



## INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

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<div style="display: flex; justify-content: space-between;"> <div style="width: 45%;"> <b>(21) International Application Number:</b> PCT/AU98/01023   <b>(22) International Filing Date:</b> 10 December 1998 (10.12.98)   <b>(30) Priority Data:</b> <table style="width: 100%; border-collapse: collapse;"> <tr><td style="width: 30%;">PP 0839</td><td style="width: 40%;">10 December 1997 (10.12.97)</td><td style="width: 30%;">AU</td></tr> <tr><td>PP 1182</td><td>31 December 1997 (31.12.97)</td><td>AU</td></tr> <tr><td>PP 1546</td><td>30 January 1998 (30.01.98)</td><td>AU</td></tr> <tr><td>PP 2264</td><td>10 March 1998 (10.03.98)</td><td>AU</td></tr> <tr><td>PP 2911</td><td>9 April 1998 (09.04.98)</td><td>AU</td></tr> <tr><td>PP 3128</td><td>23 April 1998 (23.04.98)</td><td>AU</td></tr> <tr><td>PP 3338</td><td>5 May 1998 (05.05.98)</td><td>AU</td></tr> <tr><td>PP 3654</td><td>22 May 1998 (22.05.98)</td><td>AU</td></tr> <tr><td>PP 4917</td><td>29 July 1998 (29.07.98)</td><td>AU</td></tr> <tr><td>PP 4963</td><td>30 July 1998 (30.07.98)</td><td>AU</td></tr> <tr><td>PP 5028</td><td>4 August 1998 (04.08.98)</td><td>AU</td></tr> </table> </div> <div style="width: 50%;"> <b>(71) Applicant (for all designated States except US):</b> CSL LIMITED [AU/AU]; 45 Poplar Road, Parkville, VIC 3052 (AU).   <b>(72) Inventors; and</b>  <b>(75) Inventors/Applicants (for US only):</b> ROSS, Bruce, Carter [AU/AU]; 32 Kelson Street, Coburg, VIC 3058 (AU). BARR, Ian, George [AU/AU]; 13 Shakespeare Drive, Templestowe, VIC 3106 (AU). PATTERSON, Michelle, Anne [AU/AU]; 14 Cotterell Way, Laverton, VIC 3028       </div> </div>			PP 0839	10 December 1997 (10.12.97)	AU	PP 1182	31 December 1997 (31.12.97)	AU	PP 1546	30 January 1998 (30.01.98)	AU	PP 2264	10 March 1998 (10.03.98)	AU	PP 2911	9 April 1998 (09.04.98)	AU	PP 3128	23 April 1998 (23.04.98)	AU	PP 3338	5 May 1998 (05.05.98)	AU	PP 3654	22 May 1998 (22.05.98)	AU	PP 4917	29 July 1998 (29.07.98)	AU	PP 4963	30 July 1998 (30.07.98)	AU	PP 5028	4 August 1998 (04.08.98)	AU
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<div style="display: flex; justify-content: space-between;"> <div style="width: 45%;"> <b>(74) Agent:</b> F.B. RICE &amp; CO.; 605 Darling Street, Balmain, NSW 2041 (AU).       </div> <div style="width: 50%;"> <b>(81) Designated States:</b> AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, US, UZ, VN, YU, ZW, ARIPO patent (GH, GM, KE, LS, MW, SD, SZ, UG, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG).       </div> </div>																																			
<b>Published</b> <i>With international search report.</i>																																			
<b>(54) Title:</b> PORPHORYMONAS GINGIVALIS POLYPEPTIDES AND NUCLEOTIDES																																			
<b>(57) Abstract</b>  <p>The present invention relates to isolated <i>Porphyromonas gingivalis</i> polypeptides and nucleotides. The polypeptides include: an amino acid sequence selected from the group consisting of SEQ. ID. NO. 265 to SEQ. ID. NO. 528, SEQ. ID. NO. 531 and SEQ. ID. NO. 532; or an amino acid sequence at least 85 %, preferably at least 95 %, identical to an amino acid sequence selected from the group consisting of SEQ. ID. NO. 265 to SEQ. ID. NO. 528, SEQ. ID. NO. 531 and SEQ. ID. NO. 532; or at least 40 amino acids having a contiguous sequence of at least 40 amino acids identical to a contiguous amino acid sequence selected from the group consisting of SEQ. ID. NO. 265 to SEQ. ID. NO. 528, SEQ. ID. NO. 531 and SEQ. ID. NO. 532.</p>																																			

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***Porphyromonas gingivalis* polypeptides and nucleotides****FIELD OF THE INVENTION**

5           The present invention relates to *P. gingivalis* nucleotide sequences, *P. gingivalis* polypeptides and probes for detection of *P. gingivalis*. The *P. gingivalis* polypeptides and nucleotides can be used in compositions for use in raising an immune response in a subject against *P. gingivalis* and  
10   treating or preventing or reducing the severity of the condition known as periodontitis.

**BACKGROUND OF THE INVENTION**

15           Periodontal diseases are bacterial-associated inflammatory diseases of the supporting tissues of the teeth and range from the relatively mild form of gingivitis, the non-specific, reversible inflammation of gingival tissue to the more aggressive forms of periodontitis which are characterised by the destruction of the tooth's supporting structures. Periodontitis is associated with a subgingival infection of a consortium of specific Gram-negative  
20   bacteria that leads to the destruction of the periodontium and is a major public health problem. One bacterium that has attracted considerable interest is *P. gingivalis* as the recovery of this microorganism from adult periodontitis lesions can be up to 50% of the subgingival anaerobically cultivable flora, whereas *P. gingivalis* is rarely recovered, and then in low  
25   numbers, from healthy sites. A proportional increase in the level of *P. gingivalis* in subgingival plaque has been associated with an increased severity of periodontitis and eradication of the microorganism from the cultivable subgingival microbial population is accompanied by resolution of the disease. The progression of periodontitis lesions in non-human primates  
30   has been demonstrated with the subgingival implantation of *P. gingivalis*. These findings in both animals and humans suggest a major role for *P. gingivalis* in the development of adult periodontitis.

*P. gingivalis* is a black-pigmented, anaerobic, asaccharolytic, proteolytic Gram-negative rod that obtains energy from the metabolism of  
35   specific amino acids. The microorganism has an absolute growth requirement for iron, preferentially in the form of haeme or its Fe(III)

oxidation product haemin and when grown under conditions of excess haemin is highly virulent in experimental animals. A number of virulence factors have been implicated in the pathogenicity of *P. gingivalis* including the capsule, adhesins, cytotoxins and extracellular hydrolytic enzymes.

5 In order to develop an efficacious and safe vaccine to prevent, eliminate or reduce *P. gingivalis* colonisation it is necessary to identify and produce antigens that are involved in virulence that have utility as immunogens possibly through the generation of specific antibodies. Whilst it is possible to attempt to isolate antigens directly from cultures of *P. gingivalis*  
10 this is often difficult. For example as mentioned above, *P. gingivalis* is a strict anaerobe and can be difficult to isolate and grow. It is also known that, for a number of organisms, when cultured *in vitro* that many virulence genes are down regulated and the encoded proteins are no longer expressed. If conventional chemistry techniques were applied to purify vaccine candidates  
15 potentially important (protective) molecules may not be identified. With DNA sequencing, as the gene is present (but not transcribed) even when the organism is grown *in vitro* it can be identified, cloned and produced as a recombinant DNA protein. Similarly, a protective antigen or therapeutic target may be transiently expressed by the organism *in vitro* or produced in  
20 low levels making the identification of these molecules extremely difficult by conventional methods.

With serological identification of therapeutic targets one is limited to those responses which are detectable using standard methods such as Western Blotting or ELISA. The limitation here is the both the level of  
25 response that is generated by the animal or human and determining whether this response is protective, damaging or irrelevant. No such limitation is present with a sequencing approach to the identification of potential therapeutic or prophylactic targets.

It is also well known that *P. gingivalis* produces a range of broadly  
30 active proteases (University of Melbourne International Patent Application No PCT /AU 96/00673, US Patent Nos 5,475,097 and 5,523,390), which make the identification of intact proteins difficult because of their degradation by these proteases.

## SUMMARY OF THE INVENTION

The present inventors have attempted to isolate *P. gingivalis* nucleotide sequences which can be used for recombinant production of *P. gingivalis* polypeptides and to develop nucleotide probes specific for *P. gingivalis*. The DNA sequences listed below have been selected from a large number of *P. gingivalis* sequences according to their indicative potential as vaccine candidates. This intuitive step involved comparison of the deduced protein sequence from the *P. gingivalis* DNA sequences to the known protein sequence databases. Some of the characteristics used to select useful vaccine candidates include; the expected cellular location, such as outer membrane proteins or secreted proteins, particular functional activities of similar proteins such as those with an enzymatic or proteolytic activity, proteins involved in essential metabolic pathways that when inactivated or blocked may be deleterious or lethal to the organism, proteins that might be expected to play a role in the pathogenesis of the organism eg. red cell lysis, cell agglutination or cell receptors and proteins which are paralogues to proteins with proven vaccine efficacy.

In a first aspect the present invention consists an isolated antigenic *Porphyromonas gingivalis* polypeptide, the polypeptide comprising; an amino acid sequence selected from the group consisting of SEQ. ID. NO. 265 to SEQ. ID. NO. 528, SEQ. ID. NO. 531 and SEQ. ID. NO. 532; or an amino acid sequence at least 85%, preferably at least 95%, identical to an amino acid sequence selected from the group consisting of SEQ. ID. NO. 265 to SEQ. ID. NO. 528, SEQ. ID. NO. 531 and SEQ. ID. NO. 532; or at least 40 amino acids having a contiguous sequence of at least 40 amino acids identical to a contiguous amino acid sequence selected from the group consisting of SEQ. ID. NO. 265 to SEQ. ID. NO. 528, SEQ. ID. NO. 531 and SEQ. ID. NO. 532.

In an embodiment of the present invention the polypeptide comprises;

an amino acid sequence selected from the group consisting of SEQ. ID. NO. 386 to SEQ. ID. NO. 528 and SEQ. ID. NO. 532; or

an amino acid sequence at least 85%, preferably at least 95%, identical to an amino acid sequence selected from the group consisting of SEQ. ID. NO. 386 to SEQ. ID. NO. 528 and SEQ. ID. NO. 532; or

- 5 at least 40 amino acids having a contiguous sequence of at least 40 amino acids identical to a contiguous amino acid sequence selected from the group consisting of SEQ. ID. NO. 386 to SEQ. ID. NO. 528 and SEQ. ID. NO. 532.

- 10 As used herein % identity for polypeptides is to be calculated using the alignment algorithm of Needleman and Munsch (9) using a standard protein scoring matrix (Blosum 50).

- In a preferred embodiment of the present invention the polypeptide comprises an amino acid sequence selected from the group consisting of SEQ. ID. NO. 386, SEQ. ID. NO. 424, SEQ. ID. NO. 425, SEQ. ID. NO. 434,  
15 SEQ. ID. NO. 447, SEQ. ID. NO. 458, SEQ. ID. NO. 475, SEQ. ID. NO. 498, SEQ. ID. NO. 499, SEQ. ID. NO. 500, SEQ. ID. NO. 501, SEQ. ID. NO. 387, SEQ. ID. NO. 400, SEQ. ID. NO. 411, SEQ. ID. NO. 419, SEQ. ID. NO. 420, SEQ. ID. NO. 427, SEQ. ID. NO. 429, SEQ. ID. NO. 433, SEQ. ID. NO. 437, SEQ. ID. NO. 438, SEQ. ID. NO. 443, SEQ. ID. NO. 444, SEQ. ID. NO. 448,  
20 SEQ. ID. NO. 449, SEQ. ID. NO. 452, SEQ. ID. NO. 455, SEQ. ID. NO. 457, SEQ. ID. NO. 459, SEQ. ID. NO. 461, SEQ. ID. NO. 462, SEQ. ID. NO. 463, SEQ. ID. NO. 467, SEQ. ID. NO. 468, SEQ. ID. NO. 469, SEQ. ID. NO. 482, SEQ. ID. NO. 484, SEQ. ID. NO. 485, SEQ. ID. NO. 494, SEQ. ID. NO. 508, SEQ. ID. NO. 509, SEQ. ID. NO. 510, SEQ. ID. NO. 520, SEQ. ID. NO. 521,  
25 SEQ. ID. NO. 522, SEQ. ID. NO. 525, SEQ. ID. NO. 526, SEQ. ID. NO. 528, SEQ. ID. NO. 389, SEQ. ID. NO. 390 and SEQ. ID. NO. 391.

- In another preferred embodiment of the present invention the polypeptide comprises an amino acid sequence selected from the group consisting of residue 422 to residue 531 of SEQ. ID. NO. 303, residue 534 to  
30 residue 582 of SEQ. ID. NO. 303, residue 127 to residue 232 of SEQ. ID. NO. 301, residue 240 to residue 259 of SEQ. ID. NO. 301, residue 139 to residue 156 of SEQ. ID. NO. 295, residue 160 to residue 178 of SEQ. ID. NO. 295, residue 180 to residue 207 of SEQ. ID. NO. 295, residue 221 to residue 257 of SEQ. ID. NO. 295, residue 259 to residue 323 of SEQ. ID. NO. 295, residue  
35 885 to residue 985 of SEQ. ID. NO. 299, residue 147 to residue 259 of SEQ. ID. NO. 363, residue 140 to residue 252 of SEQ. ID. NO. 344, residue 247 to

residue 356 of SEQ. ID. NO. 353, residue 359 to residue 391 of SEQ. ID. NO. 353, residue 120 to residue 254 of SEQ. ID. NO. 300, residue 287 to residue 311 of SEQ. ID. NO. 286, residue 313 to residue 352 of SEQ. ID. NO. 286, residue 354 to residue 401 of SEQ. ID. NO. 286, residue 208 to residue 252 of SEQ. ID. NO. 287, residue 259 to residue 373 of SEQ. ID. NO. 287, residue 5 to residue 120 of SEQ. ID. NO. 293, residue 123 to residue 139 of SEQ. ID. NO. 293, residue 233 to residue 339 of SEQ. ID. NO. 265, residue 67 to residue 228 of SEQ. ID. NO. 278, residue 130 to residue 172 of SEQ. ID. NO. 274, residue 174 to residue 238 of SEQ. ID. NO. 274, residue 99 to residue 112 of SEQ. ID. NO. 274, residue 114 to residue 128 of SEQ. ID. NO. 274, residue 26 to residue 69 of SEQ. ID. NO. 285, residue 71 to residue 128 of SEQ. ID. NO. 285, residue 130 to residue 146 of SEQ. ID. NO. 285, residue 620 to residue 636 of SEQ. ID. NO. 327, residue 638 to residue 775 of SEQ. ID. NO. 327, residue 397 to residue 505 of SEQ. ID. NO. 301, residue 528 to residue 545 of SEQ. ID. NO. 301, residue 556 to residue 612 of SEQ. ID. NO. 301, residue 614 to residue 631 of SEQ. ID. NO. 301, residue 633 to residue 650 of SEQ. ID. NO. 301, residue 553 to residue 687 of SEQ. ID. NO. 299, residue 305 to residue 447 of SEQ. ID. NO. 289, residue 1 to residue 52 of SEQ. ID. NO. 364, residue 65 to residue 74 of SEQ. ID. NO. 364, residue 486 to residue 604 of SEQ. ID. NO. 275, residue 158 to residue 267 of SEQ. ID. NO. 272, residue 270 to residue 282 of SEQ. ID. NO. 272, residue 163 to residue 237 of SEQ. ID. NO. 273, residue 240 to residue 251 of SEQ. ID. NO. 273, residue 213 to residue 344 of SEQ. ID. NO. 282, residue 183 to residue 324 of SEQ. ID. NO. 292, residue 327 to residue 341 of SEQ. ID. NO. 292, residue 352 to residue 372 of SEQ. ID. NO. 292, residue 141 to residue 166 of SEQ. ID. NO. 271, residue 168 to residue 232 of SEQ. ID. NO. 271, residue 1 to residue 13 of SEQ. ID. NO. 302, residue 15 to residue 28 of SEQ. ID. NO. 302, residue 30 to residue 72 of SEQ. ID. NO. 302, residue 476 to residue 529 of SEQ. ID. NO. 277, residue 41 to residue 146 of SEQ. ID. NO. 299, residue 149 to residue 162 of SEQ. ID. NO. 299, residue 166 to residue 177 of SEQ. ID. NO. 299, residue 192 to residue 203 of SEQ. ID. NO. 299, residue 71 to residue 343 of SEQ. ID. NO. 290, residue 346 to residue 363 of SEQ. ID. NO. 290, residue 36 to residue 240 of SEQ. ID. NO. 331, residue 242 to residue 270 of SEQ. ID. NO. 331, residue 1 to residue 192 of SEQ. ID. NO. 375, residue 266 to residue 290 of SEQ. ID. NO. 375, residue 23 to residue 216 of SEQ. ID. NO. 279, residue 220 to residue 270 of SEQ. ID. NO. 279, residue

285 to residue 386 of SEQ. ID. NO. 279, residue 84 to residue 234 of SEQ. ID. NO. 297, residue 248 to residue 259 of SEQ. ID. NO. 297, residue 261 to residue 269 of SEQ. ID. NO. 297, residue 275 to residue 402 of SEQ. ID. NO. 294, residue 1 to residue 171 of SEQ. ID. NO. 298, residue 403 to residue 417 of SEQ. ID. NO. 307, residue 420 to residue 453 of SEQ. ID. NO. 307, residue 456 to residue 464 of SEQ. ID. NO. 307, residue 468 to residue 690 of SEQ. ID. NO. 307, residue 1 to residue 285 of SEQ. ID. NO. 304, residue 287 to residue 315 of SEQ. ID. NO. 304, residue 318 to residue 336 of SEQ. ID. NO. 304, residue 255 to residue 269 of SEQ. ID. NO. 342, residue 271 to residue 337 of SEQ. ID. NO. 342, residue 347 to residue 467 of SEQ. ID. NO. 281, residue 116 to residue 136 of SEQ. ID. NO. 375, residue 138 to residue 357 of SEQ. ID. NO. 375, residue 133 to residue 423 of SEQ. ID. NO. 364, residue 141 to residue 299 of SEQ. ID. NO. 305, residue 202 to residue 365 of SEQ. ID. NO. 296, residue 134 to residue 426 of SEQ. ID. NO. 288, residue 1 to residue 218 of SEQ. ID. NO. 276, residue 1 to residue 246 of SEQ. ID. NO. 280, residue 444 to residue 608 of SEQ. ID. NO. 364, residue 10 to residue 686 of SEQ. ID. NO. 283, residue 1 to residue 148 of SEQ. ID. NO. 296, residue 1 to residue 191 of SEQ. ID. NO. 287, residue 193 to residue 204 of SEQ. ID. NO. 287, residue 209 to residue 373 of SEQ. ID. NO. 287, residue 211 to residue 470 of SEQ. ID. NO. 284, residue 472 to residue 482 of SEQ. ID. NO. 284, residue 133 to residue 144 of SEQ. ID. NO. 281, residue 146 to residue 336 of SEQ. ID. NO. 281, residue 1 to residue 264 of SEQ. ID. NO. 303, residue 265 to residue 295 of SEQ. ID. NO. 303, residue 297 to residue 326 of SEQ. ID. NO. 303, residue 328 to residue 338 of SEQ. ID. NO. 303, residue 247 to residue 356 of SEQ. ID. NO. 353, residue 358 to residue 391 of SEQ. ID. NO. 353, residue 257 to residue 288 of SEQ. ID. NO. 298, residue 290 to residue 385 of SEQ. ID. NO. 298, residue 245 to residue 256 of SEQ. ID. NO. 298, residue 422 to residue 802 of SEQ. ID. NO. 303, residue 803 to residue 814 of SEQ. ID. NO. 303, residue 139 to residue 156 of SEQ. ID. NO. 295, residue 160 to residue 340 of SEQ. ID. NO. 295, residue 145 to residue 361 of SEQ. ID. NO. 282, residue 363 to residue 387 of SEQ. ID. NO. 282, residue 398 to residue 471 of SEQ. ID. NO. 282, residue 573 to residue 679 of SEQ. ID. NO. 320, residue 27 to residue 168 of SEQ. ID. NO. 291, residue 170 to residue 183 of SEQ. ID. NO. 291, residue 185 to residue 415 of SEQ. ID. NO. 291, residue 1 to residue 301 of SEQ. ID. NO. 364, residue 114 to residue 702 of SEQ. ID. NO. 337, residue 377 to residue 412 of SEQ. ID. NO. 321,

residue 413 to residue 772 of SEQ. ID. NO. 321, residue 14 to residue 454 of SEQ. ID. NO. 265, residue 129 to residue 614 of SEQ. ID. NO. 268, residue 1 to residue 930 of SEQ. ID. NO. 300, residue 932 to residue 1046 of SEQ. ID. NO. 300, residue 1 to residue 301 of SEQ. ID. NO. 364, residue 1 to residue 42 of SEQ. ID. NO. 381, residue 44 to residue 973 of SEQ. ID. NO. 381, residue 1 to residue 93 of SEQ. ID. NO. 358, residue 95 to residue 179 of SEQ. ID. NO. 358, residue 181 to residue 227 of SEQ. ID. NO. 358, residue 114 to residue 702 of SEQ. ID. NO. 337, residue 1 to residue 659 of SEQ. ID. NO. 355, residue 661 to residue 907 of SEQ. ID. NO. 355, residue 1 to residue 131 of SEQ. ID. NO. 370, residue 133 to residue 601 of SEQ. ID. NO. 370, residue 1 to residue 813 of SEQ. ID. NO. 344, residue 377 to residue 412 of SEQ. ID. NO. 321, residue 413 to residue 772 of SEQ. ID. NO. 321, and residue 189 to residue 614 of SEQ. ID. NO. 364.

In a second aspect the present invention consists in an isolated antigenic *Porphyromonas gingivalis* polypeptide, the polypeptide comprising an amino acid sequence selected from the group consisting of SEQ. ID. NO. 386 to SEQ. ID. NO. 528 and SEQ. ID. NO. 532 less the leader sequence set out in Table 3.

In a third aspect the present invention consists in an isolated DNA molecule, the DNA molecule comprising a nucleotide sequence which encodes the polypeptide of the first aspect the present invention or a sequence which hybridises thereto under stringent conditions.

It is preferred that the isolated DNA molecule comprises a nucleotide sequence selected from the group consisting of SEQ. ID. NO. 1 to SEQ. ID. NO. 264, SEQ. ID. NO. 529 and SEQ. ID. NO. 530.

In a fourth aspect the present invention consists in a recombinant expression vector comprising the DNA molecule of the second aspect of the present invention operably linked to a transcription regulatory element.

The present invention also provides a cell comprising this recombinant expression vector.

In a further aspect the present invention consists in a method for producing a *P. gingivalis* polypeptide comprising culturing the cell under conditions that permit expression of the polypeptide.

In yet a further aspect the present invention provides a composition for use in raising an immune response directed against *P. gingivalis* in a subject, the composition comprising an effective amount of at least one

polypeptide of the first aspect of the present invention, or at least one DNA molecule of the second aspect of the present invention, or both, and a pharmaceutically acceptable carrier. It is preferred that the pharmaceutically acceptable carrier is an adjuvant. In other aspects the present invention provides methods of treating *P. gingivalis* infection in subject comprising the administration of the composition to the subject such that treatment of *P. gingivalis* infection occurs. The treatment may be prophylactic or therapeutic.

In yet another aspect the present invention provides an antibody raised against a polypeptide of the first aspect the invention. The antibody may be polyclonal or monoclonal. The present invention also provides compositions including these antibodies. It is preferred that these compositions are adapted for oral use and may be, for example, dentrifices, mouthwashes, etc.

In a still further aspect the present invention provides a nucleotide probe comprising at least 18 nucleotides and having a contiguous sequence of at least 18 nucleotides identical to a contiguous nucleotide sequence selected from the group consisting of SEQ. ID. NO. 1 to SEQ. ID. NO. 121, SEQ. ID. NO. 529, and sequences complementary thereto. It is preferred that the probe further comprises a detectable label.

The present invention also provides a method for detecting the presence of *P. gingivalis* nucleic acid in a sample comprising:

- (a) contacting a sample with the nucleotide probe under conditions in which a hybrid can form between the probe and a *P. gingivalis* nucleic acid in the sample; and
- (b) detecting the hybrid formed in step (a), wherein detection of a hybrid indicates the presence of a *P. gingivalis* nucleic acid in the sample.

## DETAILED DESCRIPTION

### Definitions

A purified or isolated polypeptide or a substantially pure preparation of a polypeptide are used interchangeably herein and, as used herein, mean a polypeptide that has been separated from other proteins, lipids, and nucleic acids with which it naturally occurs. Preferably, the polypeptide is also



separated from substances, e.g., antibodies or gel matrix, e.g., polyacrylamide, which are used to purify it. Preferably, the polypeptide constitutes at least 10, 20, 50 70, 80 or 95% dry weight of the purified preparation. Preferably, the preparation contains: sufficient polypeptide to  
5 allow protein sequencing; at least 1, 10, or 100 mg of the polypeptide.

A purified preparation of cells refers to, in the case of plant or animal cells, an in vitro preparation of cells and not an entire intact plant or animal. In the case of cultured cells or microbial cells, it consists of a preparation of at least 10% and more preferably 50% of the subject cells.

10 A purified or isolated or a substantially pure nucleic acid, e.g., a substantially pure DNA, (are terms used interchangeably herein) is a nucleic acid which is one or both of the following: not immediately contiguous with both of the coding sequences with which it is immediately contiguous (i.e., one at the 5' end and one at the 3' end) in the naturally occurring genome of  
15 the organism from which the nucleic acid is derived; or which is substantially free of a nucleic acid with which it occurs in the organism from which the nucleic acid is derived. The term includes, for example, a recombinant DNA which is incorporated into a vector, e.g., into an autonomously replicating plasmid or virus, or into the genomic DNA of a  
20 prokaryote or eukaryote, or which exists as a separate molecule (e.g., a cDNA or a genomic DNA fragment produced by PCR or restriction endonuclease treatment) independent of other DNA sequences. Substantially pure DNA also includes a recombinant DNA which is part of a hybrid gene encoding additional *P. gingivalis* DNA sequence.

25 A "contig" as used herein is a nucleic acid representing a continuous stretch of genomic sequence of an organism.

An "open reading frame", also referred to herein as ORF, is a region of nucleic acid which encodes a polypeptide. This region may represent a portion of a coding sequence or a total sequence and can be determined from  
30 a stop to stop codon or from a start to stop codon.

As used herein, a "coding sequence" is a nucleic acid which is transcribed into messenger RNA and/or translated into a polypeptide when placed under the control of appropriate regulatory sequences. The boundaries of the coding sequence are determined by a translation start codon at the five  
35 prime terminus and a translation stop code at the three prime terminus. A

coding sequence can include but is not limited to messenger RNA synthetic DNA, and recombinant nucleic acid sequences.

A "complement" of a nucleic acid as used herein refers to an anti-parallel or antisense sequence that participates in Watson-Crick base-pairing  
5 with the original sequence.

A "gene product" is a protein or structural RNA which is specifically encoded by a gene.

As used herein, the term "probe" refers to a nucleic acid, peptide or other chemical entity which specifically binds to a molecule of interest.  
10 Probes are often associated with or capable of associating with a label. A label is a chemical moiety capable of detection. Typical labels comprise dyes, radioisotopes, luminescent and chemiluminescent moieties, fluorophores, enzymes, precipitating agents, amplification sequences, and the like. Similarly, a nucleic acid, peptide or other chemical entity which  
15 specifically binds to a molecule of interest and immobilizes such molecule is referred herein as a "capture ligand". Capture ligands are typically associated with or capable of associating with a support such as nitro-cellulose, glass, nylon membranes, beads, particles and the like. The specificity of hybridization is dependent on conditions such as the base pair composition  
20 of the nucleotides, and the temperature and salt concentration of the reaction. These conditions are readily discernible to one of ordinary skill in the art using routine experimentation.

Homologous refers to the sequence similarity or sequence identity between two polypeptides or between two nucleic acid molecules. When a  
25 position in both of the two compared sequences is occupied by the same base or amino acid monomer subunit, e.g., if a position in each of two DNA molecules is occupied by adenine, then the molecules are homologous at that position. The percent of homology between two sequences is a function of the number of matching or homologous positions shared by the two  
30 sequences divided by the number of positions compared x 100.

The terms peptides, proteins, and polypeptides are used interchangeably herein.

An "immunogenic component" as used herein is a moiety, such as an *P. gingivalis* polypeptide, analog or fragment thereof, that is capable of  
35 eliciting a humoral and/or cellular immune response in a host animal.

An "antigenic component" as used herein is a moiety, such as *P. gingivalis* polypeptide, analog or fragment thereof, that is capable of binding to a specific antibody with sufficiently high affinity to form a detectable antigen-antibody complex.

5 As used herein, the term "cell-specific promoter" means a DNA sequence that serves as a promoter, i.e., regulates expression of a selected DNA sequence operably linked to the promoter, and which effects expression of the selected DNA sequence in specific cells of a tissue. The term also covers so-called "leaky" promoters, which regulate expression of a selected  
10 DNA primarily in one tissue, but cause expression in other tissues as well.

As used herein, the term "control sequence" refers to a nucleic acid having a base sequence which is recognized by the host organism to effect the expression of encoded sequences to which they are ligated. The nature of such control sequences differs depending upon the host organism; in  
15 prokaryotes, such control sequences generally include a promoter, ribosomal binding site, terminators, and in some cases operators; in eukaryotes, generally such control sequences include promoters, terminators and in some instances, enhancers. The term control sequence is intended to include at a minimum, all components whose presence is necessary for expression, and  
20 may also include additional components whose presence is advantageous, for example, leader sequences.

As used herein, the term "operably linked" refers to sequences joined or ligated to function in their intended manner. For example, a control sequence is operably linked to coding sequence by ligation in such a way  
25 that expression of the coding sequence is achieved under conditions compatible with the control sequence and host cell.

A "sample" as used herein refers to a biological sample, such as, for example, tissue or fluid isolated from an individual (including without limitation plasma, serum, cerebrospinal fluid, lymph, tears, saliva and tissue  
30 sections) or from *in vitro* cell culture constituents, as well as samples from the environment.

The practice of the invention will employ, unless otherwise indicated, conventional techniques of chemistry, molecular biology, microbiology, recombinant DNA, and immunology well known to those  
35 skilled in the art. Such techniques are described and explained throughout the literature in sources such as, J. Perbal, A Practical Guide to Molecular

Cloning, John Wiley and Sons (1984), J. Sambrook et al., Molecular Cloning: A Laboratory Manual, Cold Spring Harbour Laboratory Press (1989), T.A. Brown (editor), Essential Molecular Biology: A Practical Approach, Volumes 1 and 2, IRL Press (1991), D.M. Glover and B.D. Hames (editors), DNA  
5 Cloning: A Practical Approach, Volumes 1-4, IRL Press (1995 and 1996), and F.M. Ausubel et al. (Editors), Current Protocols in Molecular Biology, Greene Pub. Associates and Wiley-Interscience (1988, including all updates until present). The disclosure of these texts are incorporated herein by reference.

#### 10 Pharmaceutically Acceptable Carriers

The antibodies, polypeptides and DNA of the present invention can be included in compositions which include a carrier or diluent. These compositions include pharmaceutical compositions where the carrier or  
15 diluent will be pharmaceutically acceptable. Pharmaceutically acceptable carriers or diluents include those used in compositions suitable for oral, rectal, nasal, topical (including buccal and sublingual), vaginal, parenteral (including subcutaneous, intramuscular, intravenous, intradermal, intrathecal and epidural) administration. They are non-toxic to recipients at  
20 the dosages and concentrations employed. Representative examples of pharmaceutically acceptable carriers or diluents include, but are not limited to; water, isotonic solutions which are preferably buffered at a physiological pH (such as phosphate-buffered saline or Tris-buffered saline) and can also contain one or more of, mannitol, lactose, trehalose, dextrose, glycerol,  
25 ethanol or polypeptides (such as human serum albumin). The compositions may conveniently be presented in unit dosage form and may be prepared by any of the methods well known in the art of pharmacy.

As will be well understood by those skilled in the art alterations may  
30 be made to the amino acid sequences set out in the Sequence Listings. These alterations may be deletions, insertions, or substitutions of amino acid residues. The altered polypeptides can be either naturally occurring (that is to say, purified or isolated from a natural source) or synthetic (for example, by performing site-directed metagenesis on the encoding DNA). It is  
35 intended that such altered polypeptides which have at least 85%, preferably at least 95% identity with the sequences set out in the Sequence Listing are

within the scope of the present invention. Antibodies raised against these altered polypeptides will also bind to the polypeptides having one of the sequences set out in the Sequence Listings. The level of % identity is to be calculated as set out above.

- 5 Protein sequences are homologous if they are related by divergence from a common ancestor. Consequently, a species homologue of the protein will be the equivalent protein which occurs naturally in another species. Within any one species a homologue may exist as numerous allelic variants, and these will be considered homologues of the protein. Allelic variants and  
10 species homologues can be obtained by following standard techniques known to those skilled in the art.

An allelic variant will be a variant that is naturally occurring within an individual organism.

#### 15 Mutants, Variants and Homology - Nucleic Acids

- Mutant polynucleotides will possess one or more mutations which are deletions, insertions, or substitutions of nucleotide residues. Mutants can be either naturally occurring (that is to say, isolated from a natural source) or synthetic (for example, by performing site-directed metagenesis on  
20 the DNA). It is thus apparent that polynucleotides of the invention can be either naturally occurring or recombinant (that is to say prepared using recombinant DNA techniques).

An allelic variant will be a variant that is naturally occurring within an individual organism.

- 25 Nucleotide sequences are homologous if they are related by divergence from a common ancestor. Consequently, a species homologue of the polynucleotide will be the equivalent polynucleotide which occurs naturally in another species. Within any one species a homologue may exist as numerous allelic variants, and these will be considered homologues of the  
30 polynucleotide. Allelic variants and species homologues can be obtained by following standard techniques known to those skilled in the art.

#### Antibody Production

- Antibodies, either polyclonal or monoclonal, which are specific for a  
35 polypeptide of the present invention can be produced by a person skilled in the art using standard techniques such as, but not limited to, those described

by Harlow *et al.* Antibodies: A Laboratory Manual, Cold Springs Harbor Laboratory Press (1988), and D. Catty (editor), Antibodies: A Practical Approach, IRL Press (1988).

5 Various procedures known in the art may be used for the production of polyclonal antibodies to epitopes of a protein. For the production of polyclonal antibodies, a number of host animals are acceptable for the generation of antibodies by immunization with one or more injections of a polypeptide preparation, including but not limited to rabbits, mice, rats, etc. Various adjuvants may be used to increase the immunological response in  
10 the host animal, depending on the host species, including but not limited to Freund's (complete and incomplete), mineral gels such as aluminium hydroxide, surface active substances such as lysolecithin, pluronic polyols, polyanions, oil emulsions, keyhole limpet hemocyanins, dinitrophenol, and potentially useful human adjuvants such as BCG (bacille Calmette-Guerin)  
15 and *Corynebacterium parvum*.

A monoclonal antibody to an epitope of a protein may be prepared by using any technique which provides for the production of antibody molecules by continuous cell lines in culture. These include but are not limited to the hybridoma technique originally described by Kohler and  
20 Milstein (1975, Nature 256, 493-497), and the more recent human B-cell hybridoma technique (Kesber *et al.* 1983, Immunology Today 4:72) and EBV-hybridoma technique (Cole *et al.* 1985, Monoclonal Antibodies and Cancer Therapy, Alan R. Liss, Inc. pp. 77-96). In addition, techniques developed for the production of "chimeric antibodies" by splicing the genes from antibody  
25 molecule of appropriate antigen specificity together with genes from a human antibody molecule of appropriate biological activity may be used (Morrison *et al.* 1984, Proc. Natl. Acad. Sci., 81:6851-6855; Neuberger *et al.* 1984 Nature 312:604-608; Takeda *et al.* 1985 Nature 31:452-454). Alternatively, techniques described for the production of single chain  
30 antibodies (U.S. Patent 4,946,778) can be adapted to produce 4-specific single chain antibodies.

Recombinant human or humanized versions of monoclonal antibodies are a preferred embodiment for human therapeutic applications. Humanized antibodies may be prepared according to procedures in the  
35 literature (e.g. Jones *et al.* 1986, Nature 321:522-25; Reichman *et al.* 1988 Nature 332:323-27; Verhoeven *et al.* 1988, Science 239:1534-36). The

recently described "gene conversion metagenesis" strategy for the production of humanized monoclonal antibody may also be employed in the production of humanized antibodies (Carter et al. 1992 Proc. Natl. Acad. Sci. U.S.A. 89:4285-89). Alternatively, techniques for generating the recombinant phase  
5 library of random combinations of heavy and light regions may be used to prepare recombinant antibodies (e.g. Huse et al. 1989 Science 246:1275-81).

Antibody fragments which contain the idiotype of the molecule such as  $F_u$   $F(ab1)$  and  $F(ab2)$  may be generated by known techniques. For example, such fragments include but are not limited to: the  $F(ab)$  E2  
10 fragment which can be produced by pepsin digestion of the intact antibody molecule; the  $Fab'$  fragments which can be generated by reducing the disulfide bridges of the  $F(ab')_2$  fragment, and the two  $Fab$  fragments which can be generated by treating the antibody molecule with papain and a reducing agent. Alternatively,  $Fab$  expression libraries may be constructed  
15 (Huse et al. 1989, Science 246:1275-1281) to allow rapid and easy identification of monoclonal  $Fab$  fragment with the desired specificity to a protein.

#### Adjuvants

20 "Adjuvant" means a composition comprised of one or more substances that enhances the immunogenicity and efficacy of a vaccine composition. Non-limiting examples of suitable adjuvants include squalane and squalene (or other oils of animal origin); block copolymers; detergents such as Tween®-80; Quil® A, mineral oils such as Drakeol or Marcol,  
25 vegetable oils such as peanut oil; Corynebacterium-derived adjuvants such as Corynebacterium parvum; Propionibacterium-derived adjuvants such as Propionibacterium acne; Mycobacterium bovis (Bacillus Calmetic and Guerinn or BCG); interleukins such as interleukin 2 and interleukin-12; monokines such as interleukin 1; tumour necrosis factor; interferons such as  
30 gamma interferon; combinations such as saponin-aluminium hydroxide or Quil-A aluminium hydroxide; liposomes; ISCOM adjuvant; mycobacterial cell wall extract; synthetic glycopeptides such as muramyl dipeptides or other derivatives; Avridine; Lipid A; dextran sulfate; DEAE-Dextran or DHAE-Dextran with aluminium phosphate; carboxypolymethylene such as  
35 Carbopol' EMA; acrylic copolymer emulsions such as Neocryl A640 (e.g. U.S.

Pat. No. 5,047,238); vaccinia or animal posvirus proteins; sub-viral particle adjuvants such as cholera toxin, or mixtures thereof.

As used herein, stringent conditions are those that (1) employ low  
5 ionic strength and high temperature for washing, for example, 0.015 M NaCl/0.0015 M sodium citrate/0.1% NaDodSO<sub>4</sub> at 50°C; (2) employ during hybridisation a denaturing agent such as formamide, for example, 50% (vol/vol) formamide with 0.1% bovine serum albumin, 0.1% Ficoll, 0.1% polyvinylpyrrolidone, 50 mM sodium phosphate buffer at pH 6.5 with 750  
10 mM NaCl, 75 mM sodium citrate at 42°C; or (3) employ 50% formamide, 5 x SSC (0.75 M NaCl, 0.075 M sodium citrate), 50 mM sodium phosphate (pH 6.8), 0.1% sodium pyrophosphate, 5 x Denhardt's solution, sonicated salmon sperm DNA (50 µg/ml), 0.1% SDS and 10% dextran sulfate at 42°C in 0.2 x SSC and 0.1% SDS

15

As will be understood the present invention includes within its scope DNA vaccination. Further information regarding DNA vaccination may be found in Donnelly et al, Journal of Immunological Methods 176(1994) 145-152, the disclosure of which is incorporated herein by reference.

20 Throughout this specification the word "comprise", or variations such as "comprises" or "comprising", will be understood to imply the inclusion of a stated element or integer or group of elements or integers but not the exclusion of any other element or integer, or group of elements or integers.

## 25 Preparation of the *P. gingivalis* library for sequencing.

To determine the DNA sequence of *P. gingivalis* genomic DNA was isolated from *P. gingivalis* strain W50 (ATCC 53978) essentially by the method described by Mamur J. (J. Mol. Biol. 3, 208-218, 1961). Cloning of  
30 DNA fragments was performed essentially as described by Fleischmann et al., (Science; 269, 496-512, 1995)(2). Briefly, purified genomic DNA from *P. gingivalis* was nebulized to fragment the DNA and was treated with Bal31 nuclease to create blunt ends then run twice through preparative 1% agarose gels. DNA fragments of 1.6-2.0 kb were excised from the gel and the DNA  
35 recovered. This DNA was then ligated to the vector pUC18 (SmaI digested and dephosphorylated; Pharmacia) and electrophoresed through a 1%



preparative agarose gel. The fragment comprising linear vector plus one insert was excised, purified and this process repeated to reduce any vector without insert contamination. The recovered vector plus insert DNA was blunt-ended with T4 DNA polymerase, then a final ligation to produce  
5 circular DNA was performed. Aliquots of Epicurian Coli Electroporation-Competent Cells (Stratagene) were transformed with the ligated DNA and plated out on SOB agar antibiotic diffusion plates containing X-gal and incubated at 37°C overnight. Colonies with inserts appeared white and those without inserts (vector alone) appeared blue. Plates were stored at 4°C until  
10 the white clones were picked and expanded for the extraction of plasmid DNA for sequencing.

#### DNA sequencing

Plasmid DNA was prepared by picking bacterial colonies into 1.5ml  
15 of LB, TB or SOB broth supplemented with 50-100ug/ml Ampicillin in 96 deep well plates. Plasmid DNA was isolated using the QIAprep Spin or QIAprep 96 Turbo miniprep kits (QIAGEN GmbH, Germany). DNA was eluted into a 96 well gridded array and stored at -20C.

Sequencing reactions were performed using ABI PRISM Dye  
20 Terminator and ABI PRISM BIGDye Terminator Cycle Sequencing Ready Reaction kits with AmpliTaq DNA polymerase FS (PE Applied Biosystems, Foster City, CA) using the M13 Universal forward and reverse sequencing primers. Sequence reactions were conducted on either a Perkin-Elmer GeneAmp 9700 (PE Applied Biosystems) or Hybaid PCR Express (Hybaid,  
25 UK) thermal cyclers. Sequencing reactions were analysed on ABI PRISM 377 DNA sequencers (PE Applied Biosystems).

The sequences obtained are set out below. The relationship between these sequences is set out in Table 1. The initiation codon was calculated using a combination of sequence homology alignment (FASTA), signal  
30 sequence prediction (PSORT, SignalP) or ORF prediction (GeneMark).

**Table 1:** Reference table indicating the relationships of each sequence ID to the selected proteins.

<b>Protein name</b>	<b>DNA sequence of complete ORF</b>	<b>Amino acid sequence of complete ORF</b>	<b>DNA sequence of protein</b>	<b>Amino acid sequence of protein</b>
PG1	1	265	122	386
PG10	2	266	123	387
PG100	3	267	124	388
PG101	4	268		
PG102	5	269	125, 126	389, 390
PG104	6	270	127	391
PG105	7	271	128	392
PG106	8	272	129	393
PG107	9	273	130, 131, 132	394, 395, 396
PG108	10	274	133	397
PG109	11	275	134, 135	398, 399
PG11	12	276	136	400
PG110	13	277	137	401
PG111	14	278		
PG112	15	279	138, 139	402, 403
PG113	16	280	140	404
PG114	17	281	141	405
PG115	18	282	142	406
PG116	19	283	143	407
PG117	20	284	144	408
PG118	21	285	145	409
PG119	22	286	146	410
PG12	23	287	147	411
PG120	24	288	148	412

Protein name	DNA sequence of complete ORF	Amino acid sequence of complete ORF	DNA sequence of protein	Amino acid sequence of protein
PG121	25	289	149	413
PG122	26	290	150	414
PG123	27	291	151	415
PG124	28	292	152	416
PG125	29	293	153	417
PG126	30	294	154	418
PG13	31	295	155	419
PG14	32	296	156	420
PG15	33	297	157	421
PG16	34	298	158	422
PG18	35	299	159	423
PG2	36	300	160, 161	424, 425
PG21	37	301	162	426
PG22	38	302	163	427
PG23	39	303	164	428
PG24	40	304	165	429
PG25	41	305	166	430
PG27	42	306	167	431
PG28	43	307	168	432
PG29	44	308	169	433
PG3	45	309	170	434
PG30	46	310	171	435
PG31	47	311	172	436
PG32	48	312	173	437
PG33	49	313	174	438
PG34	50	314	175, 176	439, 440
PG35	51	315	177	441
PG36	52	316	178	442
PG37	53	317	179, 180	443, 444
PG38	54	318	181	445

Protein name	DNA sequence of complete ORF	Amino acid sequence of complete ORF	DNA sequence of protein	Amino acid sequence of protein
PG39	55	319	182	446
PG4	56	320	183	447
PG40	57	321	184	448
PG41	58	322	185	449
PG42	59	323	186	450
PG43	60	324	187	451
PG44	61	325	188	452
PG45	62	326	189	453
PG46	63	327	190	454
PG47	64	328	191	455
PG48	65	329	192	456
PG49	66	330	193	457
PG5	67	331	194	458
PG50	68	332	195	459
PG51	69	333	196	460
PG52	70	334	197	461
PG53	71	335	198	462
PG54	72	336	199	463
PG55	73	337	200	464
PG56	74	338	201, 202	465, 466
PG57	75	339	203, 204, 205	467, 468, 469
PG58	76	340	206, 207	470, 471
PG59	77	341	208, 209, 210	472, 473, 474
PG6	78	342	211	475
PG60	79	343	212	476
PG61	80	344	213	477
PG62	81	345	214	478
PG63	82	346	215	479
PG64	83	347	216	480
PG65	84	348	217	481

<b>Protein name</b>	<b>DNA sequence of complete ORF</b>	<b>Amino acid sequence of complete ORF</b>	<b>DNA sequence of protein</b>	<b>Amino acid sequence of protein</b>
PG66	85	349	218	482
PG67	86	350	219	483
PG68	87	351	220, 221	484, 485
PG69	88	352	222	486
PG7	89	353	223	487
PG70	90	354	224	488
PG71	91	355	225	489
PG72	92	356	226	490
PG73	93	357	227	491
PG74	94	358	228	492
PG75	95	359	229	493
PG76	96	360	230	494
PG77	97	361	231	495
PG78	98	362	232	496
PG79	99	363	233	497
PG8	100	364	234, 235, 236, 237	498, 499, 500, 501
PG80	101	365	238	502
PG81	102	366	102	366
PG82	103	367	239	503
PG83	104	368	240	504
PG84	105	369	241, 242	505, 506
PG85	106	370	243	507
PG86	107	371	244, 245	508, 509
PG87	108	372	246	510
PG88	109	373	247, 248, 249	511, 512, 513
PG89	110	374	250	514
PG9	111	375	251, 252, 253	515, 516, 517
PG90	112	376	254, 255	518, 519
PG91	113	377	256	520

Protein name	DNA sequence of complete ORF	Amino acid sequence of complete ORF	DNA sequence of protein	Amino acid sequence of protein
PG92	114	378	257	521
PG93	115	379	258	522
PG94	116	380	259	523
PG95	117	381	260	524
PG96	118	382	261	525
PG97	119	383	262	526
PG98	120	384	263	527
PG99	121	385	264	528
PG127	529	531	530	532

### DNA sequence analysis

5

DNA files in FASTA format were converted to GCG format files and imported into a database. The DNA files were translated into amino acid files using the program Flip obtained from ANGIS(Australian Genomic Information Service, University of Sydney, Australia). A series of

10 bioinformatic analyses were performed on the proteins in order to select potential vaccine candidates. The programs used were FASTA homology searching (1), PSORT (2,3), SignalP (4), TopPred (5), and GeneMark (6). The proteins and their bioinformatic results were stored in the custom written database for search and retrieval of proteins with the desired characteristics

15 The FASTA homology results for these proteins were then examined for any alignment with a protein suggesting surface location or vaccine efficacy. All proteins were searched for homology against a non-redundant bacterial protein database compiled by ANGIS using the FASTA algorithm. The settings used for the FASTA searches were Ktup = 2, gap creation

20 penalty = -12, gap extension penalty = -2, width for deriving alignment in opt = 16 and the Blosum 50 scoring matrix. Individual FASTA search results were examined for significant homology by statistical probability and amino acid alignments. The results are set out in Table 2.

Protein files were then trimmed to the first, second, third, fourth and fifth methionine residues using a protein trimming program (ANGIS). The trimmed proteins were then subjected to PSORT analysis for the detection of signal sequences and the prediction of cell location. Proteins exhibiting a PSORT probability of outer membrane  $>0.8$  were considered to indicate surface localisation. A second signal sequence detection program SignalP was also performed and, in certain instances, this program detected signals not identified with PSORT. All proteins identified by other methods were also analysed by PSORT and SignalP. Previously, the C-terminal amino acid of bacterial outer membrane proteins has been shown to be important for the assembly of the protein on the outer membrane (7). A typical structure definition for outer membrane proteins has been determined as the presence of a signal sequence at the N-terminus and a tyrosine or phenylalanine at the C-terminus. A number of the selected proteins exhibit this characteristic structure. The program TopPred was used to determine the presence and number of membrane spanning domains (MSDs) and the presence of such sequences indicates a preference to be attached to membranes such as the outer membrane. The results of PSORT, SignalP and TopPred analyses with the C-terminal amino acids of the selected proteins are set out in Table 3.

The 70 amino acids from the C-terminus of a number of *P. gingivalis* outer membrane proteins share 50-100% protein sequence identity. These proteins included RGP1, RGP2, KGP, HagA, HagC, HagD, prtH and prtT. This conserved motif may be involved in the attachment or sorting of proteins to the outer membrane. The protein data set was searched using FASTA homology as described above and a number of novel proteins were identified which demonstrate similar motifs at their C-termini. The results are listed in Table 4

The TonBIII box is a 30 amino acid motif present within TonB outer membrane receptors in a wide variety of bacteria. The TonBIII box of *P. gingivalis* (8) was used to search the protein data set for homology by FASTA as described above. Those proteins demonstrating significant homology are listed in Table 5.

Table 2: FASTA protein homology results of complete ORFs against a non-redundant protein database.

Protein name	Homology description	Genbank accession number	Length of homolog	Length of <i>P. gingivalis</i> protein	FASTA homology results	
					Identity %	Overlap E value
PG1	48kD outer membrane protein, <i>Actinobacillus pleuropneumoniae</i>	U24492	449aa	451aa	32	454aa 1.40E-42
PG2	Outer membrane protein (susC), <i>Bacteroides thetaiotaomicron</i>	L49338	1038aa	1017aa, 1014aa	28	1099aa 4.60E-32
PG3	Outer membrane porin F adhesin, <i>Pseudomonas fluorescens</i>	U19743	317aa	223aa	35	187aa 1.10E-10
PG4	Outer membrane protein A, <i>Escherichia fergusonii</i>	M63352	243aa	672aa	48	88aa 4.10E-10
PG5	Adhesin protein (AdcA), <i>Streptococcus pneumoniae</i>	Z71552	423aa	315aa	25	279aa 9.40E-15
PG6	Hemolysin A (phvA), <i>Prevotella melaninogenica</i>	U27567	332aa	324aa	60	306aa 3.00E-74
PG7	Hemolysin (flvC), <i>Serpulina hyodysenteriae</i>	X73141	268aa	404aa	33	266aa 1.40E-24
PG8	Heme uptake protein A, <i>Bacteriodes fragilis</i>	X97122	431aa	598aa, 550aa, 458aa, 426aa	79	417aa 6.70E-121
PG9	Internalin A (inlA), <i>Lysteria monocytogenes</i>	M67471	744aa	1266aa, 1232aa, 1174aa	38	340aa 7.30E-23



Protein name	Homology description	Genbank accession number	Length of homolog	Length of <i>P. gingivalis</i> protein	FASTA homology results	
					Identity %	Overlap E value
PG10	Macrophage infectivity potentiator (MIP), Legionella oakridgensis	U92214	234aa	195aa	50	201aa 4.70E-31
PG11	Haemagglutinin (phg), Prevotella intermedia	AF017417	309aa	313aa	44	309aa 3.60E-44
PG12	Outer membrane lipoprotein, Haemophilus influenzae	M68502	274aa	271aa	36	254aa 9.60E-27
PG13	Ferric receptor (cfrA), Campylobacter coli	U80812	696aa	757aa	24	625aa 1.20E-18
PG14	36kD antigen, Helicobacter pylori	U86610	329aa	331aa	37	326aa 1.10E-35
PG15	Outer membrane protein, Erwinia amylovora	X77921	377aa	267aa	30	253aa 5.40E-08
PG16	C terminal protease, Bartonella bacilliformis	L37094	434aa	569aa	36	357aa 3.00E-35
PG18	Protein-export membrane protein (secD), Helicobacter pylori	AE000652	503aa	981aa	32	611aa 1.10E-36
PG21	Surface antigen gene, Methanosarcina mazei	X84710	783aa	821aa	37	331aa 6.20E-33
PG22	Alpha-hemolysin gene, Aeromonas hydrophila	L36462	85aa	106aa	57	67aa 2.60E-14
PG23	clpA/clpB protease, Bacillus subtilis	D26185	810aa	859aa	45	855aa 7.10E-122
PG24	Putative hemolysin, Streptococcus mutans	AF051356	445aa	417aa	29	432aa 1.80E-29

Protein name	Homology description	Genbank accession number	Length of homolog	Length of <i>P. gingivalis</i> protein	FASTA homology results		
					Identity %	Overlap	E value
PG25	Cysteine protease, Porphyromonas gingivalis	U54591	1723aa	293aa	42	142aa	1.10E-12
PG27	TonB linked adhesin, Porphyromonas gingivalis	Y07618	1097aa	312aa	45	360aa	3.20E-41
PG28	Cysteine protease / hemagglutinin, Porphyromonas gingivalis	S75942	886aa	843aa	35	838aa	7.00E-90
PG30	Putative NlpD lipoprotein, Aquifex aeolicus	AE000754	187aa	337aa	42	142aa	1.80E-12
PG31	Hemolysin (tlyC), Serpulina hyodysenteriae	X73141	141aa	151aa	31	123aa	1.80E-07
PG32	Major outer membrane protein (oprF), Pseudomonas aeruginosa	M94078	350aa	391aa	26	382aa	3.40E-07
PG33	Major outer membrane protein (oprF), Pseudomonas fluorescens	L21200	317aa	385aa	32	163aa	2.30E-06
PG34	Putative membrane protein, Rhodobacter capsulatus	Q07396	193aa	190aa	46	190aa	2.20E-36
PG35	Colicin 1 receptor, Escherichia coli	J04229	863aa	833aa	25	590aa	2.40E-10
PG36	Outer membrane antigen (oma87), Pasteurella multocida	U60439	789aa	891aa	21	894aa	3.70E-10
PG37	Cationic outer membrane protein (ompH), Yersinia enterocolitica	M34854	164aa	174aa, 170aa	27	168aa	4.30E-07

Protein name	Homology description	Genbank accession number	Length of homolog	Length of <i>P. gingivalis</i> protein	FASTA homology results
					Identity %      Overlap      E value
PG38	Cationic outer membrane protein (ompH), Yersinia enterocolitica	M34854	164aa	163aa	23      160aa      5.90E-05
PG39	Outer membrane protein (susC) Bacteroides thetaiotaomicron	L49338	1038aa	827aa	24      347aa      1.50E-06
PG40	Heme receptor (Hut A), Vibrio cholera	Q56644	693aa	772aa	23      722aa      4.90E-09
PG41	Outer membrane protein (tolC), Escherichia coli	X54049	495aa	462aa	22      436aa      4.60E-09
PG42	Neuraminidase, Micromonospora viridifaciens	D01045	647aa	492aa	32      375aa      2.10E-22
PG43	Immunoreactive outer membrane protein (omp28), Brucella melitensis	U30815	250aa	245aa	24      178aa      0.0015
PG44	Macrophage infectivity potentiator, Legionella israelensis	U92208	242aa	276aa	35      219aa      9.10E-18
PG45	Outer membrane protein, Neisseria meningitidis	AF021245	797aa	775aa	21      699aa      0.0034
PG46	Outer membrane protein 85, Neisseria gonorrhoeae	U01959	792aa	774aa	31      117aa      0.00098
PG47	Outer membrane protein (susC) Bacteroides thetaiotaomicron	L49338	1038aa	867aa	20      962aa      1.00E-03

Protein name	Homology description	Genbank accession number	Length of homolog	Length of <i>P. gingivalis</i> protein	FASTA homology results	
					Identity %	Overlap E value
PG48	Immunoglobulin binding surface protein (sir22), <i>Streptococcus pyogenes</i>	X75750	365aa	431aa	25	269aa 5.20E-05
PG49	Fimbriillin (orf2), <i>Porphyromonas gingivalis</i>	D42067	453aa	333aa	23	296aa 0.082
PG50	Outer membrane protein (susC) <i>Bacteroides thetaiotaomicron</i>	L49338	1038aa	848aa	26	579aa 1.60E-11
PG51	PGaA antigen, <i>Porphyromonas gingivalis</i>	X95938	202aa	202aa	54	126aa 1.20E-25
PG52	Alkaline protease secretion apparatus (apnF) <i>Pseudomonas aeruginosa</i>	X64558	481aa	455aa	21	427aa 3.50E-06
PG53	Protein export protein (tolC), <i>Salmonella enteritidis</i>	U25178	491aa	444aa	23	436aa 6.20E-11
PG54	Protease I, <i>Achromobacter lyticus</i>	J5128	653aa	940aa	24	695aa 1.50E-22
PG55	Fimbriillin (orf3), <i>Porphyromonas gingivalis</i>	D42067	670aa	670aa	43	688aa 4.90E-106
PG56	Cysteine protease <i>Porphyromonas gingivalis</i>	U68468	364aa	1282aa, 1274aa	25	212aa 0.00012
PG57	Cysteine protease, <i>Porphyromonas gingivalis</i>	U68468	1358aa	924aa, 922aa, 921aa	31	742aa 1.40E-23
PG60	Outer membrane protein 11, <i>Helicobacter pylori</i>	AF000562	186aa	547aa	25	183aa 2.20E+00
PG61	Ferric pseudobactin M114 receptor protein (pbuA), <i>Pseudomonas</i> sp.	X73412	826aa	749aa	22	585aa 1.00E-05

Protein name	Homology description	Genbank accession number	Length of homolog	Length of P. gingivalis protein	FASTA homology results		
					Identity %	Overlap	E value
PG66	Attachment and invasion protein (ail), <i>Salmonella typhimurium</i>	AF007380	165aa	206aa	21	140aa	1.90E+00
PG68	Serum opacity factor, <i>Streptococcus pyogenes</i>	U02290	1025aa	1225aa	24	176aa	2.10E-01
PG69	Vacuolating cytotoxin (vacA), <i>Helicobacter pylori</i>	U63261	160aa	425aa	32	111aa	1.20E+00
PG70	Outer membrane protein, <i>Neisseria gonorrhoea</i>	U52069	174aa	266aa	22	153aa	6.90E+00
PG71	Gliding motility protein (gldA), <i>Flavobacterium johnsoniae</i>	AF007381	578aa	834aa	23	572aa	3.90E-25
PG75	Class 3 outer membrane porin (porB), <i>Neisseria meningitidis</i>	U07191	332aa	391aa	23	239aa	4.60E-01
PG81	Outer membrane protein (ompA), <i>Shigella dysenteriae</i>	V01344	351aa	>235aa	26	186aa	3.10E-01
PG82	Outer membrane protein (alkL), <i>Pseudomonas oleovorans</i>	X65936	230aa	434aa	26	136aa	2.80E+00
PG83	Gliding motility protein (gldA), <i>Flavobacterium johnsoniae</i>	AF007381	578aa	926aa	21	639aa	8.50E-09
PG87	Hypothetical protein, <i>Mycobacterium tuberculosis</i>	AL021942	877aa	781aa	29	794aa	2.20E-34

Protein name	Homology description	Genbank accession number	Length of homolog	Length of <i>P. gingivalis</i> protein	FASTA homology results		
					Identity %	Overlap	E value
PG89	NADH-ubiquinone oxidoreductase, <i>Helicobacter pylori</i>	AE000631	512aa	259aa	24	186aa	3.90E-01
PG91	Neuraminidase (nanH), <i>Bacteroides fragilis</i>	D28493	544aa	540aa	24	251aa	1.60E+00
PG92	Hypothetical protein, <i>Mycobacterium tuberculosis</i>	AL021942	877aa	771aa	29	770aa	8.00E-30
PG93	Cytoadherence protein P1, <i>Mycoplasma pneumoniae</i>	X07191	219aa	776aa	41	83aa	6.90E-01
PG94	Arginyl endopeptidase, <i>Porphyromonas gingivalis</i>	D28470	991aa	1157aa	24	328aa	7.60E-08
PG95	Sensor protein (EVGS), <i>Escherichia coli</i>	D14008	1197aa	961aa	28	511aa	2.60E-17
PG105	Plasma cell membrane glycoprotein, Human	P22413	873aa	449aa	34	404aa	5.60E-33
PG106	Hypothetical secreted protein, <i>Helicobacter pylori</i>	O24951	242aa	246aa	30	252aa	7.80E-22
PG107	Cell division ATP binding protein, <i>Mycobacterium leprae</i>	O32883	229aa	246aa, 241aa, 232aa	46	193aa	1.20E-26
PG108	ABC transporter, <i>Archaeoglobus fulgidis</i>	O29244	228aa	219aa	51	219aa	3.80E-41
PG109	Proteinase IV, <i>Escherichia coli</i>	F64936	618aa	595aa, 589aa	38	597aa	1.10E-57
PG110	Preprotein translocase, <i>Staphylococcus aureus</i>	O08446	843aa	523aa	43	521aa	6.00E-71
PG111	ABC transporter, <i>Synechocystis</i> sp.	P73758	574aa	> 720aa	40	579aa	1.70E-73
PG112	Glycosyl transferase, <i>Erwinia amylovora</i>	Q46634	351aa	375aa, 362aa	31	363aa	1.60E-32

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Protein name	Homology description	Genbank accession number	Length of homolog	Length of <i>P. gingivalis</i> protein	FASTA homology results
					Identity %      Overlap      E value
PG113	Heat shock protein (dnak), Treponema pallidum	AE001203	635aa	640aa	62      644aa      9.10E-138
PG114	Dihydrolipamide dehydrogenase, Clostridium magnum	Q59299	578aa	449aa	37      450aa      3.80E-54
PG115	Zinc protease, Escherichia coli	P31828	931aa	941aa	27      890aa      6.60E-57
PG116	Heat shock protein (HTPG), Escherichia coli	P10413	624aa	684aa	32      627aa      4.60E-48
PG117	Transcriptional regulator, Aquifex aeolicus	O66591	506aa	464aa	39      389aa      2.40E-49
PG118	ABC transporter, Bacillus subtilis	H70019	261aa	250aa	59      251aa      1.50E-60
PG119	ATP-dependent protease, Aquifex aeolicus	O66827	444aa	461aa	46      458aa      1.60E-77
PG120	Nitrogen assimilation regulatory protein, Bradyrhizobium sp.	P10576	480aa	457aa	49      242aa      3.80E-45
PG121	Cobalamin synthesis protein, Bacillus megaterium	E1331323	367aa	602aa	36      324aa      9.20E-37
PG122	Outer membrane integrity (tolA), Haemophilus influenzae	P71397	819aa	443aa	37      441aa      1.90E-54
PG123	Fimbriin, Porphyromonas gingivalis	D1034032	490aa	479aa	32      480aa      7.30E-48
PG124	Heat shock protein (dnaJ), Leptospira interrogans	AF007813	369aa	383aa	46      356aa      2.30E-57

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Protein name	Homology description	Genbank accession number	Length of homolog	Length of <i>P. gingivalis</i> protein	FASTA homology results		
					Identity %	Overlap	E value
PG125	Cobalamin biosynthesis protein(CBIK). Salmonella typhimurium	Q05592	264aa	293aa	37	259aa	3.70E-26
PG126	ABC-type permease, Pseudomonas aeruginosa	O68878	326aa	356aa	33	333aa	1.30E-30
PG127	Endonuclease excision repair protein (uvrB), Pseudomonas aeruginosa	X93486	670aa	678aa	56	675aa	1.10E-134



Table 3: Results of PSORT, SignalP and TopPred analysis of the proteins. The signal present column indicates the presence of a signal sequence detected with either PSORT or SignalP. The terms in parentheses indicates the type of signal sequence as determined by PSORT. The cell location & probability values are generated by PSORT and represent the probability of the protein being in the cell compartments outer membrane (OM), inner membrane (IM), periplasmic space (PC) or cytoplasm (C). The number of transmembrane domains (TMDs) was determined by TopPred and does not include uncleavable signal sequences.

Protein name	Protein seqID number	Protein Length	Signal Present	Methionine in ORF	SignalP cleavage site	PSORT cleavage site	Cell Location & probability				C-terminal Amino Acid	Number of TMD's
							OM	IM	PS	C		
PG1	386	451aa	Y	1	24	34	0	0	0	0.22	N	0
PG2	424	1017aa	Y	1	20	20	0.94	0	0.33	0	F	3
PG2	425	1014aa	Y	2	17	17	0.94	0	0.29	0	F	3
PG3	434	223aa	Y (lipoprotein)	1	-	18	0.79	0.76	0	0	K	3
PG4	447	672aa	Y (lipoprotein)	1	22	22	0.79	0.7	0	0	R	0
PG5	458	315aa	Y	1	40	35	0	0.25	0	0	R	0
PG6	475	324aa	N	1	-	-	0	0	0	0.2	S	1
PG7	487	404aa	N	1	7	-	0	0.42	0	0	E	3
PG8	498	598aa	N	1	-	-	0	0	0	0.22	N	0
PG8	499	550aa	N	2	-	-	0	0	0	0.25	N	0

Protein name	Protein seqID number	Protein Length	Signal Present	Methionine in ORF	SignalP cleavage site	PSORT cleavage site	Cell Location & probability				C-terminal Amino Acid	Number of TMD's
							OM	IM	PS	C		
PG8	500	458aa	N	3	-	-	0	0	0	0.34	N	0
PG8	501	426aa	N	4	-	-	0	0	0	0.24	N	0
PG9	515	1266aa	N	1	7	-	0	0	0	0.22	E	1
PG9	516	1232aa	N	2	-	-	0	0	0	0.39	E	1
PG9	517	1174aa	N	3	-	-	0	0	0	0.47	E	1
PG10	387	195aa	N	1	-	-	0	0	0	0.11	K	0
PG11	400	313aa	Y	1	22	26	0.24	0	0.93	0	R	1
PG12	411	271aa	Y (lipoprotein)	3	27	29	0.79	0.7	0	0	R	0
PG13	419	757aa	Y	1	23	25	0.94	0	0.29	0	N	0
PG14	420	331aa	Y (uncleavable)	1	35	26	0	0.58	0	0	K	1
PG15	421	267aa	Y	2	24	18	0	0.11	0	0	K	1
PG16	422	569aa	Y (lipoprotein)	1	24	18	0.79	0.7	0	0	G	0
PG18	423	981aa	Y	1	30	-	0	0.56	0	0	K	11
PG21	426	821aa	Y	2	24	27	0.34	0	0.37	0	G	1
PG22	427	106aa	Y (uncleavable)	1	41	41	0	0.29	0	0	P	0
PG23	428	859aa	N	1	-	-	0	0.12	0	0	A	1

Protein name	Protein seqID number	Protein Length	Signal Present	Methionine in ORF	SignalP cleavage site	PSORT cleavage site	Cell Location & probability				C-terminal Amino Acid	Number of TMD's
							OM	IM	PS	C		
PG24	429	417aa	Y	1	19	19	0	0.44	0	0	N	3
PG25	430	293aa	Y	1	27	28	0.2	0	0.62	0	R	0
PG27	431	312aa	N	1	-	-	0	0	0	0.28	Q	1
PG28	432	843aa	Y	1	21	21	0.93	0	0.24	0	H	1
PG29	433	290aa	Y	1	18	16	0.28	0	0.94	0	K	1
PG30	435	337aa	Y	1	21	21	0.24	0	0.4	0	K	0
PG31	436	151aa	N	1	-	-	0	0	0	0.3	T	0
PG32	437	391aa	Y	1	20	20	0.62	0	0.13	0	K	0
PG33	438	385aa	Y	1	26	26	0.81	0	0.31	0	E	1
PG34	439	190aa	Y	1	-	13	0	0.5	0	0	A	5
PG34	440	186aa	Y (uncleavable)	2	-	47	0	0.5	0	0	A	4
PG35	441	833aa	Y	1	22	22	0.94	0	0.37	0	F	1
PG36	442	891aa	Y (uncleavable)	1	-	40	0	0.31	0	0	F	2
PG37	443	174aa	Y (uncleavable)	1	28	24	0	0.35	0	0	K	0

Protein name	Protein seqID number	Protein Length	Signal Present	Methionine in ORF	SignalP cleavage site	PSORT cleavage site	Cell Location & probability				C-terminal Amino Acid	Number of TMD's
							OM	IM	PS	C		
PG37	444	170aa	Y (uncleavable)	2	24	20	0	0.35	0	0	K	0
PG38	445	163aa	Y	1	18	18	0.21	0	0.93	0	K	1
PG39	446	827aa	Y	1	36	36	0.93	0	0.25	0	F	3
PG40	448	772aa	Y	2	19	19	0.94	0	0.32	0	F	4
PG41	449	462aa	Y	2	27	27	0.25	0	0.54	0	Q	2
PG42	450	492aa	Y	5	30	-	0	0	0.00	0.13	Q	2
PG43	451	245aa	Y (uncleavable)	2	28	22	0	0.38	0	0	K	1
PG44	452	276aa	Y	1	19	24	0.15	0	0.89	0	K	0
PG45	453	775aa	Y (lipoprotein)	1	19	23	0.79	0.7	0	0	F	4
PG46	454	774aa	Y	1	27	27	0.73	0	0.22	0	F	2
PG47	455	867aa	Y	1	24	24	0.94	0	0.38	0	F	2
PG48	456	431aa	Y	1	24	24	0	0.1	0	0	R	1
PG49	457	333aa	Y (uncleavable)	1	24	18	0	0.12	0	0	I	0
PG50	459	848aa	Y	1	21	21	0.94	0	0.34	0	F	3
PG51	460	202aa	Y	1	26	25	0.2	0	0.61	0	S	0
PG52	461	455aa	Y (uncleavable)	1	23	21	0	0.18	0	0	F	1

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Protein name	Protein seqID number	Protein Length	Signal Present	Methionine in ORF	SignalP cleavage site	PSORT cleavage site	Cell Location & probability				C-terminal Amino Acid	Number of TMD's
							OM	IM	PS	C		
PG53	462	444aa	Y	1	14	17	0.36	0	0.22	0	D	2
PG54	463	940aa	Y	1	27	20	0.86	0	0.25	0	Q	5
PG55	464	670aa	Y (lipoprotein)	1	23	23	0.79	0.7	0	0	K	2
PG56	465	1282aa	Y (uncleavable)	1	-	21	0	0.04	0	0	K	4
PG56	466	1274aa	N	2	-	-	0	0	0	0.27	K	5
PG57	467	925aa	Y	1	28	24	0.53	0	0.2	0	P	3
PG57	468	922aa	Y	2	25	21	0.53	0	0.2	0	P	3
PG57	469	921aa	Y	3	24	20	0.53	0	0.2	0	P	3
PG58	470	593aa	Y	1	24	24	0.82	0	0.19	0	F	1
PG58	471	589aa	Y	2	20	20	0.82	0	0.19	0	F	1
PG59	472	346aa	Y	1	37	-	0	0.18	0	0	F	1
PG59	473	345aa	Y	2	36	56	0.92	0	0.15	0	F	1
PG59	474	330aa	Y	3	21	41	0.93	0	0.25	0	F	1
PG60	476	547aa	Y	1	28	28	0.93	0	0.25	0	F	0
PG61	477	749aa	Y	2	21	21	0.94	0	0.29	0	F	3
PG62	478	494aa	Y	1	21	21	0.93	0	0.24	0	F	2

Protein name	Protein seqID number	Protein Length	Signal Present	Methionine in ORF	SignalP cleavage site	PSORT cleavage site	Cell Location & probability				C-terminal Amino Acid	Number of TMD's
							OM	IM	PS	C		
PG63	479	294aa	Y	1	20	20	0.93	0	0.24	0	F	1
PG64	480	204aa	Y	1	20	20	0.93	0	0.19	0	F	1
PG65	481	243aa	Y	1	18	18	0.93	0	0.25	0	F	1
PG66	482	208aa	Y	1	21	21	0.94	0	0.3	0	F	1
PG67	483	950aa	Y	1	28	36	0.93	0	0.27	0	Y	4
PG68	484	1226aa	Y	1	25	25	0.91	0	0.31	0	Y	0
PG68	485	1225aa	Y	2	24	24	0.91	0	0.31	0	Y	0
PG69	486	425aa	Y	1	29	29	0.93	0	0.21	0	F	1
PG70	488	260aa	Y	1	18	24	0.93	0	0.24	0	F	0
PG71	489	834aa	Y	2	20	20	0.94	0	0.31	0	N	2
PG72	490	399aa	Y	1	27	27	0.94	0	0.32	0	H	2
PG73	491	382aa	Y	2	20	20	0.94	0	0.3	0	L	1
PG74	492	222aa	Y	1	24	24	0.94	0	0.32	0	L	0
PG75	493	391aa	Y	1	26	26	0.94	0	0.3	0	H	1
PG76	494	446aa	Y	1	21	22	0.94	0	0.32	0	V	3
PG77	495	308aa	Y	2	28	28	0.94	0	0.38	0	K	0

Protein name	Protein seqID number	Protein Length	Signal Present	Methionine in ORF	SignalP cleavage site	PSORT cleavage site	Cell Location & probability				C-terminal Amino Acid	Number of TMD's
							OM	IM	PS	C		
PG78	496	314aa	Y	1	23	23	0.94	0	0.29	0	D	0
PG79	497	285aa	Y	1	-	32	0.93	0	0.26	0	G	2
PG80	502	240aa	Y	1	19	19	0.93	0	0.22	0	N	2
PG81	366	>235aa	Y	1	28	20	0.93	0	0.21	0	Q	1
PG82	503	434aa	Y	1	30	24	0.93	0	0.2	0	N	3
PG83	504	926aa	Y	1	23	57	0.93	0	0.21	0	S	1
PG84	505	400aa	Y	1	25	25	0.93	0	0.25	0	N	1
PG84	506	398aa	Y	2	23	23	0.93	0	0.25	0	N	1
PG85	507	581aa	Y	1	20	20	0.93	0	0.46	0	L	2
PG86	508	239aa	Y	1	44	-	0	0	0	0.12	H	0
PG86	509	211aa	Y	2	16	46	0.91	0	0.03	0	H	0
PG87	510	781aa	Y	1	26	47	0.89	0	0.21	0	N	2
PG88	511	271aa	Y	2	28	19	0.89	0	0.25	0	P	0
PG88	512	270aa	Y	3	27	18	0.89	0	0.25	0	P	0
PG88	513	267aa	Y	4	24	15	0.89	0	0.23	0	P	0
PG89	514	259aa	Y	2	23	25	0.88	0	0.35	0	N	1

Protein name	Protein seqID number	Protein Length	Signal Present	Methionine in ORF	SignalP cleavage site	PSORT cleavage site	Cell Location & probability				C-terminal Amino Acid	Number of TMD's
							OM	IM	PS	C		
PG90	518	229aa	Y	1	22	21	0.85	0	0.44	0	K	0
PG90	519	228aa	Y	2	21	20	0.85	0	0.44	0	K	0
PG91	520	540aa	Y	1	25	25	0.85	0	0.30	0	E	0
PG92	521	771aa	Y	2	19	19	0.85	0	0.3	0	R	3
PG93	522	776aa	Y	1	25	25	0.85	0	0.37	0	R	4
PG94	523	1157aa	Y	1	23	28	0.8	0	0.25	0	Q	5
PG95	524	961aa	Y (lipoprotein)	1	-	19	0.79	0.87	0	0	V	1
PG96	525	563aa	Y	1	23	23	0.40	0	0.33	0	K	0
PG97	526	437aa	Y	1	23	23	0.32	0	0.65	0	Q	0
PG98	527	318aa	Y (lipoprotein)	1	19	19	0.79	0.7	0	0	L	1
PG99	528	461aa	Y (uncleavable)	1	22	20	0	0	0.3	0	R	0
PG100	388	279aa	Y	1	20	18	0.26	0	0.54	0	I	0
PG101	288	>157aa	N (ORF incomplete)	-	-	-	-	-	-	-	R	1
PG102	389	562aa	Y	1	29	29	0.19	0	0.4	0	S	3
PG102	390	558aa	Y	2	25	25	0.26	0	0.46	0	S	3
PG104	391	391aa	Y	1	17	17	0.62	0	0.22	0	R	0



Protein name	Protein seqID number	Protein Length	Signal Present	Methionine in ORF	SignalP cleavage site	PSORT cleavage site	Cell Location & probability				C-terminal Amino Acid	Number of TMD's
							OM	IM	PS	C		
PG105	392	449aa	Y	1	22	19	0.31	0	0.91	0	P	3
PG106	393	246aa	Y	2	41	49	0	0	0	0.02	L	0
PG107	394	246aa	N	1	-	-	0	0	0	0.32	D	1
PG107	395	241aa	N	2	-	-	0	0	0	0.3	D	1
PG107	396	232aa	N	3	-	-	0	0	0	0.21	D	1
PG108	397	219aa	N	1	-	-	0	0	0	0.19	R	1
PG109	398	595aa	Y	1	35	37	0.26	0	0.93	0	Y	3
PG109	399	589aa	Y	2	29	31	0.27	0	0.93	0	Y	3
PG110	401	>523aa	N	1	-	-	0	0	0	0.38	incomplete	0
PG111	278	>720aa	N (ORF incomplete)	-	-	-	-	-	-	-	G	1
PG112	402	375aa	Y	1	-	43	0	0.12	0	0	N	1
PG112	403	362aa	Y	2	-	30	0	0	0.12	0	N	1
PG113	404	540aa	N	1	-	-	0	0	0	0.25	K	1
PG114	405	449aa	N	1	-	-	0	0.12	0	0	G	4
PG115	406	941aa	Y	1	23	22	0.13	0	0.92	0	Q	2
PG116	407	964aa	N	1	-	-	0	0.12	0	0	L	2

SUBSTITUTE SHEET (Rule 26) (RO/AU)

Protein name	Protein seqID number	Protein Length	Signal Present	Methionine in ORF	SignalP cleavage site	PSORT cleavage site	Cell Location & probability				C-terminal Amino Acid	Number of TMD's
							OM	IM	PS	C		
PG117	408	464aa	N	1	-	-	0	0.19	0	0	L	1
PG118	409	250aa	N	1	-	-	0	0	0	0.27	E	1
PG119	410	461aa	N	1	-	-	0	0.28	0	0	E	2
PG120	412	457aa	N	1	-	-	0	0	0	0.21	E	0
PG121	413	602aa	N	1	-	-	0	0	0	0.31	E	3
PG122	414	443aa	N	1	-	-	0	0	0	0.14	Q	4
PG123	415	479aa	Y	2	22	22	0.26	0	0.94	0	K	0
PG124	416	383aa	N	1	-	-	0	0	0	0.29	D	2
PG125	417	293aa	Y	1	23	15	0.18	0	0.93	0	R	1
PG126	418	356aa	N	1	-	-	0	0.52	0	0	D	9
PG127	532	678aa	N	1	-	-	0	0	0	0.28	A	2

**Table 4:** Percentage identity and percentage similarity of various proteins with the 70 amino acids from the C-terminal of the *P. gingivalis* arginine protease 1 (RGP1), arginine protease 2 (RGP2), and the cysteine protease/hemagglutinin (prtT).

5

Protein name	Percent identity			Percent similarity		
	RGP1	RGP2	prtT	RGP1	RGP2	prtT
PG21	17	29	21	40	57	49
PG25	43	41	9	64	73	14
PG27	41	33	7	73	74	11
PG28	21	26	34	49	57	74
PG54	19	13	16	40	43	33
PG57	11	14	19	20	24	34
PG91	31	21	39	57	53	74
PG96	0	13	20	0	24	43
PG97	10	26	33	14	47	61
PG98	16	20	0	47	54	0
PG99	19	0	26	41	0	54
PG100	20	21	24	39	57	41
PG101	11	16	27	17	39	60
PG102	27	20	31	50	61	61
PG104	16	23	26	46	44	49

**Table 5:** Percentage identity and percentage similarity of various proteins with the TonBIII box of *P. gingivalis*.

Protein name	Percent identity	Percent similarity
PG2	46	71
PG13	57	93
PG35	50	96
PG47	39	71
PG50	54	93

### Cloning, expression and purification of recombinant *P. gingivalis* genes.

#### PG1

5           Oligonucleotides to the 5' and 3' regions of the deduced protein were used to amplify the gene of interest from a preparation of *P. gingivalis* W50 genomic DNA using the TaqPlus Precision PCR System (Stratagene) and a PTC-100 (MJ Research) thermal cycler or similar device. The 5' oligonucleotide primer sequence was GCGCCATATGCTGGCCGAACCGGCC, 10 the 3' oligonucleotide primer sequence was GCGCCTCGAGTCAATTCATTTCCTTATAGAG. The PCR fragment was purified, digested with Nde I, Xho I restriction enzymes (Promega) and ligated into the corresponding sites of the plasmid pProEx-1 (Gibco-BRL) and transformed into *E. coli* ER1793 cells (a gift from Elizabeth Raleigh, New 15 England Biolabs). A resulting clone expressing the correct insert was selected and induced with or without 0.1mM IPTG (Promega) for expression of the recombinant protein. Expression of the recombinant protein was determined by SDS-PAGE analysis and Western Blot using the one of the rabbit antisera described above or an anti-hexahistidine antibody (Clontech) 20 that detects the hexahistidine tag that was fused to the *P. gingivalis* recombinant protein. PG1 was purified by disruption of the *E. coli* cells by sonication in binding buffer (Novagen) and solubilisation by the addition of sarkosyl (N-Lauroyl sarcosine) to a 1% final concentration. There after the preparation was diluted to 0.1% sarkosyl in binding buffer, bound to a 25 Nickel-nitrilotriacetic acid column (Ni-NTA; Qiagen), after washing bound proteins were eluted with 1M imidazole in elution buffer (Novagen) according to the Qiagen recommendations with 0.1% sarkosyl added to all buffers. Following purification samples were dialysed against 500mM NaCl, 20mM Tris, 0.1% sarkosyl at pH7.4 to remove the imidazole, concentrated as 30 required and stored at 4°C until used. Purity and antigenicity were assessed by SDS-PAGE and Western blot using selected antisera (from those described above) and the protein concentration was determined by the BCA assay (Pierce).

**PG2**

The methods used for PG2 were essentially the same as for PG1 with the following exceptions. The 5' oligonucleotide primer sequence was CGCGGTATACATGAAAAGAATGACGC, the 3' oligonucleotide primer  
5 sequence was CGCGAGATCTGAAAGACAACCTGAATACC and the PCR product was cloned into pGex-stop RBS(IV) (Patent application WO9619496, JC Cox, SE Edwards, I Frazer and EA Webb. Variants of human papilloma virus antigens) using the BstZ 171 and Bgl II restriction sites. 2% sarkosyl was used to solubilise PG2 and 8M urea was added to the solubilisation buffer  
10 and to all other buffers. Urea was removed from the purified protein by sequential dialysis (4M then 2M then 1M then 0.5M then 0M urea all in 50mM Tris, 500mM NaCl, 0.1% sarkosyl, pH7.4). Purified protein was stored at 4°C until required.

**PG3**

The methods used for PG3 were essentially the same as for PG1 with the following exceptions. The 5' oligonucleotide primer sequence was GCGCGTATACATGAAGAAATCAAGTGTAG, the 3' oligonucleotide primer  
20 sequence was GCGCAGATCTCTTCAGCGTACCTTGCTGTG and DNA was amplified with Pfu DNA polymerase (Stratagene). The PCR product was cloned directly into pCR-Blunt and transformed into *E. coli* Top10F'(InVitrogen) before subcloning into the expression plasmid pGex-stop RBS(IV) using the Bst Z171 and Bgl II restriction sites and transformed  
25 into *E. coli* BL21DE3 (Pharmacia Biotech). The following modifications were made to the purification of PG3 from the PG1 method. Cells expressing the recombinant protein were disrupted by sonication in binding buffer and the insoluble inclusion bodies concentrated by centrifugation. Inclusion bodies  
30 were then solubilised in 6M urea (Sigma) in binding buffer and eluted with 6M urea added to the elution buffer. In some instances 6M guanidine hydrochloride (Sigma) was used instead of urea for these steps. Urea (or guanidine hydrochloride when it was substituted) was removed from the purified protein by sequential dialysis against reducing levels of urea (3M  
35 then 1.5M then 0.5M then 0M urea all in 50mM Tris, 500mM NaCl, 8% glycerol, pH7.4). Purified protein was stored frozen at -80°C until required. Protein concentration was determined by the Coomassie Plus protein assay (Pierce).

**PG4**

The methods used for PG4 were essentially the same as for PG3 with the following exceptions. The 5' oligonucleotide primer sequence was CTTCTGTATACTTACAGCGGACATCATAAAATC, the 3' oligonucleotide  
5 primer sequence was TTCCAGGAGGGTACCACGCAACTCTTCTTCGAT and DNA was amplified with the Tth XL PCR kit (Perkin Elmer). The PCR product was cloned into the expression plasmid pGex-stop RBS(IV) using the Bst Z171 and Kpn I restriction sites and transformed into *E. coli* ER1793.

**10 PG5**

The methods used for PG5 were essentially the same as for PG3 with the following exceptions. The 5' oligonucleotide primer sequence was TTGCAACATATGATCAGAACGATACTTTCA, the 3' oligonucleotide primer  
15 sequence was AGCAATCTCGAGCGGTTTCATGAGCCAAAGC and DNA was amplified with the Tth XL PCR kit. The PCR product was cloned into the expression plasmid pET24 (Novagen) using the Nde I and Xho I restriction sites and transformed into *E. coli* BL21 (Pharmacia Biotech). Removal of urea was not proceeded past 1M urea as the protein was insoluble at lower  
20 concentrations of urea. Purified protein was stored at 4°C until required.

**PG6**

The methods used for PG6 were essentially the same as for PG3 with the following exceptions. The 5' oligonucleotide primer sequence was TAAACATATGTGCCTCGAACCCATAATTGCTCCG, the 3' oligonucleotide  
25 primer sequence was CGTCCGCGGAAGCTTTGATCGGCCATTGCTACT and DNA was amplified with the Tth XL PCR kit. The PCR product was cloned into the expression plasmid pET24a using the Nde I and Hind III restriction sites and transformed into *E. coli* BL21.

**30 PG8**

The methods used for PG8 were essentially the same as for PG3 with the following exceptions. The 5' oligonucleotide primer sequence was CGCGGTATACATGGAGTTCAAGATTGTG, the 3' oligonucleotide primer  
35 sequence was CGCGAGATCTGTTTTCTGAAAGCTTTTC and DNA was amplified with the TaqPlus Precision PCR System. The PCR product was

cloned into the expression plasmid pProEx-1 using the Nde I and Xho I restriction sites and transformed into *E. coli* ER1793.

#### PG8A

5 PG8A is a shortened version of PG8 and has the first 173 amino acids removed. The methods used for PG8A were essentially the same as for PG3 with the following exceptions. The 5' oligonucleotide primer sequence was CGCGGTATACATGGAAAACCTTAAAGAAC, the 3' oligonucleotide primer sequence was CGCGAGATCTGTTTTCTGAAAGCTTTTC and DNA was  
10 amplified with the TaqPlus Precision PCR System. The PCR product was cloned into the expression plasmid pGex-stop RBS(IV) using the Bst Z171 and Bgl II restriction sites and transformed into *E. coli* ER1793. Prior to dialysis of the purified protein EDTA (Sigma) was added to a final concentration of 10mM.

15

#### PG10

The methods used for PG10 were essentially the same as for PG3 with the following exceptions. The 5' oligonucleotide primer sequence was CGCGGATATCATGGATAAAGTGAGCTATGC, the 3' oligonucleotide primer  
20 sequence was CGCGAGATCTTTTGTTGATACTCAATAATTC and DNA was amplified with the TaqPlus Precision PCR System. The PCR product was digested with Eco RV and Bgl II and ligated into the expression plasmid pGex-stop RBS(IV) using the Bst Z171 and Bgl II restriction sites and transformed into *E. coli* ER1793.

25

#### PG11

The methods used for PG11 were essentially the same as for PG1 with the following exceptions. The 5' oligonucleotide primer sequence was GCGCGTATACATGAGAGCAAACATTTGGCAGATACTTTCCG, the 3'  
30 oligonucleotide primer sequence was GCGCAGATCTGCGCAAGCGCAGTATATCGCC and DNA was amplified with Tli DNA polymerase (Promega). The PCR product was cloned into pCR-Blunt and transformed into *E. coli* Top10F' before subcloning into the expression plasmid pGex-stop RBS(IV) using the Bst Z171 and Bgl II restriction sites and  
35 transformed into *E. coli* ER1793. PG11 was purified by solubilisation of *E. coli* cells with 2% sarkosyl in binding buffer (Qiagen) which was diluted to

0.1% sarkosyl in binding buffer, bound to a Nickel-nitrilotriacetic acid column (Ni-NTA; Qiagen), after washing bound proteins were eluted with 1M imidazole (0.7% CHAPS (Sigma) in elution buffer; Qiagen) according to the Qiagen recommendations. Following purification samples were dialysed  
5 against 500mM NaCl, 20mM Tris, 0.7% CHAPS, 20% glycerol (Sigma) at pH7.4 to remove the imidazole, concentrated as required and stored at 4°C until used.

### PG12

10 The methods used for PG12 were essentially the same as for PG1 with the following exceptions. The 5' oligonucleotide primer sequence was GCGCGTATACATGAATAGCAGACATCTGACAATCACAATCATTGCCGG, the 3' oligonucleotide primer sequence was  
15 GCGCAGATCTGCTGTTCTGTGAGTGCAGTTGTTTAAGTG and DNA was amplified with Tli DNA polymerase. The PCR product was cloned into pCR-Blunt and transformed into *E. coli* Top10F' cells before subcloning into the expression plasmid pGex-stop RBS(IV) using the Bst Z171 and Bgl II restriction sites and transformed into *E. coli* BL21. Purification of the recombinant protein was essentially the same as PG11 except 0.5% DHPC  
20 (1,2-Diheptanoyl-*sn*-glycero-3-phosphocholine; Avanti) in 50mM Tris, 50mM NaCl, pH8.0 was used to solubilise the inclusion bodies instead of sarkosyl and the DHPC was diluted to 0.1% before addition to the Ni-NTA and 0.1% DHPC was added to all buffers.

### 25 PG13

The methods used for PG13 were essentially the same as for PG3 with the following exceptions. The 5' oligonucleotide primer sequence was GCGCCATATGCGGACAAAACTATCTTTTTTGCG, the 3' oligonucleotide primer sequence was  
30 GCGCCTCGAGGTTGTTGAATCGAATCGCTATTTGAGC and DNA was amplified with Tli DNA polymerase. The PCR product was cloned the expression plasmid pET24b using the Nde I and Xho I restriction sites and transformed into *E. coli* BL21. Purification of the recombinant protein was essentially the same as PG3 using 6M urea and 1% NOG (n-octyl glucoside;  
35 Sigma) was added to the dialysis buffer. Removal of urea was not proceeded



past 2M urea as the protein was insoluble at lower concentrations of urea. Purified protein was stored at 4°C until required.

#### PG14

- 5           The methods used for PG12 were essentially the same as for PG1 with the following exceptions. The 5' oligonucleotide primer sequence was GCGCGGCGCCATGACGGACAACAAACGTAATATCG, the 3' oligonucleotide primer sequence was GCGCCTCGAGTTACTTGCGTATGATCACGGACATACCC and DNA was  
10   amplified with Tli DNA polymerase. The PCR product was cloned the expression plasmid pProEx-1 using the Ehe I and Xho I restriction sites and transformed into *E. coli* BL21. Purification of the recombinant protein was essentially the same as PG12.

#### 15   PG15

- The methods used for PG15 were essentially the same as for PG3 with the following exceptions. The 5' oligonucleotide primer sequence was CAAAAGTATACTAATAAATATCATTCTCAA, the 3' oligonucleotide primer sequence was GCTTATGGTACCTTTGGTCTTATCTATTAT and DNA was  
20   amplified with the Tth XL PCR kit. The PCR product was cloned into the expression plasmid pGex-stop RBS(IV) using the Bst Z171 and Kpn I restriction sites and transformed into *E. coli* ER1793.

#### PG22

- 25           The methods used for PG22 were essentially the same as for PG1 with the following exceptions. The 5' oligonucleotide primer sequence was CCCCCGATCCGATGCGACTGATCAAGGC, the 3' oligonucleotide primer sequence was CCCCCTCGAGCGGAACGGGGTCATAGCC and DNA was amplified with the TaqPlus Precision PCR System. The PCR product was  
30   cloned into the expression plasmid pET24b using the Bam HI and Xho I restriction sites and transformed into *E. coli* BL21DE3. Once PG22 was purified dialysis was performed in the same manner as for PG1 but in the presence of 1M imidazole.

**PG24**

The methods used for PG24 were essentially the same as for PG3 with the following exceptions. The 5' oligonucleotide primer sequence was CGCGGTATACATGAATTACCTGTACATAC, the 3' oligonucleotide primer  
5 sequence was CGCGGGATCCGTTTCGATTGGTCGTCGATGG and DNA was amplified with the TaqPlus Precision PCR System. The PCR product was digested with Bst Z171 and Bam HI and ligated into the expression plasmid pGex-stop RBS(IV) using the Bst Z171 and Bgl II restriction sites and transformed into *E. coli* ER1793. Due to the low level of expression of PG24  
10 purification was not proceeded with except on small scale.

**PG24A**

A modified version of PG24 was also cloned and expressed. PG24A is the same as PG24 with the predicted N-terminal sequence removed. The  
15 methods used for PG24A were essentially the same as for PG3 with the following exceptions. The 5' oligonucleotide primer sequence was CGCGCATATGGAGATTGCTTTTCCTTTCTTCG, the 3' oligonucleotide primer sequence was CGCGCTCGAGTTAGTTTCGATTGGTCGTCG and DNA was amplified with the TaqPlus Precision PCR System. The PCR product was  
20 cloned into the expression plasmid pProEx-1 using the Nde I and Xho I restriction sites and transformed into *E. coli* ER1793. Purification of the recombinant protein was essentially the same as PG3 except 8M urea was used to solubilise the inclusion bodies and in the buffers used for the Ni-NTA column purification. Urea was removed by sequential dialysis (4M then 2M,  
25 then 1M then 0.5M then 0M urea all in 50mM Tris, 500mM NaCl, 8% glycerol, pH7.4). Purified protein was stored frozen at -80°C until required.

**PG29**

The methods used for PG29 were essentially the same as for PG3 with  
30 the following exceptions. The 5' oligonucleotide primer sequence was GCGCGATATCGCTAGCATGAAAAAGCTATTTCTC, the 3' oligonucleotide primer sequence was GCGCAGATCTCTCGAGTTTGCCATCGGATTGCGGATTG and DNA was amplified with Pfu DNA polymerase being used. The PCR product was  
35 cloned into pCR-Blunt (InVitrogen) and transformed into *E. coli* Top10F' before subcloning into the expression plasmid pGex-stop RBS(IV)

using the EcoR V and Bgl II restriction sites and transformed into *E. coli* BL21. 6M urea was used throughout the purification process.

### PG30

5       The methods used for PG30 were essentially the same as for PG3 with the following exceptions. The predicted N-terminal signal sequence was removed from the recombinant protein. The 5' oligonucleotide primer sequence was TACGGAATTTCGTGACCCCCGTCAGAAATGTGCGC, the 3' oligonucleotide primer sequence was  
10   CTATGCGGCCGCTTTGATCCTCAAGGCTTTGCCCGG and DNA was amplified with the Tth XL PCR kit. The PCR product was cloned into the expression plasmid pET24a using the Eco RI and Not I restriction sites and transformed into *E. coli* BL21DE3. Expression studies and immunoreactivity studies were carried out on whole *E. coli* lysates of PG30. 10ml cultures of  
15   recombinant *E. coli* were grown to an OD of 2.0 ( $A_{600nm}$ ) in terrific broth and the cells were induced with 0.5mM IPTG and samples taken for analysis at 4 hours post induction. Purification was not done for these studies.

### PG31

20       The methods used for PG31 were essentially the same as for PG30 with the following exceptions. The 5' oligonucleotide primer sequence was CGGGGAATTTCGAAAAATCAATTTCTATGCTGAA, the 3' oligonucleotide primer sequence was CTATGCGGCCGCTGTATGCAATAGGGAAAGCTCCGA and DNA was amplified with the Tth XL PCR kit. The PCR product was  
25   cloned into the expression plasmid pET24a using the Eco RI and Not I restriction sites and transformed into *E. coli* BL21DE3. Expression studies and immunoreactivity studies were carried out on whole *E. coli* lysates. Purification was not done for these studies.

### PG32

30       The methods used for PG32 were essentially the same as for PG30 with the following exceptions. The predicted N-terminal signal sequence was removed from the recombinant protein. The 5' oligonucleotide primer sequence was CGCAGAATTCCAGGAGAATACTGTACCGGCAACG, the 3'  
35   oligonucleotide primer sequence was CTATGCGGCCGCTTGGAGCGAACGATTACAACAC and DNA was

amplified with the Tth XL PCR kit. The PCR product was cloned into the expression plasmid pET24a using the Eco RI and Not I restriction sites and transformed into *E. coli* BL21DE3. Expression studies and immunoreactivity studies were carried out on whole *E. coli* lysates. Purification was not done  
5 for these studies.

### PG33

The methods used for PG33 were essentially the same as for PG30 with the following exceptions. The predicted N-terminal signal sequence was  
10 removed from the recombinant protein.

The 5' oligonucleotide primer sequence was TGCAGAATTCCAAGAAGCTACTACACAGAACAAA, the 3' oligonucleotide primer sequence was CTATGCGGCCGCTTCCGCTGCAGTCATTACTACAA and DNA was amplified with the Tth XL PCR kit. The PCR product was  
15 cloned into the expression plasmid pET24a using the Eco RI and Not I restriction sites and transformed into *E. coli* BL21DE3. Expression studies and immunoreactivity studies were carried out on whole *E. coli* lysates. Purification was not done for these studies.

### 20 PG35

The methods used for PG35 were essentially the same as for PG30 with the following exceptions. The 5' oligonucleotide primer sequence was GCGCGAATTCATGAAACAACATAACATTATCAGC, the 3' oligonucleotide primer sequence was GCGTGCGGCCGCGAAATTGATCTTTGTACCGACGA  
25 and DNA was amplified with the Tth XL PCR kit. The PCR product was cloned into the expression plasmid pET24a using the Eco RI and Not I restriction sites and transformed into *E. coli* BL21DE3. Expression studies and immunoreactivity studies were carried out on whole *E. coli* lysates. Purification was not done for these studies.

30

### PG36

The methods used for PG36 were essentially the same as for PG30 with the following exceptions. The 5' oligonucleotide primer sequence was AAAGGAATTCTACAAAAAGATTATTGCCGTAGCA, the 3' oligonucleotide  
35 primer sequence was CTATGCGGCCGCGAACTCCTGTCCGAGCACAAAGT and DNA was amplified with the Tth XL PCR kit. The PCR product was

cloned into the expression plasmid pET24a using theEco RI and Not I restriction sites and transformed into *E. coli* BL21DE3. Expression studies and immunoreactivity studies were carried out on whole *E. coli* lysates. Purification was not done for these studies.

5

**PG37**

The methods used for PG37 were essentially the same as for PG30 with the following exceptions. The 5' oligonucleotide primer sequence was TGGCGAATTCAAACGGTTTTTGATTTTGATCGGC, the 3' oligonucleotide  
10 primer sequence was CTATGCGGCCGCTTGCTAAAGCCCATCTTGCTCAG and DNA was amplified with the Tth XL PCR kit. The PCR product was cloned into the expression plasmid pET24a using the Eco RI and Not I restriction sites and transformed into *E. coli* BL21DE3. Expression studies and immunoreactivity studies were carried out on whole *E. coli* lysates.  
15 Purification was not done for these studies.

**PG38**

The methods used for PG38 were essentially the same as for PG30 with the following exceptions. The predicted N-terminal signal sequence was  
20 removed from the recombinant protein. The 5' oligonucleotide primer sequence was CCTCGAATTCCAAAAGGTGGCAGTGGTAAACACT, the 3' oligonucleotide primer sequence was CTATGCGGCCGCTTGATTCCGAGTTTCGCTTTTAC and DNA was amplified with the Tth XL PCR kit. The PCR product was cloned into the  
25 expression plasmid pET24a using the Eco RI and Not I restriction sites and transformed into *E. coli* BL21DE3. Expression studies and immunoreactivity studies were carried out on whole *E. coli* lysates. Purification was not done for these studies.

**PG39**

The methods used for PG39 were essentially the same as for PG30 with the following exceptions. The predicted N-terminal signal sequence was removed from the recombinant protein. The 5' oligonucleotide primer  
30 sequence was AGCTGGATCCCAAGGEGTCAGGGTATCGGGCTAT, the 3' oligonucleotide primer sequence was  
35 CTATGCGGCCGCGAATTCGACGAGGAGACGCAGGT and DNA was

amplified with the Tth XL PCR kit. The PCR product was cloned into the expression plasmid pET24a using the Bam HI and Not I restriction sites and transformed into *E. coli* BL21DE3. Expression studies and immunoreactivity studies were carried out on whole *E. coli* lysates. Purification was not done  
5 for these studies.

#### PG40

The methods used for PG40 were essentially the same as for PG30 with the following exceptions. The predicted N-terminal signal sequence was  
10 removed from the recombinant protein. The 5' oligonucleotide primer sequence was GGCTGAATTCAAGACGGACAACGTCCCGACAGAT, the 3' oligonucleotide primer sequence was CTATGCGGCCGCGAAGTTGACCATAACCTTACCCA and DNA was amplified with the Tth XL PCR kit. The PCR product was cloned into the  
15 expression plasmid pET24a using the Eco RI and Not I restriction sites and transformed into *E. coli* BL21DE3. Expression studies and immunoreactivity studies were carried out on whole *E. coli* lysates. Purification was not done for these studies.

#### 20 PG41

The methods used for PG41 were essentially the same as for PG30 with the following exceptions. The predicted N-terminal signal sequence was removed from the recombinant protein. The 5' oligonucleotide primer sequence was GACTGAATTCCAAAACGCCTCCGAAACGACGGTA, the 3'  
25 oligonucleotide primer sequence was CTATGCGGCCGCTTGTTGCGGAATCCCCATGCCGTT and DNA was amplified with the Tth XL PCR kit. The PCR product was cloned into the expression plasmid pET24a using the Eco RI and Not I restriction sites and transformed into *E. coli* BL21DE3. Expression studies and immunoreactivity  
30 studies were carried out on whole *E. coli* lysates. Purification was not done for these studies.

#### PG42

The methods used for PG42 were essentially the same as for PG30  
35 with the following exceptions. The 5' oligonucleotide primer sequence was GTTTGAATTCGCAAATAATACTCTTTTGGCGAAG, the 3' oligonucleotide

primer sequence was

GAGTGC GGCCGCTTTGCCGGACATCGAAGAGATCGTC and DNA was amplified with the Tth XL PCR kit. The PCR product was cloned into the expression plasmid pET24a using the Eco RI and Not I restriction sites and transformed into *E. coli* BL21DE3. Expression studies and immunoreactivity studies were carried out on whole *E. coli* lysates. Purification was not done for these studies.

#### PG43

The methods used for PG43 were essentially the same as for PG30 with the following exceptions. The 5' oligonucleotide primer sequence was GCGCGAATTCAAAAAAGAAAAACTTTGGATTGCG, the 3' oligonucleotide primer sequence was CTATGCGGCCGCTTCAAAGCGAAAGAAGCCTTAAC and DNA was amplified with the Tth XL PCR kit. The PCR product was cloned into the expression plasmid pET24a using the Eco RI and Not I restriction sites and transformed into *E. coli* BL21DE3. Expression studies and immunoreactivity studies were carried out on whole *E. coli* lysates. Purification was not done for these studies.

#### PG44

The methods used for PG44 were essentially the same as for PG30 with the following exceptions. The predicted N-terminal signal sequence was removed from the recombinant protein. The 5' oligonucleotide primer sequence was AGCCGAATTCTGTAAGAAAAATGCTGACACTACC, the 3' oligonucleotide primer sequence was CTATGCGGCCGCTTTTCCCGGGCTTGATCCCGAT and DNA was amplified with the Tth XL PCR kit. The PCR product was cloned into the expression plasmid pET24a using the Eco RI and Not I restriction sites and transformed into *E. coli* BL21DE3. Expression studies and immunoreactivity studies were carried out on whole *E. coli* lysates. Purification was not done for these studies.

#### PG45

The methods used for PG45 were essentially the same as for PG30 with the following exceptions. The predicted N-terminal signal sequence was removed from the recombinant protein. The 5' oligonucleotide primer

sequence was GACAGGATCCTGCTCCACCACAAAGAATCTGCCG, the 3' oligonucleotide primer sequence was CTATGCGGCCGCGAAGGGATAGCCGACAGCCAAAT and DNA was amplified with the Tth XL PCR kit. The PCR product was cloned into the expression plasmid pET24a using the Bam HI and Not I restriction sites and transformed into *E. coli* BL21DE3. Expression studies and immunoreactivity studies were carried out on whole *E. coli* lysates. Purification was not done for these studies.

#### 10 PG46

The methods used for PG46 were essentially the same as for PG30 with the following exceptions. The predicted N-terminal signal sequence was removed from the recombinant protein. The 5' oligonucleotide primer sequence was CTCGGAATTCCGTTATGTGCCGGACGGTAGCAGA, the 3' oligonucleotide primer sequence was CTATGCGGCCGCGAACGGATAGCCTACTGCAATGT and DNA was amplified with the Tth XL PCR kit. The PCR product was cloned into the expression plasmid pET24a using the Eco RI and Not I restriction sites and transformed into *E. coli* BL21DE3. Expression studies and immunoreactivity studies were carried out on whole *E. coli* lysates. Purification was not done for these studies.

#### PG47

The methods used for PG47 were essentially the same as for PG30 with the following exceptions. The predicted N-terminal signal sequence was removed from the recombinant protein. The 5' oligonucleotide primer sequence was CGCCGAATTCCAAACAGTGGTGACCGGTAAGGTGATCGATTCAGAA, the 3' oligonucleotide primer sequence was CTATGCGGCCGCGAAGTTTACACGAATACCGGTAGACCAAGTGCGGCC and DNA was amplified with the Tth XL PCR kit. The PCR product was cloned into the expression plasmid pET24a using the Eco RI and Not I restriction sites and transformed into *E. coli* BL21DE3. Expression studies and immunoreactivity studies were carried out on whole *E. coli* lysates. Purification was not done for these studies.



**PG48**

The methods used for PG48 were essentially the same as for PG30 with the following exceptions. The predicted N-terminal signal sequence was removed from the recombinant protein. The 5' oligonucleotide primer  
5 sequence was TGCTGAATTCCAAAAATCCAAGCAGGTACAGCGA, the 3' oligonucleotide primer sequence was CTATGCGGCCGCTCGTAACCATAGTCTTGGGTTTTG and DNA was amplified with the Tth XL PCR kit. The PCR product was cloned into the expression plasmid pET24a using the Eco RI and Not I restriction sites and  
10 transformed into *E. coli* BL21DE3. Expression studies and immunoreactivity studies were carried out on whole *E. coli* lysates. Purification was not done for these studies.

**PG49**

15 The methods used for PG49 were essentially the same as for PG30 with the following exceptions. The predicted N-terminal signal sequence was removed from the recombinant protein. The 5' oligonucleotide primer sequence was GAACGGATCCAACGAGCCGGTGAAGACAGATCC, the 3' oligonucleotide primer sequence was  
20 GAGTGC GGCCGCTAATCTCGACTTCATACTTGTACCA and DNA was amplified with the Tth XL PCR kit. The PCR product was cloned into the expression plasmid pET24a using the Bam HI and Not I restriction sites and transformed into *E. coli* BL21DE3. Expression studies and immunoreactivity studies were carried out on whole *E. coli* lysates. Purification was not done  
25 for these studies.

**PG50**

The methods used for PG50 were essentially the same as for PG30 with the following exceptions. The predicted N-terminal signal sequence was removed from the recombinant protein. The 5' oligonucleotide primer  
30 sequence was GCTGGGATCCGCGACAGACACTGAGTTCAAGTAC, the 3' oligonucleotide primer sequence was CTATGCGGCCGCGAACTTCACTACCAAGCCCATGT and DNA was amplified with the Tth XL PCR kit. The PCR product was cloned into the expression plasmid pET24a using the Bam HI and Not I restriction sites and  
35 transformed into *E. coli* BL21DE3. Expression studies and immunoreactivity

studies were carried out on whole *E. coli* lysates. Purification was not done for these studies.

#### PG51

- 5           The methods used for PG51 were essentially the same as for PG30 with the following exceptions. The predicted N-terminal signal sequence was removed from the recombinant protein. The 5' oligonucleotide primer sequence was TCTTGAATTTCGCGCAAAGTCTTTTCAGCACCGAA, the 3' oligonucleotide primer sequence was
- 10   CTATGCGGCCGCACTTTTTCGTGGGATCACTCTCTT and DNA was amplified with the Tth XL PCR kit. The PCR product was cloned into the expression plasmid pET24a using the Eco RI and Not I restriction sites and transformed into *E. coli* BL21DE3. Expression studies and immunoreactivity studies were carried out on whole *E. coli* lysates. Purification was not done
- 15   for these studies.

#### PG52

- The methods used for PG52 were essentially the same as for PG30 with the following exceptions. The 5' oligonucleotide primer sequence was
- 20   AGAAGAATTCAAACGGACAATCCTCCTGACGGCA, the 3' oligonucleotide primer sequence was CTATGCGGCCGCGAAGTCTTTGCCCTGATAGAAATC and DNA was amplified with the Tth XL PCR kit. The PCR product was cloned into the expression plasmid pET24a using the Eco RI and Not I restriction sites and transformed into *E. coli* BL21DE3. Expression studies
- 25   and immunoreactivity studies were carried out on whole *E. coli* lysates. Purification was not done for these studies.

#### PG53

- The methods used for PG53 were essentially the same as for PG30 with the following exceptions. The predicted N-terminal signal sequence was removed from the recombinant protein. The 5' oligonucleotide primer sequence was GGCTGAATTTCGCGAATCCCCTTACGGGGCCAATCG, the 3' oligonucleotide primer sequence was
- 30   CTATGCGGCCGCGTCCGAAAGGCAGCCGTAATAGG and DNA was amplified with the Tth XL PCR kit. The PCR product was cloned into the expression plasmid pET24a using the Eco RI and Not I restriction sites and
- 35

transformed into *E. coli* BL21DE3. Expression studies and immunoreactivity studies were carried out on whole *E. coli* lysates. Purification was not done for these studies.

5 **PG54**

The methods used for PG54 were essentially the same as for PG30 with the following exceptions. The predicted N-terminal signal sequence was removed from the recombinant protein. The 5' oligonucleotide primer sequence was CGCTGAATTCCAGATTTTCGTTTCGGAGGGGAACCC, the 3'  
10 oligonucleotide primer sequence was CTATGCGGCCGCTGCTTCACGATCTTTTGGCTCA and DNA was amplified with the Tth XL PCR kit. The PCR product was cloned into the expression plasmid pET24a using the Eco RI and Not I restriction sites and transformed into *E. coli* BL21DE3. Expression studies and immunoreactivity  
15 studies were carried out on whole *E. coli* lysates. Purification was not done for these studies.

**PG55**

The methods used for PG55 were essentially the same as for PG30 with the following exceptions. The predicted N-terminal signal sequence was removed from the recombinant protein. The 5' oligonucleotide primer sequence was CGAGGGATCCGAGCTCTCTATTTGCGATGGCGAG, the 3'  
20 oligonucleotide primer sequence was GAGTGC GGCCGCTCTTACCTGACTTCTTGTCACGAAT and DNA was amplified with the Tth XL PCR kit. The PCR product was cloned into the expression plasmid pET24a using the Bam HI and Not I restriction sites and transformed into *E. coli* BL21DE3. Expression studies and immunoreactivity  
25 studies were carried out on whole *E. coli* lysates. Purification was not done for these studies.

30

**PG56**

The methods used for PG56 were essentially the same as for PG30 with the following exceptions. The 5' oligonucleotide primer sequence was AAATGGATCCCGAAAAATTTTGAGCTTTTGGATG, the 3' oligonucleotide  
35 primer sequence was CTATGCGGCCGCTTTGATTTCGTAATTTTCCGTATC and DNA was amplified with the Tth XL PCR kit. The PCR product was

cloned into the expression plasmid pET24a using the Bam HI and Not I restriction sites and transformed into *E. coli* BL21DE3. Expression studies and immunoreactivity studies were carried out on whole *E. coli* lysates. Purification was not done for these studies.

5

**PG57**

The methods used for PG57 were essentially the same as for PG30 with the following exceptions. The predicted N-terminal signal sequence was removed from the recombinant protein. The 5' oligonucleotide primer  
10 sequence was TGCTGGATCCCAAGAGATCTCAGGCATGAATGCA, the 3' oligonucleotide primer sequence was  
GAGTGCGGCCGCTCGGCCTCTTTATCTCTACCTTTTC and DNA was amplified with the Tth XL PCR kit. The PCR product was cloned into the expression plasmid pET24a using the Bam HI and Not I restriction sites and  
15 transformed into *E. coli* BL21DE3. Expression studies and immunoreactivity studies were carried out on whole *E. coli* lysates. Purification was not done for these studies.

**PG58**

The methods used for PG58 were essentially the same as for PG30 with the following exceptions. The predicted N-terminal signal sequence was removed from the recombinant protein. The 5' oligonucleotide primer  
20 sequence was CGGTGAATTCCAAACCCACGAAATACAGAAACC, the 3' oligonucleotide primer sequence was  
25 GAGTGCGGCCGCTGAAAGTCCAGCTAAAACCGGCGAA and DNA was amplified with the Tth XL PCR kit. The PCR product was cloned into the expression plasmid pET24a using the Eco RI and Not I restriction sites and transformed into *E. coli* BL21DE3. Expression studies and immunoreactivity  
30 studies were carried out on whole *E. coli* lysates. Purification was not done for these studies.

**PG59**

The methods used for PG59 were essentially the same as for PG30 with the following exceptions. The predicted N-terminal signal sequence was  
35 removed from the recombinant protein. The 5' oligonucleotide primer sequence was TGCTGAATTCCAACAAGAGAAGCAGGTGTTTCAT, the 3'

oligonucleotide primer sequence was

GAGTGCGGCCGCTGAAGATGCTCTTATCGTCCAAACG and DNA was

amplified with the Tth XL PCR kit. The PCR product was cloned into the expression plasmid pET24a using the Eco RI and Not I restriction sites and

- 5 transformed into *E. coli* BL21DE3. Expression studies and immunoreactivity studies were carried out on whole *E. coli* lysates. Purification was not done for these studies.

#### PG60

- 10 The methods used for PG60 were essentially the same as for PG30 with the following exceptions. The predicted N-terminal signal sequence was removed from the recombinant protein. The 5' oligonucleotide primer sequence was GCGGAATTCCAGATGCTCAATACTCCTTTCGAG, the 3' oligonucleotide primer sequence was

- 15 GAGTGCGGCCGCTGAAGAGGTAGGAGATATTGCAGAT and DNA was amplified with the Tth XL PCR kit. The PCR product was cloned into the expression plasmid pET24a using the Eco RI and Not I restriction sites and transformed into *E. coli* BL21DE3. Expression studies and immunoreactivity studies were carried out on whole *E. coli* lysates. Purification was not done  
20 for these studies.

#### PG61

- The methods used for PG61 were essentially the same as for PG30 with the following exceptions. The predicted N-terminal signal sequence was  
25 removed from the recombinant protein. The 5' oligonucleotide primer sequence was AGCAGAATTCCCCGTCTCCAACAGCGAGATAGAT, the 3' oligonucleotide primer sequence was  
GAGTGCGGCCGCTGAAATCGATTGTCAGACTACCCAG and DNA was  
30 amplified with the Tth XL PCR kit. The PCR product was cloned into the expression plasmid pET24a using the Eco RI and Not I restriction sites and transformed into *E. coli* BL21DE3. Expression studies and immunoreactivity studies were carried out on whole *E. coli* lysates. Purification was not done for these studies.

**PG62**

The methods used for PG62 were essentially the same as for PG30 with the following exceptions. The predicted N-terminal signal sequence was removed from the recombinant protein. The 5' oligonucleotide primer sequence was TGCTGAATTCCAGCGGTTTCCGATGGTGCAGGGA, the 3' oligonucleotide primer sequence was GAGTGCGGCCGCTGAAGTGAAATCCGACACGCAGCTG and DNA was amplified with the Tth XL PCR kit. The PCR product was cloned into the expression plasmid pET24a using the Eco RI and Not I restriction sites and transformed into *E. coli* BL21DE3. Expression studies and immunoreactivity studies were carried out on whole *E. coli* lysates. Purification was not done for these studies.

**PG63**

The methods used for PG63 were essentially the same as for PG30 with the following exceptions. The predicted N-terminal signal sequence was removed from the recombinant protein. The 5' oligonucleotide primer sequence was GGCAGAATTCCAAGAAGCAAACACTGCATCTGAC, the 3' oligonucleotide primer sequence was GAGTGCGGCCGCTGAAAGTGACGCAACACCCACGCC and DNA was amplified with the Tth XL PCR kit. The PCR product was cloned into the expression plasmid pET24a using the Eco RI and Not I restriction sites and transformed into *E. coli* BL21DE3. Expression studies and immunoreactivity studies were carried out on whole *E. coli* lysates. Purification was not done for these studies.

**PG64**

The methods used for PG64 were essentially the same as for PG30 with the following exceptions. The predicted N-terminal signal sequence was removed from the recombinant protein. The 5' oligonucleotide primer sequence was TGCTGAATTCCAGAGTCGTCCTGCTCTTAGACTG, the 3' oligonucleotide primer sequence was GAGTGCGGCCGCTGAAGCGAACACCGAGACCCACAAA and DNA was amplified with the Tth XL PCR kit. The PCR product was cloned into the expression plasmid pET24a using the Eco RI and Not I restriction sites and transformed into *E. coli* BL21DE3. Expression studies and immunoreactivity

studies were carried out on whole *E. coli* lysates. Purification was not done for these studies.

#### PG65

- 5           The methods used for PG65 were essentially the same as for PG30 with the following exceptions. The predicted N-terminal signal sequence was removed from the recombinant protein. The 5' oligonucleotide primer sequence was GGCCGGATCCATCGGACAAAGCCGCCCGGCACTT, the 3' oligonucleotide primer sequence was
- 10 GAGTGCGGCCGCTAAAGCGGTAACCTATGCCCCACGAA and DNA was amplified with the Tth XL PCR kit. The PCR product was cloned into the expression plasmid pET24a using the Bam HI and Not I restriction sites and transformed into *E. coli* BL21DE3. Expression studies and immunoreactivity studies were carried out on whole *E. coli* lysates. Purification was not done
- 15 for these studies.

#### PG66

- The methods used for PG66 were essentially the same as for PG30 with the following exceptions. The predicted N-terminal signal sequence was
- 20 removed from the recombinant protein. The 5' oligonucleotide primer sequence was GTTTGAATTCCAAGACGTTATCAGACCATGGTCA, the 3' oligonucleotide primer sequence was
- GAGTGCGGCCGCTAAAATGAGTGGAGAGCGTGGCCAT and DNA was amplified with the Tth XL PCR kit. The PCR product was cloned into the
- 25 expression plasmid pET24a using the Eco RI and Not I restriction sites and transformed into *E. coli* BL21DE3. Expression studies and immunoreactivity studies were carried out on whole *E. coli* lysates. Purification was not done for these studies.

#### 30 PG67

- The methods used for PG67 were essentially the same as for PG30 with the following exceptions. The predicted N-terminal signal sequence was removed from the recombinant protein. The 5' oligonucleotide primer sequence was GAACGAGCTCGCGGAACGTCCTATGGCCGGAGCA, the 3'
- 35 oligonucleotide primer sequence was
- GAGTGCGGCCGCTATACCAAGTATTCGTGATGGGACG and DNA was

amplified with the Tth XL PCR kit. The PCR product was cloned into the expression plasmid pET24a using the Sac I and Not I restriction sites and transformed into *E. coli* BL21DE3. Expression studies and immunoreactivity studies were carried out on whole *E. coli* lysates. Purification was not done  
5 for these studies.

#### PG68

The methods used for PG68 were essentially the same as for PG30 with the following exceptions. The predicted N-terminal signal sequence was  
10 removed from the recombinant protein. The 5' oligonucleotide primer sequence was GCTTGCGGCCGCCCTTATGAAAGATTTGCAGAT, the 3' oligonucleotide primer sequence was GGTGCTCGAGTATACTCAACAAGCACCTTATGCAC and DNA was  
15 amplified with the Tth XL PCR kit. The PCR product was cloned into the expression plasmid pET24a using the Not I and Xho I restriction sites and transformed into *E. coli* BL21DE3. Expression studies and immunoreactivity studies were carried out on whole *E. coli* lysates. Purification was not done  
for these studies.

#### 20 PG69

The methods used for PG69 were essentially the same as for PG30 with the following exceptions. The predicted N-terminal signal sequence was removed from the recombinant protein. The 5' oligonucleotide primer  
sequence was TGCTGAATTCCAGGAAGGGGAGGGGAGTGCCCCGA, the 3'  
25 oligonucleotide primer sequence was GAGTGCGGCCGCTGAAGCTGTAGCGGGCTTTGAACCA and DNA was amplified with the Tth XL PCR kit. The PCR product was cloned into the expression plasmid pET24a using the Eco RI and Not I restriction sites and transformed into *E. coli* BL21DE3. Expression studies and immunoreactivity  
30 studies were carried out on whole *E. coli* lysates. Purification was not done for these studies.

#### PG70

The methods used for PG70 were essentially the same as for PG30  
35 with the following exceptions. The predicted N-terminal signal sequence was removed from the recombinant protein. The 5' oligonucleotide primer



sequence was CGGTGGATCCTCGCAAATGCTCTTCTCAGAGAAT, the 3' oligonucleotide primer sequence was GAGTGCGGCCGCTAAACGAAATATCGATACCAACATC and DNA was amplified with the Tth XL PCR kit. The PCR product was cloned into the expression plasmid pET24a using the Bam HI and Not I restriction sites and transformed into *E. coli* BL21DE3. Expression studies and immunoreactivity studies were carried out on whole *E. coli* lysates. Purification was not done for these studies.

#### 10 PG71

The methods used for PG71 were essentially the same as for PG30 with the following exceptions. The predicted N-terminal signal sequence was removed from the recombinant protein. The 5' oligonucleotide primer sequence was TGCTGAATTCCAGAACAATACCCTCGATGTACAC, the 3' oligonucleotide primer sequence was GAGTGCGGCCGCTATTGCCGGTAGGATTTTCCTTGTCC and DNA was amplified with the Tth XL PCR kit. The PCR product was cloned into the expression plasmid pET24a using the Eco RI and Not I restriction sites and transformed into *E. coli* BL21DE3. Expression studies and immunoreactivity studies were carried out on whole *E. coli* lysates. Purification was not done for these studies.

#### PG72

The methods used for PG72 were essentially the same as for PG30 with the following exceptions. The predicted N-terminal signal sequence was removed from the recombinant protein. The 5' oligonucleotide primer sequence was TGCTGAATTCGGAGAGCGACTGGAGACGGACAGC, the 3' oligonucleotide primer sequence was GAGTGCGGCCGCTATGATTGCCTTTCAGAAAAGCTAT and DNA was amplified with the Tth XL PCR kit. The PCR product was cloned into the expression plasmid pET24a using the Eco RI and Not I restriction sites and transformed TGCTGAATTCGGAGAGCGACTGGAGACGGACAGC into *E. coli* BL21DE3. Expression studies and immunoreactivity studies were carried out on whole *E. coli* lysates. Purification was not done for these studies.

**PG73**

The methods used for PG73 were essentially the same as for PG30 with the following exceptions. The predicted N-terminal signal sequence was removed from the recombinant protein. The 5' oligonucleotide primer  
5 sequence was CGGTGAATTCCAACAGACAGGACCGGCCGAACGC, the 3' oligonucleotide primer sequence was  
GAGTGCGGCCGCTTAAGAAAGGTATCTGATAGATCAG and DNA was amplified with the Tth XL PCR kit. The PCR product was cloned into the expression plasmid pET24a using the Eco RI and Not I restriction sites and  
10 transformed into *E. coli* BL21DE3. Expression studies and immunoreactivity studies were carried out on whole *E. coli* lysates. Purification was not done for these studies.

**PG74**

15 The methods used for PG74 were essentially the same as for PG30 with the following exceptions. The predicted N-terminal signal sequence was removed from the recombinant protein. The 5' oligonucleotide primer sequence was TGCTGAATTCCAAGAAAATAATACAGAAAAGTCA, the 3' oligonucleotide primer sequence was  
20 GAGTGCGGCCGCTGAGGTTTAATCCTATGCCAATACT and DNA was amplified with the Tth XL PCR kit. The PCR product was cloned into the expression plasmid pET24a using the Eco RI and Not I restriction sites and transformed into *E. coli* BL21DE3. Expression studies and immunoreactivity studies were carried out on whole *E. coli* lysates. Purification was not done  
25 for these studies.

**PG75**

The methods used for PG75 were essentially the same as for PG30 with the following exceptions. The predicted N-terminal signal sequence was  
30 removed from the recombinant protein. The 5' oligonucleotide primer sequence was GGCGGGATCCGCTCAGGAGCAACTGAATGTGGTA, the 3' oligonucleotide primer sequence was  
GAGTGCGGCCGCTGTGGAACAAATTGCGCAATCCATC and DNA was amplified with the Tth XL PCR kit. The PCR product was cloned into the  
35 expression plasmid pET24a using the Bam HI and Not I restriction sites and transformed into *E. coli* BL21DE3. Expression studies and immunoreactivity

studies were carried out on whole *E. coli* lysates. Purification was not done for these studies.

#### PG76

5           The methods used for PG76 were essentially the same as for PG30 with the following exceptions. The predicted N-terminal signal sequence was removed from the recombinant protein. The 5' oligonucleotide primer sequence was AGCAGAATTTCGGAAACGCACAGAGCTTTTGGGAA, the 3' oligonucleotide primer sequence was  
10 GAGTGCGGCCGCTTACCTGCACCTTATGACTGAATAC and DNA was amplified with the Tth XL PCR kit. The PCR product was cloned into the expression plasmid pET24a using the Eco RI and Not I restriction sites and transformed into *E. coli* BL21DE3. Expression studies and immunoreactivity studies were carried out on whole *E. coli* lysates. Purification was not done  
15 for these studies.

#### PG77

          The methods used for PG77 were essentially the same as for PG30 with the following exceptions. The predicted N-terminal signal sequence was  
20 removed from the recombinant protein. The 5' oligonucleotide primer sequence was TGCTGAATTCCAAGAGAAAAAGGATAGTCTCTCT, the 3' oligonucleotide primer sequence was GAGTGCGGCCGCTCTTCTTATCGCCATAGAATACAGG and DNA was amplified with the Tth XL PCR kit. The PCR product was cloned into the  
25 expression plasmid pET24a using the Eco RI and Not I restriction sites and transformed into *E. coli* BL21DE3. Expression studies and immunoreactivity studies were carried out on whole *E. coli* lysates. Purification was not done for these studies.

#### 30 PG78

          The methods used for PG78 were essentially the same as for PG30 with the following exceptions. The predicted N-terminal signal sequence was removed from the recombinant protein. The 5' oligonucleotide primer sequence was GGCAGAATTCCAGGATTCTTCCCACGGTAGCAAT, the 3'  
35 oligonucleotide primer sequence was GAGTGCGGCCGCTATCATGATAGTAAAGACTGGTTCT and DNA was

amplified with the Tth XL PCR kit. The PCR product was cloned into the expression plasmid pET24a using the Eco RI and Not I restriction sites and transformed into *E. coli* BL21DE3. Expression studies and immunoreactivity studies were carried out on whole *E. coli* lysates. Purification was not done  
5 for these studies.

#### PG79

The methods used for PG79 were essentially the same as for PG30 with the following exceptions. The 5' oligonucleotide primer sequence was  
10 TGCTGAATTCGTAGTGACGCTGCTCGTAATTGTC, the 3' oligonucleotide primer sequence was  
GAGTGCGGCCGCTGCCGTCCTGCCTTTCTGCCTGACG and DNA was amplified with the Tth XL PCR kit. The PCR product was cloned into the expression plasmid pET24a using the Eco RI and Not I restriction sites and  
15 transformed into *E. coli* BL21DE3. Expression studies and immunoreactivity studies were carried out on whole *E. coli* lysates. Purification was not done for these studies.

#### PG80

The methods used for PG80 were essentially the same as for PG30 with the following exceptions. The predicted N-terminal signal sequence was removed from the recombinant protein. The 5' oligonucleotide primer sequence was GGCCGAATTCCAAAACGTGCAGTTGCACTACGAT, the 3' oligonucleotide primer sequence was  
25 GAGTGCGGCCGCTGTTGAAAGTCCATTTGACCGCAAG and DNA was amplified with the Tth XL PCR kit. The PCR product was cloned into the expression plasmid pET24a using the Eco RI and Not I restriction sites and transformed into *E. coli* BL21DE3. Expression studies and immunoreactivity studies were carried out on whole *E. coli* lysates. Purification was not done  
30 for these studies.

#### PG81

The methods used for PG81 were essentially the same as for PG30 with the following exceptions. The predicted N-terminal signal sequence was  
35 removed from the recombinant protein. The 5' oligonucleotide primer sequence was GTTTGAATTCCAGGATTTTCTCTATGAAATAGGA, the 3'

oligonucleotide primer sequence was

GAGTGCGGCCGCTTTGTTTATTACAAAAAGTCTTACG and DNA was

amplified with the Tth XL PCR kit. The PCR product was cloned into the  
expression plasmid pET24a using the Eco RI and Not I restriction sites and

- 5 transformed into *E. coli* BL21DE3. Expression studies and immunoreactivity studies were carried out on whole *E. coli* lysates. Purification was not done for these studies.

#### PG82

- 10 The methods used for PG82 were essentially the same as for PG30 with the following exceptions. The predicted N-terminal signal sequence was removed from the recombinant protein. The 5' oligonucleotide primer sequence was GAACGAATTCCAGAACAACAACCTTACCGAGTCG, the 3' oligonucleotide primer sequence was

- 15 GAGTGCGGCCGCTGTTTCAGTTTCAGCTTTTAAACCA and DNA was amplified with the Tth XL PCR kit. The PCR product was cloned into the expression plasmid pET24a using the Eco RI and Not I restriction sites and transformed into *E. coli* BL21DE3. Expression studies and immunoreactivity studies were carried out on whole *E. coli* lysates. Purification was not done  
20 for these studies.

#### PG84

- The methods used for PG84 were essentially the same as for PG30 with the following exceptions. The predicted N-terminal signal sequence was  
25 removed from the recombinant protein. The 5' oligonucleotide primer sequence was TGCTGGATCCCAGAATGATGACATCTTCGAAGAT, the 3' oligonucleotide primer sequence was  
GAGTGCGGCCGCTATTGCGTCCCCGGCCACTACGTCC and DNA was  
30 amplified with the Tth XL PCR kit. The PCR product was cloned into the expression plasmid pET24a using the Bam HI and Not I restriction sites and transformed into *E. coli* BL21DE3. Expression studies and immunoreactivity studies were carried out on whole *E. coli* lysates. Purification was not done for these studies.

**PG85**

The methods used for PG85 were essentially the same as for PG30 with the following exceptions. The predicted N-terminal signal sequence was removed from the recombinant protein. The 5' oligonucleotide primer  
5 sequence was CGGTGAATTCGTACCAACGGACAGCACGGAATCG, the 3' oligonucleotide primer sequence was  
GAGTGCGGCCGCTCAGATTGGTGCTATAAGAAAGGTA and DNA was amplified with the Tth XL PCR kit. The PCR product was cloned into the expression plasmid pET24a using the Eco RI and Not I restriction sites and  
10 transformed into *E. coli* BL21DE3. Expression studies and immunoreactivity studies were carried out on whole *E. coli* lysates. Purification was not done for these studies.

**PG86**

15 The methods used for PG86 were essentially the same as for PG30 with the following exceptions. The predicted N-terminal signal sequence was removed from the recombinant protein. The 5' oligonucleotide primer sequence was TGCTGGATCCCAAACGCATGATCATCTCATCGAA, the 3' oligonucleotide primer sequence was  
20 GAGTGCGGCCGCTGTGGTTCAGGCCGTGGGCAAATCT and DNA was amplified with the Tth XL PCR kit. The PCR product was cloned into the expression plasmid pET24a using the Bam HI and Not I restriction sites and transformed into *E. coli* BL21DE3. Expression studies and immunoreactivity studies were carried out on whole *E. coli* lysates. Purification was not done  
25 for these studies.

**PG87**

The methods used for PG87 were essentially the same as for PG30 with the following exceptions. The predicted N-terminal signal sequence was  
30 removed from the recombinant protein. The 5' oligonucleotide primer sequence was GGCGGAATTCCAGAGCTATGTGGACTACGTCGAT, the 3' oligonucleotide primer sequence was  
GAGTGCGGCCGCTATTACTGTGATTAGCGCGACGCTG and DNA was amplified with the Tth XL PCR kit. The PCR product was cloned into the  
35 expression plasmid pET24a using the Eco RI and Not I restriction sites and transformed into *E. coli* BL21DE3. Expression studies and immunoreactivity

studies were carried out on whole *E. coli* lysates. Purification was not done for these studies.

#### PG88

5           The methods used for PG88 were essentially the same as for PG30 with the following exceptions. The predicted N-terminal signal sequence was removed from the recombinant protein. The 5' oligonucleotide primer sequence was AGCAGAATTCCGCCGAATCGAAGTCTGTCTCTTTC, the 3' oligonucleotide primer sequence was  
10 GAGTGCGGCCGCTCGGCAAGTAACGCTTTAGTGGGGA and DNA was amplified with the Tth XL PCR kit. The PCR product was cloned into the expression plasmid pET24a using the Eco RI and Not I restriction sites and transformed into *E. coli* BL21DE3. Expression studies and immunoreactivity studies were carried out on whole *E. coli* lysates. Purification was not done  
15 for these studies.

#### PG89

          The methods used for PG89 were essentially the same as for PG30 with the following exceptions. The predicted N-terminal signal sequence was  
20 removed from the recombinant protein. The 5' oligonucleotide primer sequence was TGCTGAATTCCAATCGAAGTTAAAGATCAAGAGC, the 3' oligonucleotide primer sequence was GAGTGCGGCCGCTATTAGTCCAAAGACCCACGGTAAA and DNA was amplified with the Tth XL PCR kit. The PCR product was cloned into the  
25 expression plasmid pET24a using the Eco RI and Not I restriction sites and transformed into *E. coli* BL21DE3. Expression studies and immunoreactivity studies were carried out on whole *E. coli* lysates. Purification was not done for these studies.

#### 30 PG90

          The methods used for PG90 were essentially the same as for PG30 with the following exceptions. The predicted N-terminal signal sequence was removed from the recombinant protein. The 5' oligonucleotide primer sequence was GGCAGAATTCCAAACAACGACGAACAGTAGCCGG, the 3'  
35 oligonucleotide primer sequence was GAGTGCGGCCGCTTTTTTGTGTGATACTGTTTGGGC and DNA was

amplified with the Tth XL PCR kit. The PCR product was cloned into the expression plasmid pET24a using the Eco RI and Not I restriction sites and transformed into *E. coli* BL21DE3. Expression studies and immunoreactivity studies were carried out on whole *E. coli* lysates. Purification was not done  
5 for these studies.

#### PG91

The methods used for PG91 were essentially the same as for PG30 with the following exceptions. The predicted N-terminal signal sequence was  
10 removed from the recombinant protein. The 5' oligonucleotide primer sequence was TGCTGAATTCCAGACGATGGGAGGAGATGATGTC, the 3' oligonucleotide primer sequence was GAGTGCGGCCGCTTTCCACGATGAGCTTCTCTACGAA and DNA was amplified with the Tth XL PCR kit. The PCR product was cloned into the  
15 expression plasmid pET24a using the Eco RI and Not I restriction sites and transformed into *E. coli* BL21DE3. Expression studies and immunoreactivity studies were carried out on whole *E. coli* lysates. Purification was not done for these studies.

#### 20 PG92

The methods used for PG92 were essentially the same as for PG30 with the following exceptions. The predicted N-terminal signal sequence was removed from the recombinant protein. The 5' oligonucleotide primer sequence was GGCCGAATTCGCCGATGCACAAAGCTCTGTCTCT, the 3'  
25 oligonucleotide primer sequence was GAGTGCGGCCGCTTCGAGGACGATTGCTTAGTTCGTA and DNA was amplified with the Tth XL PCR kit. The PCR product was cloned into the expression plasmid pET24a using the Eco RI and Not I restriction sites and transformed into *E. coli* BL21DE3. Expression studies and immunoreactivity  
30 studies were carried out on whole *E. coli* lysates. Purification was not done for these studies.

#### PG93

The methods used for PG93 were essentially the same as for PG30  
35 with the following exceptions. The predicted N-terminal signal sequence was removed from the recombinant protein. The 5' oligonucleotide primer



sequence was GGCCGAGCTCCAAGAGGAAGGTATTTGGAATACC, the 3' oligonucleotide primer sequence was GAGTGCGGCCGCTGCGAATCACTGCGAAGCGAATTAG and DNA was amplified with the Tth XL PCR kit. The PCR product was cloned into the expression plasmid pET24a using the Sac I and Not I restriction sites and transformed into *E. coli* BL21DE3. Expression studies and immunoreactivity studies were carried out on whole *E. coli* lysates. Purification was not done for these studies.

#### 10 PG94

The methods used for PG94 were essentially the same as for PG30 with the following exceptions. The predicted N-terminal signal sequence was removed from the recombinant protein. The 5' oligonucleotide primer sequence was GGCCGAGCTCCAAGAGGAAGGTATTTGGAATACC, the 3' oligonucleotide primer sequence was GAGTGCGGCCGCTTTGTCCTACCACGATCATTTTCTT and DNA was amplified with the Tth XL PCR kit. The PCR product was cloned into the expression plasmid pET24a using the Eco RI and Not I restriction sites and transformed into *E. coli* BL21DE3. Expression studies and immunoreactivity studies were carried out on whole *E. coli* lysates. Purification was not done for these studies.

#### PG95

The methods used for PG95 were essentially the same as for PG30 with the following exceptions. The predicted N-terminal signal sequence was removed from the recombinant protein. The 5' oligonucleotide primer sequence was GGCCGAGCTCTGTGGAAAAAAGAAAAACACTCT, the 3' oligonucleotide primer sequence was GAGTGCGGCCGCTAACTGTCTCCTTGTGCTCCCCGG and DNA was amplified with the Tth XL PCR kit. The PCR product was cloned into the expression plasmid pET24a using the Sac I and Not I restriction sites and transformed into *E. coli* BL21DE3. Expression studies and immunoreactivity studies were carried out on whole *E. coli* lysates. Purification was not done for these studies.

**PG96**

The methods used for PG96 were essentially the same as for PG30 with the following exceptions. The predicted N-terminal signal sequence was removed from the recombinant protein. The 5' oligonucleotide primer sequence was TGCTGAGCTCCAAACGCAAATGCAAGCAGACCGA, the 3' oligonucleotide primer sequence was GAGTGCGGCCGCTTTTGAGAATTTTCATTGTCTCACG and DNA was amplified with the Tth XL PCR kit. The PCR product was cloned into the expression plasmid pET24a using the Sac I and Not I restriction sites and transformed into *E. coli* BL21DE3. Expression studies and immunoreactivity studies were carried out on whole *E. coli* lysates. Purification was not done for these studies.

**PG97**

The methods used for PG97 were essentially the same as for PG30 with the following exceptions. The predicted N-terminal signal sequence was removed from the recombinant protein. The 5' oligonucleotide primer sequence was GCGGGATCCCAGTTTGTTCGCGCTCCCACCACA, the 3' oligonucleotide primer sequence was GAGTGCGGCCGCTCTGTTTGATGAGCTTAGTGGTATA and DNA was amplified with the Tth XL PCR kit. The PCR product was cloned into the expression plasmid pET24a using the Bam HI and Not I restriction sites and transformed into *E. coli* BL21DE3. Expression studies and immunoreactivity studies were carried out on whole *E. coli* lysates. Purification was not done for these studies.

**PG98**

The methods used for PG98 were essentially the same as for PG30 with the following exceptions. The predicted N-terminal signal sequence was removed from the recombinant protein. The 5' oligonucleotide primer sequence was AGCAGAATTCCAAGAAAGAGTCGATGAAAAAGTA, the 3' oligonucleotide primer sequence was GAGTGCGGCCGCTTAGCTGTGTAACATTAAGTTTTTTATTGAT and DNA was amplified with the Tth XL PCR kit. The PCR product was cloned into the expression plasmid pET24a using the Eco RI and Not I restriction sites and transformed into *E. coli* BL21DE3. Expression studies and

immunoreactivity studies were carried out on whole *E. coli* lysates. Purification was not done for these studies.

#### PG99

- 5           The methods used for PG99 were essentially the same as for PG30 with the following exceptions. The predicted N-terminal signal sequence was removed from the recombinant protein. The 5' oligonucleotide primer sequence was TGCTGAATTCAAGGACAATTCTTCTTACAAACCT, the 3' oligonucleotide primer sequence was
- 10 GAGTGCGGCCGCTTCGAATCAGCACTTTTCTCACAAA and DNA was amplified with the Tth XL PCR kit. The PCR product was cloned into the expression plasmid pET24a using the Eco RI and Not I restriction sites and transformed into *E. coli* BL21DE3. Expression studies and immunoreactivity studies were carried out on whole *E. coli* lysates. Purification was not done
- 15 for these studies.

#### PG100

- The methods used for PG100 were essentially the same as for PG30 with the following exceptions. The predicted N-terminal signal sequence was removed from the recombinant protein. The 5' oligonucleotide primer sequence was GGCAGAATTCCAGTCTTTGAGCACAAATCAAAGTA, the 3' oligonucleotide primer sequence was
- 20 GAGTGCGGCCGCTGATAGCCAGCTTGATGCTCTTAGC and DNA was amplified with the Tth XL PCR kit. The PCR product was cloned into the expression plasmid pET24a using the Eco RI and Not I restriction sites and transformed into *E. coli* BL21DE3. Expression studies and immunoreactivity studies were carried out on whole *E. coli* lysates. Purification was not done for these studies.

#### 30 PG101

- The methods used for PG101 were essentially the same as for PG30 with the following exceptions. The 5' oligonucleotide primer sequence was TGCTGAATTCAAAGGCAAGGGCGATCTGGTCGGG, the 3' oligonucleotide primer sequence was
- 35 GAGTGCGGCCGCTTCTCTTCTCGAACTTGGCCGAGTA and DNA was amplified with the Tth XL PCR kit. The PCR product was cloned into the

expression plasmid pET24a using the Eco RI and Not I restriction sites and transformed into *E. coli* BL21DE3. Expression studies and immunoreactivity studies were carried out on whole *E. coli* lysates. Purification was not done for these studies.

5

**PG102**

The methods used for PG102 were essentially the same as for PG30 with the following exceptions. The predicted N-terminal signal sequence was removed from the recombinant protein. The 5' oligonucleotide primer  
10 sequence was GGCCGAATTCCAGATGGATATTGGTGGAGACGAT, the 3' oligonucleotide primer sequence was GAGTGCGGCCGCTCTCTACAATGATTTTTTCCACGAA and DNA was amplified with the Tth XL PCR kit. The PCR product was cloned into the expression plasmid pET24a using the Eco RI and Not I restriction sites and  
15 transformed into *E. coli* BL21DE3. Expression studies and immunoreactivity studies were carried out on whole *E. coli* lysates. Purification was not done for these studies.

**PG104**

20 The methods used for PG104 were essentially the same as for PG30 with the following exceptions. The predicted N-terminal signal sequence was removed from the recombinant protein. The 5' oligonucleotide primer sequence was GAACGGATCCAACGTGTCTGCTCAGTCACCCCGA, the 3' oligonucleotide primer sequence was  
25 GAGTGCGGCCGCTTCTGAGCGATACTTTTGCACGTAT and DNA was amplified with the Tth XL PCR kit. The PCR product was cloned into the expression plasmid pET24a using the Bam HI and Not I restriction sites and transformed into *E. coli* BL21DE3. Expression studies and immunoreactivity studies were carried out on whole *E. coli* lysates. Purification was not done  
30 for these studies.

**Animal antisera and human patient sera.**

Various antisera were raised for detecting the expression and  
35 refolding of the recombinant *P. gingivalis* proteins. A whole cell antisera was raised by injecting New Zealand White rabbits with 3 doses of sonicated

*P. gingivalis* (strain W50) containing approximately 2mg of protein. The first dose was given in Freund's complete adjuvant (FCA) and the second and third doses were given in Freund's incomplete adjuvant (IFA) at 3 week intervals. Doses (1ml) were given intramuscularly into the hind legs and rabbits bled 7 days after the last dose, the blood clotted and serum removed and stored at -20°C until required. A second rabbit antiserum was produced in a similar manner but using a sarkosyl insoluble fraction (each dose was 0.69mg of protein) derived from *P. gingivalis* W50 according to the method of Doidg and Trust T. *et al* 1994 as the immunogen. A third rabbit antiserum was produced in a similar manner to the first only the sarkosyl soluble fraction (1mg of protein per dose) derived from *P. gingivalis* W50 cells according to the method of Doidg P. and Trust TJ. (1994 Infect Immun 62:4526-33) was used as the immunogen.

A "protected rat serum" pool was also used in these studies and was obtained from rats immunised with formalin killed whole *P. gingivalis* cells in FIA (strain ATCC 33277; 2 doses of  $2 \times 10^9$  cells, 3 weeks apart). Rats were then challenged 2 weeks after their last dose with live *P. gingivalis* cells (strain 33277) given orally as previously described (Klaussen B. *et al.* 1991, Oral Microbiol Immunol 6:193-201) and the serum obtained from these rats 6 weeks after the final challenge inoculation at the time of sacrifice.

Human sera were obtained from adult patients undergoing treatment or assessment for periodontitis at an outpatient clinic. These patients had at least 6 teeth with 6mm attachment loss and had *P. gingivalis* present in their sub-gingival plaque as detected using a *P. gingivalis* specific DNA probe. Sera was pooled from these patients and compared to a pool of sera from periodontally healthy patients.

### Immunization and Murine Lesion Model Protocols

The mouse abscess model was used to assess the efficacy of immunising mice with recombinant *P. gingivalis* proteins in protecting mice from formation of a subcutaneous abscess. This model has been used by others as a predictor of potential vaccines against periodontal disease (Bird PS, *et al.* 1995 J. Periodontol. 66:351-362. BALB/c mice 6-8 weeks old were immunised by subcutaneously injecting them with 0.1 ml containing either 10 or 20µg of recombinant *P. gingivalis* protein, 20µg of *E. coli* lysate protein,

2 x 10<sup>9</sup> formalin killed cells of *P. gingivalis* strain 33277 emulsified in incomplete Freund's adjuvant (IFA; Sigma) on day 0. At day 21 mice were re-injected with the same dose and then bled 1 week later and evaluated for antibody levels. At day 35 mice all mice were challenged with approximately 2 x 10<sup>9</sup> cells of live *P. gingivalis* (ATCC 33277) by subcutaneous injection in the abdomen. Following challenge mice were monitored daily for weight loss and the size of the lesion measured for the next 10 days. Lesion sizes were measured by length and width and expressed as mm<sup>2</sup>. Groups were statistically analysed using a Kruskal-Wallis one-way ANOVA and were also individually examined using the unpaired t test or Mann-Whitney rank sum test using the Instat statistical package.

Figure 1 shows the results of one experiment at day 4 after challenge (lesions were at maximum size at this time point). Control mice immunised with *E. coli* lysate showed large lesions while mice immunised with killed cells of *P. gingivalis* strain 33277 were fully protected. This indicates that whole cells provide protection against *P. gingivalis* while *E. coli* protein immunised mice were not protected. Mice given the various PG recombinant proteins showed significant levels of protection for PG2, PG22, PG24 and PG29 (p<0.05 unpaired t test) while PG8A was not quite significantly different (p=0.07) compared to the *E. coli* control group.

Figure 2 shows the results of a separate experiment using combinations of recombinant proteins. Mice given PG1 + PG2 showed a significant level of protection compared to control mice give *E. coli* lysate (p<0.026 unpaired t test).

### Immunoscreening

Cloned candidates were cultured in 15ml of Terrific broth, induced with IPTG and sampled at 4h post-induction. One ml of culture was removed, pelleted and the cells resuspended in a volume of PBS determined by dividing the OD A<sub>600nm</sub> of the culture by 8. An aliquot of lysate (100µl) was added to 100µl of 2x sample reducing buffer (125mM Tris pH 6.8, 20% glycerol, 4% SDS, 80mM DTT, 0.03% bromophenol blue) and boiled for 10min. SDS-PAGE was performed according to the method of Laemmli UK. 1970 (Nature 227:680-685) using 4-20% 1.0mm Tris-Glycine gels (Novex) according to the manufacturers recommendations. Proteins were transferred

onto Hybond-C Extra nitrocellulose membranes (Amersham) by transblotting and the membranes were then blocked for 2h at room temperature (RT) in 5% skim milk in 20mM Tris, 0.5M NaCl, 0.05% Tween-20, pH 7.5 (TTBS).

Immunoscreening was performed separately with the rabbit  
5 anti-*P. gingivalis* whole cell serum, the rat protective serum, a pool of human periodontal patients serum, and in many cases an anti-T7-Tag antibody HRP conjugate (Novagen). Prior to use, the rabbit, rat and human sera were diluted 1/5000, 1/1000 and 1/500 respectively in 5% skim milk in TTBS and absorbed with 100µl (for the rabbit serum) or 250µl (for the rat and human  
10 sera) *E. coli* extract (20mg/ml; Promega) for 6h at RT.

Membranes were incubated overnight at RT with the absorbed antisera, or for 1 hr at RT with 1/5000 diluted anti-T7-Tag conjugate. Following 3x10min washes with TTBS, HRP-conjugated anti-rabbit (Silenus), anti-mouse (Silenus) or anti-human (KPL) antibody, diluted 1/5000 in 5%  
15 skim milk in TTBS, was added for 1h at RT. Membranes were washed as before, prior to addition of TMB membrane peroxidase substrate (KPL) for detection of immunoreactive proteins. Results of reactivity for the recombinant *P. gingivalis* proteins is shown in Table 7.

In addition some of the sera (pooled sera diluted 1/1000) from the  
20 mice immunised with *P. gingivalis* recombinant proteins (prior to challenge) were analysed for their reactivity against Western blots of whole native W50 *P. gingivalis* proteins using similar techniques as those outlined above. PG2, PG8A, PG29 and PG3 all showed bands at a similar molecular weight to that of the recombinant PG protein in the native W50 blot. This indicates that PG  
25 proteins are expressed in the W50 strain and that the recombinant proteins have at least some identical immunogenicity to the native proteins.

### m-RNA analysis

#### 30 Hot Phenol RNA Extraction

*P. gingivalis* W50 cells (150ml culture) were grown anaerobically to mid log phase (OD  $A_{600}$ =0.18) mixed with 50% glycerol and stored at -70°C until RNA extraction. Cells were pelleted by centrifugation at 6000g, and  
35 resuspended in 8ml ASE (20mM NaOAc, 0.5% SDS, 1mM EDTA). An equal volume of 20mM NaOAc(pH 4.5)-saturated phenol was added and mixed by

shaking for 30 seconds, incubated at 65°C for 5 minutes, followed by a further 5 second shaking and repeated incubation. After cooling, 2ml chloroform was added and mixed by shaking for 5 seconds, and the mixture spun at 10000g for 10 minutes at 4°C. The top aqueous phase was transferred and re-extracted by repeating the phenol and chloroform steps. The aqueous phase was transferred again and 100U RNase inhibitor (RNasin; Promega) were added. RNA was precipitated with 3 volumes 100% ethanol at -20°C overnight. The RNA precipitate was recovered by centrifugation at 10000g at 4°C for 15 minutes, then washed with 100% ethanol, dried and resuspended in 600µl sterile, deionised, dH<sub>2</sub>O with 1µl of fresh RNase inhibitor. RNA was aliquoted and stored at -70°C. The RNA concentration was determined spectrophotometrically. A formaldehyde RNA gel confirmed RNA integrity (Sambrook J. et al. 1989, Molecular Cloning. A laboratory manual. Cold Spring Laboratory Press, New York. 2nd Edition).

#### RT-PCR

The isolated RNA was used as a template for Reverse Transcription (RT) to produce cDNA. Varying RNA concentrations were used for the RT as each RNA transcript was potentially present at different levels. Subsequent amplification of the cDNA was performed using Polymerase Chain Reaction (PCR). RT-PCR was performed using GeneAmp® RNA PCR Kit (Perkin Elmer) according to the manufacturer's protocol with the following exception to the PCR; 35 cycles were performed as follows: Melt phase 95°C for 30 seconds, Anneal phase varied between 50-60°C for 30 seconds, Extension phase 72°C for 1 minute. Amplification was performed in a PTC-100 Programable Thermal Controller (MJ Research Inc.). As a control to demonstrate that the amplified product did not arise from contaminating DNA, Reverse Transcriptase (RTase) was omitted from a parallel tube. The PCR products were examined against DNA markers (GIBCO 1kB ladder) on a 1% agarose gel stained with ethidium bromide.

RT-PCR results are shown in Table 6 using the oligonucleotide primers as used in "Cloning, expression and purification of recombinant *P. gingivalis* genes" section described above, except for the following changes. For PG1 the 3' reverse primer used was



- GCGCCTCGAGATTCATTTTCCTTATAGAG, for PG4 the 5' forward primer was CTTCTTGTCGACTACAGCGGACATCATAAAATC and the 3' reverse primer was TTCCACCTCGAGTTAACGCAACTCTTCTTCGAT, for PG6 the 5' forward primer was TAAAGAATTCTGCCTCGAACCCATAATTGCTCCG, for PG10 the 5' forward primer was CGCGCATATGGATAAAGTGAGCTATGC and the 3' reverse primer was CGCGCTCGAGTTTGTGATACTCAATAATTC, for PG13 the 5' forward primer was GCCCGGCGCCATGCGGACAAAACTATCTTTTTTGCG and the 3' reverse primer was GCCCGGCGCCTTAGTTGTTGAATCGAATCGCTATTTGAGC. Amplification of *P. gingivalis* transcripts is a likely indication that RNA for a specific candidate is present and that the protein is produced. However, where there is no amplification achieved this does not indicate that this gene is never transcribed and may be the result of the culture conditions or the state of the cells when harvested.

Table 6. Expression of PG m-RNA with *in vitro* grown *P. gingivalis* W50. The symbols are + band visible on agarose gel, - no band present on agarose gel, ND not detected.

PG #	RNA µg	Annealing temp. °C	RT-PCR	PCR (-RT)	Approx. fragment size bp	Expected fragment size bp
1	0.15	55	+	-	1300	1362
2	1.0	50	+	-	3200	3051
3	0.15	60	+	-	720	690
4	2.9	55	-	-	N.D.	2000
5	0.02	50	+	-	1000	947
6	1.0	55	+	-	1000	972
8A	0.15	50	+	-	1200	1278
10	0.15	55	+	-	590	585
11	0.10	60	+	-	960	942
12	0.02	60	+	-	880	831
13	1.0	50	+	-	2150	2274
14	0.15	60	+	-	1050	996

PG #	RNA μg	Annealing temp. °C	RT-PCR	PCR (-RT)	Approx. fragment size bp	Expected fragment size bp
22	1.0	60	-	-	N.D.	228
24	1.0	55	+	+	1150	1194
29	0.15	60	+	-	880	885

**Table 7:** Immunoblot results of proteins expressed in *E.coli* against rabbit, rat and human antisera. Deduced MW was calculated from amino acid sequence of the *P. gingivalis* proteins, some of which had their N-terminal signal sequences removed. Apparent MW was determined from SDS-PAGE gels. The N- and C-terminal tags add approximately 2.5 KDa to the deduced MW of the recombinant proteins. The symbols are + positive, - negative, +/- weak positive, ND not done.

Protein number	Deduced MW (KDa)	Apparent MW (KDa)	Antisera reactivity			
			T7	Rabbit	Rat	Human
PG1	47.5	63	ND	-	-	-
PG2	112.4	125.7	ND	+	-	-
PG3	22.6	18.3	ND	- <sup>a</sup>	-	-
PG4	75	90.6	ND	-	-	-
PG5	34.9	43.8	ND	-	-	-
PG6	36.7	47.1	ND	-	-	-
PG8	67.5	63.1	ND	- <sup>b</sup>	-	-
PG8A	47.7	90.6	ND	-	-	-
PG10	21.3	25.5	ND	+	-	+
PG11	36.2	42.4	ND	-	-	-
PG12	30.7	30.6	ND	-	-	-
PG13	84.5	101	ND	-	-	-
PG14	36	42.4	ND	-	+	+
PG22	8.6	11.1	ND	-	-	-
PG24A	47	63.1	ND	-	-	-
PG29	31.1	40.9	ND	+	+	+

Protein number	Deduced MW (KDa)	Apparent MW (KDa)	Antisera reactivity			
			T7	Rabbit	Rat	Human
PG30	35.1	46.9	+	-	-	-
PG31	16.7	-	-	-	-	-
PG32	41.2	59.5	+	+	+	-
PG33	39.9	52.7	+	+	+	-
PG35	92.6	116.6	+	-	-	-
PG36	98.9	120.2	-	-	-	-
PG37	18.8	23.1	+	+	-	-
PG38	16.1	22.9	+	-	-	-
PG39	87.9	116.6	+	-	-	-
PG40	76.6	103.1	+	-	-	-
PG41	48.3	81.1	+	-	+	+
PG42	59.3	73.9	+	-	-	-
PG43	27.1	50.3	+	-	-	-
PG44	28.6	32.3	+	-	+	-
PG45	84	100.6	+	-	-	-
PG46	83	97.7	+	-	-	-
PG47	93.7	42.5	+	+	-	+
PG48	45.2	37.9	+	-	-	-
PG49	33.3	64.1	+	-	+	-
PG50	91.9	113.2	+	+	-	-
PG51	19.6	27.2	+	-	-	-
PG52	50.4	64.4	+	+	-	+
PG53	47.4	45.4	+	-	-	+
PG54	101.4	46.7	+	+	-	-
PG55	70.4	68.4	+	-	-	-
PG56	142.3	-	-	-	-	-
PG57	100	134.5	+	+	+	+
PG58	63	82.9	+	-	-	-
PG59	33.3	43.6	+	-	-	-
PG60	55.6	77.8	+	-	-	-
PG61	81.5	107.3	+	-	-	-

Protein number	Deduced MW (KDa)	Apparent MW (KDa)	Antisera reactivity			
			T7	Rabbit	Rat	Human
PG62	51.9	58.4	+	-	-	-
PG63	29.6	43.6	+	-	-	-
PG64	18.5	26.9	+	-	-	-
PG65	25.9	28.8	+	-	-	-
PG66	22.2	25.1	+	+	-	-
PG67	103.7	105	+	-	-	-
PG68	133.3	30.7	+	-	+	+
PG69	44.4	50.8	+	-	-	-
PG70	25.9	30.8	+	-	-	-
PG71	88.9	105.5	+	-	-	-
PG72	40.7	49.8	+	-	-	-
PG73	40.7	29	+/-	-	-	-
PG74	22.2	32.5	+	-	-	-
PG75	40.7	46.7	+	-	-	-
PG76	48.1	55.6	+	-	-	+
PG77	29.6	36.9	+	-	-	-
PG78	33.3	35.4	+	-	-	-
PG79	33.3	-	-	-	-	-
PG80	25.9	20.5	+	-	-	-
PG81	23	25.8	+	-	-	-
PG82	44.8	48.5	+	-	-	-
PG84	41.7	52.4	+	-	-	+/-
PG85	62.7	72.4	+	-	-	-
PG86	21.7	27.4	+	-	-	+/-
PG87	83	91.3	+	-	-	+
PG88	27	40.1	+	-	-	-
PG89	26.2	29.4	+	-	-	-
PG90	23	28.4	+	-	-	-
PG91	57.2	85.7	+	+	+	+
PG92	83.6	110.4	+	-	-	+
PG93	83.4	110.4	+	-	-	+

Protein number	Deduced MW (KDa)	Apparent MW (KDa)	Antisera reactivity			
			T7	Rabbit	Rat	Human
PG96	59.3	70.3	+	+	+	+
PG97	44.4	57.5	+	-	+	+
PG98	33.3	36	+	-	-	-
PG99	40.7	55.6	+	-	+	+
PG100	29.6	10.8	+	-	-	-
PG101	14.8	19.7, 14.1	+	-	-	-
PG102	59.3	70.3	+	-	-	+
PG104	40.7	57.5	+	-	-	+

- a. Positive reaction detected with the rabbit antiserum to sarkosyl insoluble
- 5 *P. gingivalis* antigen.
- b. Purified protein demonstrated weak positive reaction with the rabbit antiserum to whole *P. gingivalis*.

- 10 It will be appreciated by persons skilled in the art that numerous variations and/or modifications may be made to the invention as shown in the specific embodiments without departing from the spirit or scope of the invention as broadly described. The present embodiments are, therefore, to be considered in all respects as illustrative and not restrictive.

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- 30

## CLAIMS:-

1. An isolated antigenic *Porphyromonas gingivalis* polypeptide, the polypeptide comprising;  
an amino acid sequence selected from the group consisting of SEQ.  
5 ID. NO. 265 to SEQ. ID. NO. 528, SEQ. ID. NO. 531 and SEQ. ID. NO. 532; or  
an amino acid sequence at least 85%, preferably at least 95%, identical to an amino acid sequence selected from the group consisting of SEQ. ID. NO. 265 to SEQ. ID. NO. 528, SEQ. ID. NO.  
10 531 and SEQ. ID. NO. 532; or  
at least 40 amino acids having a contiguous sequence of at least 40 amino acids identical to a contiguous amino acid sequence selected from the group consisting of SEQ. ID. NO. 265 to SEQ. ID. NO. 528, SEQ. ID. NO. 531 and SEQ. ID. NO. 532.
- 15 2. A polypeptide as claimed in claim 1 in which the polypeptide comprises an amino acid sequence selected from the group consisting of SEQ. ID. NO. 265 to SEQ. ID. NO. 528, SEQ. ID. NO. 531 and SEQ. ID. NO. 532.
- 20 3. A polypeptide as claimed in claim 1 in which the polypeptide comprises an amino acid sequence at least 85%, preferably at least 95%, identical to an amino acid sequence selected from the group consisting of SEQ. ID. NO. 265 to SEQ. ID. NO. 528, SEQ. ID. NO. 531 and SEQ. ID. NO. 532.
- 25 4. A polypeptide as claimed in claim 1 in which the polypeptide comprises at least 40 amino acids having a contiguous sequence of at least 40 amino acids identical to a contiguous amino acid sequence selected from the group consisting of SEQ. ID. NO. 265 to SEQ. ID. NO. 528, SEQ. ID. NO. 531 and SEQ. ID. NO. 532.
- 30 5. A polypeptide as claimed in claim 1 in which the polypeptide comprises;  
an amino acid sequence selected from the group consisting of SEQ.  
ID. NO. 386 to SEQ. ID. NO. 528 and SEQ. ID. NO. 532; or  
an amino acid sequence at least 85%, preferably at least 95%,  
35 identical to an amino acid sequence selected from the group consisting of SEQ. ID. NO. 386 to SEQ. ID. NO. 528 and SEQ. ID. NO. 532; or

at least 40 amino acids having a contiguous sequence of at least 40 amino acids identical to a contiguous amino acid sequence selected from the group consisting of SEQ. ID. NO. 386 to SEQ. ID. NO. 528 and SEQ. ID. NO. 532.

5 6. A polypeptide as claimed in claim 1 in which the polypeptide comprises an amino acid sequence selected from the group consisting of SEQ. ID. NO. 386 to SEQ. ID. NO. 528 and SEQ. ID. NO. 532.

7. A polypeptide as claimed in claim 1 in which the polypeptide comprises an amino acid sequence at least 85%, preferably at least 95%,  
10 identical to an amino acid sequence selected from the group consisting of SEQ. ID. NO. 386 to SEQ. ID. NO. 528 and SEQ. ID. NO. 532.

8. A polypeptide as claimed in claim 1 in which the polypeptide comprises at least 40 amino acids having a contiguous sequence of at least 40 amino acids identical to a contiguous amino acid sequence selected from the  
15 group consisting of SEQ. ID. NO. 386 to SEQ. ID. NO. 528 and SEQ. ID. NO. 532.

9. A polypeptide as claimed in claim 6 in which the polypeptide comprises an amino acid sequence selected from the group consisting of SEQ. ID. NO. 386, SEQ. ID. NO. 424, SEQ. ID. NO. 425, SEQ. ID. NO. 434,  
20 SEQ. ID. NO. 447, SEQ. ID. NO. 458, SEQ. ID. NO. 475, SEQ. ID. NO. 498, SEQ. ID. NO. 499, SEQ. ID. NO. 500, SEQ. ID. NO. 501, SEQ. ID. NO. 387, SEQ. ID. NO. 400, SEQ. ID. NO. 411, SEQ. ID. NO. 419, SEQ. ID. NO. 420, SEQ. ID. NO. 427, SEQ. ID. NO. 429, SEQ. ID. NO. 433, SEQ. ID. NO. 437, SEQ. ID. NO. 438, SEQ. ID. NO. 443, SEQ. ID. NO. 444, SEQ. ID. NO. 448,  
25 SEQ. ID. NO. 449, SEQ. ID. NO. 452, SEQ. ID. NO. 455, SEQ. ID. NO. 457, SEQ. ID. NO. 459, SEQ. ID. NO. 461, SEQ. ID. NO. 462, SEQ. ID. NO. 463, SEQ. ID. NO. 467, SEQ. ID. NO. 468, SEQ. ID. NO. 469, SEQ. ID. NO. 482, SEQ. ID. NO. 484, SEQ. ID. NO. 485, SEQ. ID. NO. 494, SEQ. ID. NO. 508, SEQ. ID. NO. 509, SEQ. ID. NO. 510, SEQ. ID. NO. 520, SEQ. ID. NO. 521,  
30 SEQ. ID. NO. 522, SEQ. ID. NO. 525, SEQ. ID. NO. 526, SEQ. ID. NO. 528, SEQ. ID. NO. 389, SEQ. ID. NO. 390 and SEQ. ID. NO. 391.

10. An isolated antigenic *Porphyromonas gingivalis* polypeptide, the polypeptide comprising an amino acid sequence selected from the group consisting of SEQ. ID. NO. 386 to SEQ. ID. NO. 528 and SEQ. ID. NO. 532  
35 less the leader sequence set out in Table 3.



11. An isolated DNA molecule, the DNA molecule comprising a nucleotide sequence which encodes the polypeptide as claimed in any one of claims 1 to 10 or a sequence which hybridises thereto under conditions of high stringency.
- 5 12. An isolated DNA molecule as claimed in claim 11 in which the DNA molecule comprises a nucleotide sequence selected from the group consisting of SEQ. ID. NO. 1 to SEQ. ID. NO. 264, SEQ. ID. NO. 529 and SEQ. ID. NO. 530.
- 10 13. A recombinant expression vector comprising the DNA molecule as claimed in claim 11 or claim 12 operably linked to a transcription regulatory element.
14. A cell comprising the recombinant expression vector as claimed in claim 13.
- 15 15. A method for producing a *P. gingivalis* polypeptide comprising culturing the cell as claimed in claim 14 under conditions that permit expression of the polypeptide.
16. A composition for use in raising an immune response directed against *P. gingivalis* in a subject, the composition comprising an effective amount of at least one polypeptide as claimed in any one of claims 1 to 10 and a pharmaceutically acceptable carrier.
- 20 17. A composition as claimed in claim 16 in which the composition further comprises at least one DNA molecule as claimed in claim 11 or claim 12.
18. A composition as claimed in claim 16 or claim 17 in which the pharmaceutically acceptable carrier is an adjuvant.
- 25 19. A method of treating a subject for *P. gingivalis* infection comprising administering to the subject a composition as claimed in any one of claims 16 or claim 18 such that treatment of *P. gingivalis* infection occurs.
20. A method as claimed in claim 19, wherein the treatment is a prophylactic treatment.
- 30 21. A method as claimed in claim 19, wherein the treatment is a therapeutic treatment.
22. A composition for use in raising an immune response directed against *P. gingivalis* in a subject, the composition comprising an effective amount of at least one DNA molecule as claimed in claim 11 or claim 12 and a pharmaceutically acceptable carrier.
- 35

23. A composition as claimed in claim 22 in which the pharmaceutically acceptable carrier is an adjuvant.
24. A method of treating a subject for *P. gingivalis* infection comprising administering to the subject a composition as claimed in claim 22 or claim 23  
5 such that treatment of *P. gingivalis* infection occurs.
25. A method as claimed in claim 24, wherein the treatment is a prophylactic treatment.
26. A method as claimed in claim 24, wherein the treatment is a therapeutic treatment.
- 10 27. An antibody raised against a polypeptide as claimed in any one of claims 1 to 10.
28. An antibody as claimed in claim 27 in which the antibody is polyclonal.
29. An antibody as claimed in claim 27 in which the antibody is  
15 monoclonal.
30. A composition comprising at least one antibody as claimed in any one of claims 27 to 29.
31. A composition as claimed in claim 30 in which the composition adapted for oral use.
- 20 32. A nucleotide probe comprising at least 18 nucleotides and having a contiguous sequence of at least 18 nucleotides identical to a contiguous nucleotide sequence selected from the group consisting of SEQ. ID. NO. 1 to SEQ. ID. NO. 121, SEQ. ID. NO. 529 and sequences complementary thereto.
33. A nucleotide probe as claimed in claim 32 in which the probe further  
25 comprises a detectable label.
34. A method for detecting the presence of *P. gingivalis* nucleic acid in a sample comprising:
- 30 (a) contacting a sample with the nucleotide probe as claimed in claim 32 or claim 33 under conditions in which a hybrid can form between the probe and a *P. gingivalis* nucleic acid in the sample; and
- (b) detecting the hybrid formed in step (a), wherein detection of a hybrid indicates the presence of a *P. gingivalis* nucleic acid in the sample.

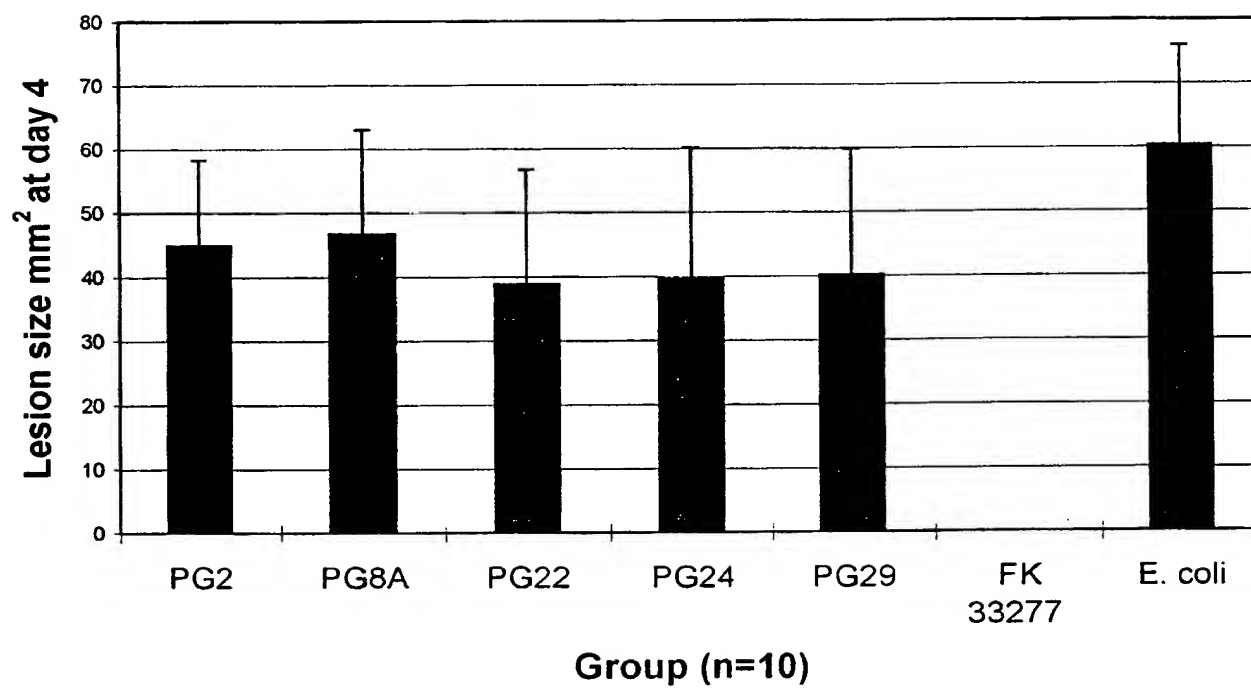


Figure 1

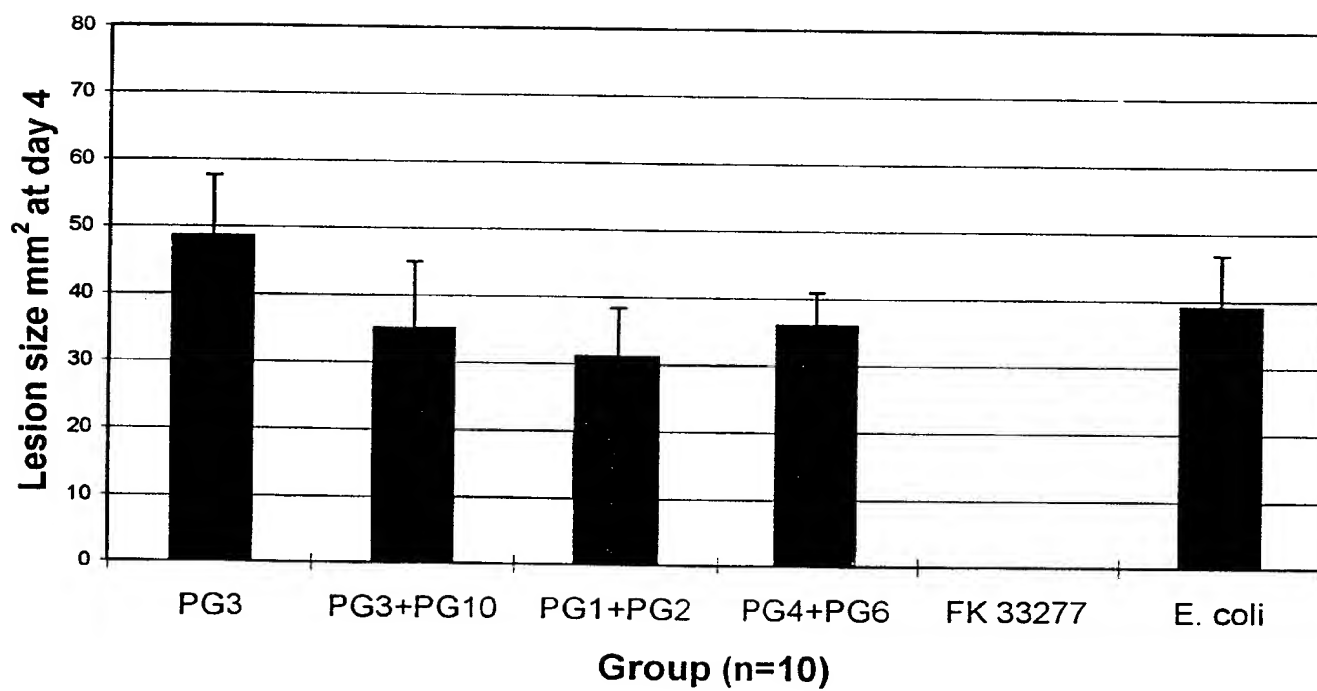


Figure 2

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## (2) INFORMATION FOR SEQ ID NO:1

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 1362 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:  
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:  
(A) NAME/KEY: misc\_feature  
(B) LOCATION 1...1362

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1

25	TTCTGTGTCA TGGCAAAAGT TATAAAAACA AAAAAAGGCC TTGCACTTAA TCTGAAAGGA	60
	AAACCGCTGC CCGAGATGCT GGCCGAACCG GCCCAAAGTC CTACTTACGC GGTGCTGCCC	120
	GACGATTTTG AAGGTGTTAT CCCCAAGGTG ACGGCTCGTC CGGGGGATAA GGTGCTGCCC	180
	GGCTCAGCAC TGATGCACCA CAAGGCATAT CCGGAGATGA AGTTTACAAG TCCGGTTAGC	240
	GGCGAAGTGA TCGCGGTGAA TCGCGGTGCC AAGCGCAAGG TGTTGAGCAT CGAGGTGAAA	300
	CCGGACGGAC TGAACGAATA CGAGTCATTC CCTGTGCGGG ATCCGTCTGC CCTCTCTGCC	360
30	GAACAGATCA AGGAGCTTTT ACTGTGCGAGC GGTATGTGGG GTTTTATTAA GCAACGTCCT	420
	TACGACATAG TGGGTACACC GGATATAGCT CCACGCGACA TTTATATTAC TGCCAACTTT	480
	ACTGCACCAT TGGTCCGGGA CTTGATTTTC ATCGTTCGAG GAGAAGAACG CGCCTGCGAG	540
	ACTGCCATCG ATGCCTTGGC CAAACTCACG ACAGGAAAGG TGATGTGGG CCTGAAGCCG	600
	GGTTCATCTC TGGGCTTGCA CAATGCAGAA ATCGTAGAAG TACACGGACC TCATCCGGCA	660
35	GGTAACGTGG GCGTGCTGAT CAATCATACG AAGCCAATCA ATCGGGGCGA AACGGTGTGG	720
	ACGCTCAAGG CTACCGACCT GATCGTGATC GGACGTTTCC TGCTTACGGG CAAAGCCGAT	780
	TTTACCAGAA TGATTGCCAT GACCGGCTCA GACGCTGCAG CTCACGGATA CGTCCGTATT	840
	ATGCCGGGTT GCAATGTCTT TGCTTCCTTC CCCGGCCGAC TGACAATAAA GGAATCTCAC	900
	GAGCGTGTGA TCGATGGCAA TGTGCTGACC GGTAAAGAGC TCTGCGAGAA GGAGCCTTTC	960
40	CTGTCAGCCC GGTGTGACCA GATCACGGTG ATCCCGAAG GCGACGATGT GGACGAACTC	1020
	TTCCGGTGGG CTGCACCCCG TCTCGATCAG TACAGCATGA GCAGAGCTTA TTTCTCTTGG	1080
	TTGCAGGGGA AAAACAAAGA GTACGTACTC GATGCCCGGA TCAAGGGTGG CGAACGTGCT	1140
	ATGATCATGA GCAACGAGTA TGACCGCGTT TTCCCGATGG ACATCTATCC GGAGTATTTG	1200
	CTCAAGGCTA TTATAGCATT CSACATCGAC AAGATGGAGG ACTTAGGCAT ATATGAAGTG	1260
45	GCTCCGGAGG ACTTTGCCAC TTGCGAATTT GTGGATACAT CCAAGATCGA GCTGCAGCGT	1320
	ATCGTTCGGG AGGGCTTGA TATGCTCTAT AAGGAAATGA AT	1362

## (2) INFORMATION FOR SEQ ID NO:2

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 603 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:  
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:  
(A) NAME/KEY: misc\_feature  
(B) LOCATION 1...603

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2

50	GAACAAAGCA AGTGTACAT GGATAAAGTG AGCTATGCTC TGGGATTGAG CATCGGTAAT	60
	AATTTCAAGT CTTGGGGCAT CGACAGCGTC GTTATGGATG ATTTTCATGCA AGTCTGTCT	120
	GATGTAAGTG AAGAAAAAGC CCCTCAGCTC TCGTATGACG AGGCCAAGCG CGAAATAGAG	180
75	GCGTATTTCA TGGATTTGCA GCAGAAGGCT GTCAAACTGA ACAAAGAGGC CGGAGAAGAA	240

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5 TTCCTCAAGA TAAATGCACA CAAGGAAGGT GTGACGACCT TACCGAGCGG CTTGCAATAC 300  
 GAAATCATTA AGATGGGAGA GGGCCCCGAAA CCCACCCCTT CGGACACGGT AACCTGTCAT 360  
 TATCACGGTA CGCTCATCAA CGGTATCSTT TTCGATAGCT CTATGGACAG GGGAGAACCG 420  
 GCCAGTTTCC CTCTAAGAGG AGTTATAGCC GGCTGGACGG AGATTCTTCA ATTAATGCCT 480  
 GTAGGATCCA AGTGGAAAGT AACTATACCG AGCGATCTGG CGTATGGAGA TCGTGGTGCC 540  
 GGCGAACATA TCAAACCGGG TAGTACGCTC ATTTTATATA TCGAATTATT GAGTATCAAC 600  
 AAA 603

10 (2) INFORMATION FOR SEQ ID NO:3

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 837 base pairs  
 (B) TYPE: nucleic acid  
 15 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- 20 (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:  
 25 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:  
 (A) NAME/KEY: misc feature  
 (B) LOCATION 1...837
- 30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3

35 CAAAAAACA AACGAAAGAT GAAAAAAGCA TTACTTATTG GTGCTGCTCT TTTGGGAGCA 60  
 GTCAGTTTTG CAAGTGCTCA GTCTTTGAGC ACAATCAAAG TACAGAACAA TTCAGTACAG 120  
 CAACCTCGTG AGGAAGCCAC TATTCAGGTT TGTGGAGAAT TGGCAGAGCA AGTTGACTGC 180  
 ATTGGGACAG GTAATTCTGC AATCATAGCC GCTGCAGCGA AATTTGAAAG CGATGATCTC 240  
 GAAAGCTATG TTGGCTGGGA GATCATGAGT GTTGATTCT TCCCTGGATA TAAAGCGTGC 300  
 AAGTACACAT CTGCAGTCTG GGCTGATGAT ATGACCATTT TGGGCCAATC AGAAGATAGT 360  
 GATCCCGAAA TGCAGACTAT CAACAATCTT GCTCTCAAGA CTAGTGTCAG GATTGAAGCC 420  
 40 GGCAAGAATT ACATAGTTGG TTATATTGCT AATACCGCAG GTGGACATCC TATCGGATGT 480  
 GATCAGGGCC CTGCCGTTGA TGGTTATGGA GATTTGGTTT CTATATCAGA AGATGGTGGT 540  
 GCTACTTTCC CTCCGTTTCA ATCTCTTCAT CAAGCAGTTC CTACCTTAAA TTACAACATC 600  
 TATGTCGTTG TTCATTTGAA GAAGGGTGAA GGTGTTGAGG CTGTTCTTAC CAACGACAAG 660  
 GCTAATGCTT ATGTTTCAGAA TGGCGTTATC TATGTAGCCG GAGCTAATGG TCGTCAGGTA 720  
 45 TCTCTGTTCC ACATGAACGG TAAGGTGTT TATACCGGCG TTAGCGAAAC GATTGCAGCT 780  
 CCTCAGAAGG GCATGTATAT CCTCCGTGTA GGTGCTAAGA GCATCAAGCT GGCTATC 837

50 (2) INFORMATION FOR SEQ ID NO:4

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 471 base pairs  
 (B) TYPE: nucleic acid  
 55 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- 60 (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- 65 (ix) FEATURE:  
 (A) NAME/KEY: misc feature  
 (B) LOCATION 1...471
- 70 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4

75 CGTGnATTCC TGCCGGAGAA AGCTCTCTAT ATCGGCTGCC GCGTGGAGAC GCAAGAGGGG 60  
 CATGCCGTAG GTTTCGGACT GGATGACGGC CCTGCGATGA AAGGCAAGGG CGATCTGGTC 120  
 GGGAGCTATC TTCCCGGTGC TGCTCCGATG CCTTTTGTCC CGCTTTCTGA TATTCGGGCT 180  
 CGTTCGATGG ATGCCAATTT TTATATCTAT TCTCGTATTT CACTGGGTTC GGGCACGCA 240

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GATGTTCTCC AGCATAGGAT GAAAGTGTAT CCCAACCCCTG CCACGACGGA GCTGCATGTG 300  
 GAAGCCCTGT CCGCATGGGT GGGCGAGCAG GCTGCGGTAT ATGATATGCG TGGTCGTGCG 360  
 GTATCGGCTC GGACGGTGGA TAGCGAGAAG CTGTGCATCG ACATTGCCTC ACTGCCCGTG 420  
 GGCGTCTATA TGCTGCGCAT CGGCAGCTAC TCGGCCAAGT TCGAGAAGAG A 471

5

## (2) INFORMATION FOR SEQ ID NO:5

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1686 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...1686
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5

30 ACAAGAAATG TTTCACTCAT AAAAATGCCA AGAATTATGA AATTAAAAAT TGCACTCAGA 60  
 CTGCTGCTGG CGACTTTTGC CATAGTTTTA TTTAGCCCTC TGGCCAAGGC CCAGATGGAT 120  
 ATTGGTGGAG ACGATGTATT GATCGAGACG ATGTCCACCC TATCAGGATA TTCAGAGGAT 180  
 TTTTATTACA AGATGGCTGT GGCAGACAAT GGATGGATCT ATGTGATGTT GGATTTCTCT 240  
 CGTATTTAT TTTGATGATG CAGGCTGTAT CGTTCCAAAG ACGGTGGTGC TACTTACCAA 300  
 35 AAGTTAGGGT CTTTGGGGTC TTTGGTGCCT TATGACTTCG ATGTCTCGCA TTGCGATTTT 360  
 ATTGTAACGG GAAAGGATGA AGATGATATC AATGTTTGGG CAGTCATGAC AGCATTCGAA 420  
 TATGTAGGTG GTACTATTGG CAATGGCGTT TTGCTGATGC ATCGCCATGA TGCAGATATC 480  
 AATAATACAG AGTGTGTGTA CAAGAAGGAT TTCCCTAATA ATAGACTGAT GGGTGTAGCC 540  
 ATCGCCTCCA ACTACCGTGC GCCCTCTCCT TACGGTTTGG GGGGCGATCC TTTTGCTCTC 600  
 40 GCTGTGCGCC TTAGTGGCTC CGGAAGCGAT CACAGCTTCT TGGACTATAT TTTTTCGTTA 660  
 GATGGTGGAG TACACTTTGA GCAAAAGCGT ATTTACACAA GACCCCAAAA ACTGACTATC 720  
 AATAGAGTAG ACCTTTCATT AGGCAGTACA TCTCCTTCTC TTGGATTAA TACTTGGCCA 780  
 CTAATGGGAG TCGTATTCGA AATGAATAAG AACCTTGATG GCTTCGACAT TGGTTTCATT 840  
 TCCAACTTTG TGGACTATGA TCCCCTCTAT GCGTGGTCTG AACCGATAAT AATAGAAGAA 900  
 45 GACTGTGGAT GGAATGATT TAATCCTTTG GGAGCACTAA GTATAGAGAT CCAATGATG 960  
 TTGGATGACA ATTCCGATAA TACCGTGGGT GGAGAACGCT CCCATAACTT CCTGATCACT 1020  
 TACCCGGGCC ATTACGTATA TCCGAAGCAA TCTTTCAATT ATTCTCCCGG ACATACACCG 1080  
 ACAAGAAAG ATCTGGTCTT TAAACACTGT ATAGGTATTC CGGCTTTGGC ATACGATAAG 1140  
 50 GAAGGCGATC GTTATCTGAC TACTTTTCAA GATCACAATC TAATGAGATA CAGATGGATC 1200  
 AAATACGATG ACATTAACTC TTTTATGGT TGGAGTTGGC CATATGTATA TGCAAAAGAA 1260  
 GCTAAAGATA AAAAGAGGCG CCGTCCGCAA GTAGCACTCA ATCCTACCAA TGGAAAGGCT 1320  
 TGT'TGGGTAT GGCATACTCG CAAGAGCCCA TATGATGAAA CCAAACCACA TCCTACTCCT 1380  
 GTAATTATTA AACATTTTCT ATGGTCCGAT ACGGAGTGGG TACATGCTCT GGACGTGGGG 1440  
 55 GACGTATTGC AGAAGGAGGG TAGCATGAAG CTCTACCCCA ATCCTGCCAA AGAATATGTT 1500  
 CTGATCAACC TACCCAAAGA AGGGGGGCAC GAGGCAGTCG TATACGACAT GCAGGGCCGA 1560  
 ATCGTGGAGA AAGTTTCATT TTCAGGGAAA GAATATAAGC TGAATGTGCA GTATCTGTCC 1620  
 AAAGGTACGT ACATGCTGAA AGTGTAGCG GATACGGAGT ATTTCTGTGA AAAAATCATT 1680  
 GTAGAG 1686

60

## (2) INFORMATION FOR SEQ ID NO:6

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1173 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:

75

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(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc feature

(B) LOCATION 1...1173

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6

10 CAAATGAAAC GATTACTCCC CTTTCTCCTT TTAGCAGGAC TCGTAGCCGT AGGAAACGTG 60  
TCTGCTCAGT CACCCCGAAT CCCTCAAGTG GATGTACACA CTCGCATCGC AAGAAATGCC 120  
CGTTATCGAC TGGACAAGAT CAGTGTCCCG GATTCTCGTC AGATATTCGA TTAATTCTAT 180  
AAAGAAGAAA CGATACCCAC TAAATACAA ACCACCACAG GAGGTGCAAT TACAAGCATC 240  
GATTGCTTTT TCTATGAAGA CGACAGGTTG GTTCAGGTGC GCTATTTTGA CAATAACCTT 300  
15 GAATTAAGAA AAGCGGAGAA GTATGTATAC GACGTTCTA AGCTGGTCTT TCGAGAAATT 360  
CGCAAGTCGC CGACAGACGA AACGCCAATA AAGAAAGTTA GCTATCACTA TCTCTGTGGC 420  
AGCGATATGC CTTTGTAGAT TACGACAGAG ATGAGCGATG GCTATTTTGA AAGCCATACG 480  
CTTAACATATC TGAATGGAAA GATTGCCCGA ATAGATATCA TGAATCAACA GAACCCATCG 540  
GCCGAATTGA TCGAAACGGG TAGAATGGTA TAGGAGTTTG ATGCCAATAA TGATGCTGTA 600  
CTGCTTCGTG ACAGTGTATT TCTTCTCTT CAAAACAAGT GGGTAGAAAT GTTACTCAC 660  
20 CGTTATACAT ACACAATAA GCATAATTGT ATTCGTTGGG AACAGACGA ATTCGGCACC 720  
CTCACCTTGG CCAACAACCT CGAATACGAC ACCACTATCC CTCTGTCGTC TGTATTGTTT 780  
CCACGCGATG AGGAGTTCTT CCGTCTCTT CTCCCAATT TTATGAAGCA TATGCGTACG 840  
AAGCAAACST ATTTCAATAA CTCGGGAGAA GGCTTGTGAG AGGTATGCGA TTACAACACT 900  
TTCTATACCG ATATGACGGG TAATGCACTG ACCGATGTTG CCGTGAACGA ATCGATCAAG 960  
25 ATTTATCCTC GTCTGCGCAC GGATTTTCTG CGTATAGAAG GTTCGCAACT GCTTCGCTT 1020  
TCGTATTTCG ACATGAACGG GAAGCTCATC AGAGCTACCG AATTGACAGG CGATTTGGCC 1080  
ATTATCGGAG TTGCATCTCT TCCGAGAGGC ACTTACATCG CAGAAATAAC TGCTGCAAA 1140  
AGCAAAACCA TACGTGCAAA AGTATCGCTC AGA 1173

30

(2) INFORMATION FOR SEQ ID NO:7

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1284 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

35

(ii) MOLECULE TYPE: DNA (genomic)

40

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

45

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc feature

(B) LOCATION 1...1284

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7

55 AAGAGGAATC CCTTACCTTT GACGGCATCA AATCGAAAGA TTTTATAAAA AATGAGACAG 60  
CATTATATCT TATTTCCTTT TATCTTGTTT CTGCTTCTTG CCTTCTCTTA TGTCGGTTGC 120  
AGAACAGTCC GACAAACACC TAAGCAGTCG GAACGGTACG TCGTAGTCTT GTCTTTGGAC 180  
GGCTTCCGAC CGGACTATAC CGATCGGGCA CGTACACCGG CGTTGGATCG GATGGCACAG 240  
GAGGGATTGA GCGGGTCGCT CCAACCATGC TTCCCTCTGC TTACATTTC CAATCATTAC 300  
60 AGCATGGCTA CGGGGCTTTA CCCCATCAT CACGGTATCG TAGCCAATGA GTTTGTGGAT 360  
TCGCTACTGG GCATCTTTTG TATATCCGAC CGAAAAGCCG TGGAGACCCC CGGATTTTGG 420  
GGCGGCGAGC CGGTTTGGA TACGGCCGCA CGCCAAGGCA TCCGTACCGG TGTCTACTTT 480  
TGGGTAGGAT CCGAAACGGC TGTGAACGGA AATCGGCCGT GGCGGTGGAA AAAATTCTCC 540  
TCCACCGTTC CGTTTCGTGA CCGTGCCGAC TCCGTCTATG CGTGGCTCGG ACTGCCCGAA 600  
AAGGAGCGAC CGCGCTTGCT CATGTGGTAC ATCGAGGAGC CGGATATGAT CGGACACAGC 660  
65 CAAACGCCCG AAAGCCCGCT GACACTGGCA ATGGTAGAGC GGTGGACAG TGTGGTCGGC 720  
TATTTCCGCA AGCGGTTGGA CTCTCTGCC ATAGCCGCA AGACCGACTT CATCATAGTA 780  
TCCGATCAGC GTATGGCCAC GTACGAAAT GAGAAATGT TCAATCTGTC GCATTATCTG 840  
CCTGCGGACA GTTTCCTCTA CATGGCCACC GGGGCTTCA CCCACTTGTA CCCGAAGCCC 900  
TCCTATACCG AGCGAGCCTA TGAGATCTTG CGGGCCATTC CACATATATC GGTTTACCGC 960  
70 AAGGGGGAGG TGCCCAAGCG TTTGCGCTGT GGCACCAATC CTCGTTTGGG CGAACTGCTC 1020  
GTGATTCCGG ACATAGGCTC CACCGTCTTT TTCGCAATAA ATGAAGACGT TCGTCCGGGA 1080  
GCCGCACATG GCTATGACAA CCAAGCACCG GAAATGCGGG CTTTACTCCG GCTGTGCGGA 1140  
CCGATTTTCC GTCCGGGCG TAGGGTGGAA AACCTGCCGA ATATCACCAT CTATCCGCTC 1200  
ATATGCAGGC TGTGCGGTAT AGAGCCTGCA CCCAACGATG CGGACGAAAC GTTGCTGAAC 1260  
75 GGCTGATCC GAGACAAACG ACCA 1284



## (2) INFORMATION FOR SEQ ID NO:8

- 5 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 846 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
10 (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- 15 (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:  
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- 20 (ix) FEATURE:  
(A) NAME/KEY: misc\_feature  
(B) LOCATION 1...846

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8

25 CTTTCCCGTG GAGTTTTTCC CCTGATGTAT GGCCGAAGAG GAAGCATTCTG TGCCTCTTCA 60  
GGGCATAGGG ACAAATTTT TAAGAATACA ATTATCAGAT TTATCACAAT GAAAGTAGGT 120  
TTGTTTCATCC CCTGTTATGT CAATGCAGTG TATCCGGAAG TGGGTATCGC CACGTACAAA 180  
CTGCTGAAGA GTTTGGACAT AGATGTCGAC TACCCGATGG ATCAGACATG TTGCGGCCAG 240  
30 CCTATGGCCA ATGCCGGATT CGAACAGAAA GCTCAAAAGC TGGCTTTGCG ATTCTGAAGAG 300  
CTGTTCTGAGT CGTATGATGT AGTCGTAGGG CCATCGGCCA GTTGCCTTGC TTTCGTGAAA 360  
GAAAACTATG ATCATATCCT CAGACCGACA GGACATGTCT GCAAGTCGGC AGCCAAGGTT 420  
CGGGATATAT GCGAGTTCTT GCACGATGAC CTGAAGATCA CCAGCCTCCC CTCCCGATTCT 480  
35 GCCCATTAAGG TGAGCCTGCA CAACAGTTGC CACGGTGTGC GCGAACTGCA TCTGTCCACC 540  
CCAGTGAAG TGCACCGACC GTACCACAAC AAGGTGCGCC GGCTATTGGA GATGGTGCAG 600  
GGCATAGAGG TATTCGAGCC GAAGCGAATA GACGAATGCT GCGGTTTCGG CGGTATGTAC 660  
TCGGTGGAGG AGCCGGAGGT ATCCACCTGT ATGGGGCATG ACAAGGTGCT GGATCACATA 720  
TCCACAGGTG CCGAGTACAT CACAGGGCCG GACAGCTCGT GCCTCATGCA TATGCAGGGA 780  
40 GTGATAGACA GAGAGAAATT GCCGATCAAG ACAATTCATG CAGTAGAAAT TTAGCAGCA 840  
AACTTA 846

## (2) INFORMATION FOR SEQ ID NO:9

- 45 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 753 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
50 (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- 55 (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:  
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- 60 (ix) FEATURE:  
(A) NAME/KEY: misc\_feature  
(B) LOCATION 1...753

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9

65 CCTCTGAAAA AACGAATGGA TATTGTAAGT ATGGCCGATA AAGCTCTTGT AGTGGAGATG 60  
AGAGATGTGA CGCTCTGTCA GGAGGAAAAC GTCATTTTTC AAAATTTGAA TCTGACCCCTT 120  
TCCGCCGGAG ACTTCGTCTA TCTGATAGGC TCAGTGGGAT CGGGGAAGAG CACTTTGCTG 180  
AAGGCTTTGT ATGCTGAGGT GCCTATCTCT GCCGGTTATG CCCCGTGAT AGATTATGAT 240  
70 CTGGCAAAGT TGAAACGGAA GCAAGTGCCC TATCTGCGCA GGAATTTGGG CATTGTGTTT 300  
CAGGATTTCC AGTTGCTGAA CGGACGTACT GTTGGGAGA ATTTGGATTT CGTTTTCGCA 360  
GCTACGSACT GGAAGAACCG AGCCGATCGC GAGCAGCGTA TCGAGGAGGT TTTGACCCGT 420  
GTGGGAATGT CTCGGAAGGC TTATAAGAGA CCGCACGAAC TGTCGGGAGG GGAGCAACAA 480  
CGTGTGGSTA TAGCCAGAGC TTTGCTGGCG AAGCCTGCGT TGATCCTGGC CGACGAACCC 540  
75 ACAGGCAACC TCGATTCCGT GACCGGATTG CAGATCGCTT CTCTGCTCTA CGAAATCAGT 600

AAGCAGGGCA CTGCACTACT TATGAGCAGC CACAACAGCA GCCTGCTGTC GCATCTGCCG 660  
GCACGGACAT TGGCCGTTTC TAAGAATGGC GATGCCTCCT CTTTGGTCGA GCTGAGTGCA 720  
GATGCTGTTT CAAGAAAAA TACGGAATA GAT 753

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(2) INFORMATION FOR SEQ ID NO:10

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 714 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: circular

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(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

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(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

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(A) NAME/KEY: misc\_feature  
(B) LOCATION 1...714

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10

30 ACCAGGCATT GTCCGGCTTG TCGCTCTTCC TTTCACCTCA TAAAAACAAG TAAAAACAATG 60  
ATTGAAATCA GCAACCTCAC CAAGGTTTTC AGAACAGAAG AAATAGAGAC GGTAGCCCTC 120  
GATGGCGTAT CGCTCAAAGT GGACAAAGGC GAATTTATCG CCATAATGGG GCCTTCGGGA 180  
TGCGGTAAAT CCACTCTGCT CAATATCCTC GGCTTCTCG ACAATCCAC TTCCGGTATC 240  
TACAAGCTCG ATGGGGCAGA AGTGGGCAAC CTCGGGAAA AAGACAGGAC TGCCGTCCGT 300  
AAGGGCAATA TCGGCTTCGT ATTCCAGAGC TTCAACCTCA TCGAAGAGAT GACGGTAAGC 360  
35 GAGAACGTGG AGTTGCCGCT CGTCTATCTG GGTGTGAAGG CCTCCGAGCG GAAAGAGCGA 420  
GTGGAGGAGG CACTGCGCAA GATGAGCATC AGCCACCGGG CCGGCCACTT CCCCAATCAG 480  
CTCTCCGGAG GACAACAGCA GCGCGTGGCT ATCGCCCGTG CCGTGGTGGC CAATCCGAAG 540  
CTCATCTCG CCGATGAACC CACGGGTAAAC CTCGACTCCA AAAACGGAGC CGATGTCATG 600  
40 GAACTGCTCA GAGGTCTCAA TCGCGAAGGT GCAACCATCG TCATGGTGAC GCACTCCGAG 660  
CACGATGCAC GTAGTGCCGG CCGCATCATC AATCTGTTCG ACGGTAAGAT TCGC 714

(2) INFORMATION FOR SEQ ID NO:11

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(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 1812 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: circular

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(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

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(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

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(ix) FEATURE:

(A) NAME/KEY: misc\_feature  
(B) LOCATION 1...1812

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11

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AGCACAGAAA CAAATAGCAA ATCTGAAATG AAAGAATTTT TCAAAATGTT TTTCGCCTCG 60  
ATCCTCGGGG TTATAACGGC AGGAATCATC TTGTTCTGTA TCTTTCTATT TATCTTTTTC 120  
GGCATCGTAG CCGGTATTGC CTCCAAGGCA ACGGGAGGAA CCATTCCGAA GATCGAAGCA 180  
70 AACTCCATCC TACATATANA CAATTCCTCT TTCCCTGAGA TCGTATCGGC CAATCCCTGG 240  
AGCATGCTCA CAGGCAAAGA CGAGTCCGTA TCGCTCTCAC AGGCAGTCGA AGCCATCGGC 300  
CAAGCCAAA ATAATCCCAA CATAACCGGT ATCTTCTCG ATCTGGACAA CCTTCCGTG 360  
GGTATGGCAT CGGCAGAGGA ATTGCGTCGC GCGTTGCAGG ATTTCAAGAT GTCGGGCAAG 420  
TTCGTCTGAT CCTATGCCGA CAGATACACC CAAAAGGGT ACTACCTCTC CAGTATTGCA 480  
75 GACAACTCT ACCTCAATCC GAAAGGAATG TTGGGGCTTA TCGGGATTGC GACCCAAACA 540  
ATGTTCTACA AAGATGCCCT CGACAAATC GCGGTGAAGA TGGAGATCTT CAAGGTAGGC 600

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ACCTACAAGG	CAGCCGTAGA	GCCATTCATG	CTCAACAGGA	TGAGCGATGC	CAATCGCGAA	660
CAAATCACCA	CATACATAAA	CGGGCTTTGG	GACAAGATCA	CATCCGATAT	TGCAGAGTCG	720
CGCAAGACGG	CAATGGATTG	CGTGAAAATG	TTTGCCGACA	AAGGCGAAAT	GTTCGGTCTT	780
GCCGAGAAAG	CGSTGGAGAT	GAAGCTCGTG	GATGAGCTGG	CTTACCGTAC	CGATGTGGAG	840
AAAGAACTCA	AAAAGATGTC	CCAACGCGGA	GAGAAAGATG	AACTTCGGTT	CGTATCGCTT	900
TCTCAGGTTT	TGGCCAATGG	CCCGATGAAC	AAAACGAAAG	GCAGTCGGAT	CGCCGTTCTC	960
TTTGCCGAAG	GTGAAATAAC	GGAAGAAATA	ATAAAGAAGC	CGTTCGACAC	TGACGGTAGC	1020
TCCATCACAC	AAGAACTCGC	CAAAGAAATC	AAGGCAGCAG	CCGATGACGA	TGATATCAAA	1080
GCCGTAGTAC	TTCTGTGCAA	TTCTCCGGGA	GGTAGTGCTT	TCACTTCCGA	ACAGATATGG	1140
AAGCAGGTAG	CCGATCTCAA	GGCCAAAAG	CCTATCGTGG	TCTCCATGGG	CGACGTAGCA	1200
GCCTCGGGCG	GATACTACAT	AGCCTGCGCA	GCCAACAGTA	TCTGTGGCAGA	GCATACGACT	1260
CTGACCGGCT	CCATCGGCAT	ATTCTGGCAT	TTCCCGAACT	TCCGCGGCGT	AGCCAAGAAG	1320
ATAGGAGTGA	ATATGGACGT	CGTACAGACA	TCCAAGTAGT	CAGACTTGGG	CAACACCTTC	1380
GCTCCGATGA	CGGTGGAAGA	TCTGTCCCTC	ATCCAACGCT	ACATAGAGCA	GGGCTACGAC	1440
CTCTTCTCTCA	CTCGCGTATC	GGAAGGCCGC	AACCGCACCA	AGGCACAGAT	CGACAGCATC	1500
GCTCAAGGCC	GTGTATGGCT	CGGCGACAAA	GCTCTTGCAAC	TCCGTTTGGT	GGATGAGCTT	1560
GGAGTTTTGG	ACACAGCTAT	CAAACGGGCC	GCGAAGCTGG	CTCAGCTCGG	TGGCAACTAC	1620
AGCATAGAST	ATGGCAAGAC	CAAGCGCAAC	TTCTTCGAAG	AGTTGCTCTC	CTCATCAGCA	1680
GCGGATATGA	AGTCTGCCAT	CCTGAGTACC	ATTCTCTCCG	ATCCGGAAT	AGAAGTTCTG	1740
CGCGAACTCC	GCTCCATGCC	GCCCCGTCTT	TCCGGCATAC	AGGCACGTCT	CCCCATTATC	1800
TTTCATGCCGT	AC					1812

25 (2) INFORMATION FOR SEQ ID NO:12

30 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 972 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: circular

35 (ii) MOLECULE TYPE: DNA (genomic)

40 (iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:  
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

45 (ix) FEATURE:  
(A) NAME/KEY: misc feature  
(B) LOCATION 1...972

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12

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CTAACGTGT	TTTGTGCAA	CTATTTCAA	CAGATGAGAG	CAAACATTTG	GCAGATACTT	60
TCCGTTTCGS	TTCTCTTTT	CTTCCGGACA	GCGATCGGAC	AGGCTCAGAG	TCGAAACCGT	120
ACATACGAGG	CTTATGTGAA	ACAGTACGCC	GACGAAGCTA	TCCGACAGAT	GAGCCGCTAC	180
AATATACCGG	CAAGCATCAC	CATAGCACAG	GCTTTGGTGG	AGACAGGAGC	CGGAGCCAGT	240
ACACTGGCCA	GCGTACACAA	CAATCACTTC	GGGATCAAAT	GCCACAAATC	GTGGACGGGC	300
AAGCGCACCT	ATCGTACCGA	CGATGCGCCG	AACGAATGCT	TCCGACAGCTA	TTCCGCGGCT	360
CGCGAATCGT	ATGAAGATCA	TTCCCGATTT	CTGCTCCAAC	CACGCTATCG	TCCCTGTGTC	420
AAACTCGACA	GAGAAGACTA	TCCGGGCTGG	GCTACGGGGT	TGCAACGCTG	TGGCTATGCC	480
ACCAATCGGG	GCTATGCCAA	TCTGCTGATC	AAGATGGTGG	AGCTGTATGA	GCTATATGCT	540
TTGGATCGCG	AGAAGTACCC	CTCATGGTTC	CACAAGTCTT	ACCCCGGGTC	CAACAAAAAA	600
TCCATCAAAA	CGACCAAGCA	GAAGCAGAGC	GGACTCAAGC	ACGAAGCTTA	CTTCAGCTAC	660
GGACTGCTCT	ACATCATAGC	CAAGCAAGGC	GATACCTTCG	ATTCTTTGGC	CGAAGAGTTC	720
GACATGAGAG	CCTCCAAACT	GGCCAAATAC	AACGATGCTC	CCGTGGATT	CCCGATCGAA	780
AAGGGCGATG	TGATCTATCT	GGAGAAAAAG	CACGCATGCT	CCATCTCCAA	ACACACACAG	840
CACGTAGTGC	GTGTGGGCGA	TTCCATGCAC	AGTATCTCCC	AACGCTATGG	CATCCGGATG	900
AAGAACCCTCT	ACAAAGCTCAA	CGACAAGGAT	GGCGAATATA	TACCCCAAGA	GGSCGATATA	960
CTGCGCTTGC	GC					972

70 (2) INFORMATION FOR SEQ ID NO:13

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 1599 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: circular

75 (ii) MOLECULE TYPE: DNA (genomic)

- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- 5 (vi) ORIGINAL SOURCE:  
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:  
(A) NAME/KEY: misc feature  
10 (B) LOCATION 1...1599
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:13
- |    |            |             |            |             |             |            |      |
|----|------------|-------------|------------|-------------|-------------|------------|------|
| 15 | AGGATCCCCG | ACGAGCAGAC  | CGGACGTATC | ATGGACGGAC  | GTCGATATTC  | GGATGGCCTC | 60   |
|    | CATCAGGCTA | TGGAAGCCAA  | AGAGCATGTG | AAAGTAGAGG  | CTGCGACACA  | GACATTTGCA | 120  |
|    | ACTATCACTT | TGCAGAACTA  | TTTCCGCATG | TATCATAAGC  | TGGCAGGGAT  | GACCGGTACT | 180  |
|    | GCTGAAACTG | AAGCGGGAGA  | GCTTTGGGAC | ATCTACAAAC  | TGGACGTTGT  | AGTTATTCCG | 240  |
|    | ACAACAAGC  | CTATCGCCCG  | TAAGGATATG | AATGATCGTA  | TCTATAAGAC  | GGCACGTGAA | 300  |
|    | AAATATGCAG | CAGTTATCGA  | AGAGATTGTA | CGTCTTGTG   | AAGAGGGCAG  | ACCTGTACTT | 360  |
| 20 | GTCCGTA    | CTTCGGTGA   | AATATCGAA  | TTGTTGAGCC  | GTATGTTACG  | CTTGGCTGGC | 420  |
|    | ATCCAACACA | ATGTA       | CTCAA      | ATG         | AGG         | CCGAGAT    | 480  |
|    | GCCGCTCAG  | AAGGA       | ACTGT      | TACCATCGCA  | ACGAACATGG  | CCGGTCGTGG | 540  |
|    | AAGCTCTCTG | CCGAGGTTAA  | GAAAGCCGGG | GGTTTGGCTA  | TCATTGGTAC  | GGAAAGGCAC | 600  |
|    | GAATCCAGAC | GAGTGGACAG  | ACAGCTTCGT | GGTCGTTCCG  | GCCGTCAGGG  | TGATCCCGGT | 660  |
| 25 | TCGTCCATAT | TCTATGTTTC  | CCTTGAAGAT | CATCTGATGC  | GCCTCTTTGC  | CACAGAAAAG | 720  |
|    | ATTGCATCAT | TGATCGATCG  | TTTAGGTTTC | AAGGAAGGAG  | AAGTGCTCGA  | AAACAACATG | 780  |
|    | CTGAGTAAGT | CCGTGGAGCG  | TGCTCAAAAG | AAGGTGGAAG  | AGAACAACCTT | CGGTATCCGT | 840  |
|    | AAACATCTGC | TTGAGTACGA  | TGATGTAATG | AATTTCGCAGC | GTGAAGTCAT  | TTATACCCGT | 900  |
|    | CGCCGTCATG | CTTTGATGGG  | AGAGCGTATC | GGTATGGATG  | TACTCAATAC  | CATATACGAC | 960  |
| 30 | GTATGTAAGG | CTCTGATTGA  | CAATTATGCA | GAAGCCAATG  | ATTTCGAAGG  | CTTCAAGGAA | 1020 |
|    | GATCTGATGC | GTGCACTCGC  | GATAGAATCT | CCTATCACGC  | AAGAAATATT  | CAGAGGTAAG | 1080 |
|    | AAAGCAGAAG | AGCTGACCGA  | TATGCTTTTC | GATGAAGCTT  | ACAAGTCTTT  | CCAACGTAAG | 1140 |
|    | ATGGATCTGA | TGCGAGAAGT  | GGCCCCACCT | GTGGTTCATC  | AGGTATTCGA  | GACCCAGGCC | 1200 |
|    | GCCGTGTACG | AGCGCATTCT  | AATCCCCATT | ACGGATGGTA  | AACGTGTCTA  | TAACATAGGA | 1260 |
| 35 | TGCAATTTGC | GTGAAGCGGA  | TGAAACTCAA | GGGAAAAGCA  | TCATCAAAGA  | ATTTGAGAAA | 1320 |
|    | GCTATCGTAC | TGCATACTAT  | CGATGAGTCT | TGGAAAGAAC  | ATCTGCGTGA  | GATGGACGAG | 1380 |
|    | CTTCGTAATT | CCGTTTCAGAA | TGCCAGCTAC | GAAAACAAAG  | ATCCACTACT  | TATCTATAAA | 1440 |
|    | CTCGAATCTT | ACGAACTGTT  | CCGCAAGATG | GTAGAAGCCA  | TGAACCGTAA  | GACCGTAGCG | 1500 |
|    | ATCCTAATGC | GTGCTCGGAT  | ACCGGTACCG | GAGGCTCCTT  | CCCAAGAAGA  | GCTGGAACAC | 1560 |
| 40 | AGGCGGCAAA | TAGAAATCCG  | ACATGCAACC | CAACAACGT   |             |            | 1599 |
- (2) INFORMATION FOR SEQ ID NO:14
- 45 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 2160 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: circular
- 50 (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- 55 (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:  
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- 60 (ix) FEATURE:  
(A) NAME/KEY: misc feature  
(B) LOCATION 1...2160
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:14
- |    |            |            |            |            |            |            |     |
|----|------------|------------|------------|------------|------------|------------|-----|
| 65 | AAATCTTGCC | GTGTTATTGG | CCAGACGAGG | CGATACGGAT | GCTGCCCTGT | CGGACTACGA | 60  |
|    | CCGTGCCATC | AAAGCCTATC | CGGAGTTTGC | CGATGCCTAT | TTCAATCGCG | GCCTGCTGTT | 120 |
|    | GCTTTTCGCG | GGAAAGGCCA | AAGAAGGCAT | CGCCGATCTG | AGTCGGGCG  | GCGAATACGG | 180 |
|    | GCTCTACAAG | GCGTACAACA | TCATCAAACG | AATGAGCACG | AAGTCATGAT | CTCCGTCAAT | 240 |
| 70 | AACCTGACTG | TGCAATTCGG | CACCCGCTCG | CTCTTCGATC | AGGTATCATT | CGTCATCAAC | 300 |
|    | AGGGCGGACC | GTATCGCTCT | TGTAGGGAAG | AACGGTGCCG | GCAAGAGTAC | GCTGCTCAAG | 360 |
|    | CTGATTGCCG | GCATGGAAGA | ACCGACATCC | GGACACATAG | CACGCCCAA  | GGGGATCCGC | 420 |
|    | ATAGGCTATC | TGCCGCAGGT | GATGCGTTTG | CAGGAACGAC | ACACGGTTTA | CGAAGAGGTC | 480 |
|    | GAGCAGGCTT | TCAACGATAT | TGCCCCAATA | GAGGAAGAGA | TACGGCGTCT | GTCCGATGAA | 540 |
| 75 | ATGGCCGGAC | GTACGGACTA | CGAATCGGAT | GACTATATCC | GACTGATAGA | GCATTATACG | 600 |

5 AATATGAGCG AGACCCCTCTC TCTCATGCAG CAGGGCAACT ATCATGCTGC GATCGAACAG 660  
ACATTGATCG GTCTGGGCTT CGGCCGAGAG GACTTCCACC GCCCCACAGC CGATTTCAGC 720  
GGAGGATGGC GTATGCGGAT AGAGCTGGCC AAACCTTCTGC TCCAACGCCG CGAAGTTTTG 780  
CTGCTCGACG AGCCGACCAA TCACCTCGAC ATCGAATCCA TCGGCTGGCT GGAGCAGTTC 840  
ATCGCCACCA ATGCGAGGAGC CGTTATCCTG GTGTCGCACG ACAGGGCATT CATCGACAAT 900  
ACCCAGCACG GCACTATCGA AATAGAACTG GGACATATAT ACGACTACAA GACCAACTAC 960  
AGCCACTATG TGGAGCTGCG CGAAGAGCGG CTGCGACAGC AGATGCGTGC CTACGAGAAT 1020  
CAGCAGAAGA TGATCCGCGA TACGGAGGAC TTCATCGAAC GATTTCAGATA CAAGGCCACG 1080  
AAGTCCGTAC AGGTACAGAG CCGGATCAAA CAGTTGGAGA AAGTAGAGCG CGTGGAGATA 1140  
10 GACGAGCGGG ATCGTTCGGC ATTTCACTTC CGCTTTATCC CGGCACAGCC TTCCGGCAGT 1200  
TATCCGCTAA TAGTGGATGA TTTGGCCAAG GCTTATGGCG ATCACCAGGT GTTTTCCGGA 1260  
GCTACATACA CCATCGAAAG AGGCCGAAAAG GTGGCTTTTC TAGGCAAAAA CGGTGCCGGC 1320  
AAAAGTACCA TGGTCAAGTG TATCATGGGA GAGCTGACAG ACTACACCGG CAAGCTCGAA 1380  
CTGGGGCACA ACGTGCAGCT GGGCTACTTT GCCCAAAACG AAGCCCAAGA GCTAAGAGGG 1440  
15 GATCTCAGCG TATTTCGACG GATAGACCGT GAGGCCGTGG GCGACATCCG TCTGCGCCTG 1500  
AACGATTTGC TCGGGGCTTT TCTCTTCGGG GGCGAAGCAT CGGAAAAGAA AGTAAGTGTC 1560  
CTGAGTGGAG GAGAACGAGC ACGATTGGCT ATTATCAGGC TTTTGCTACA GCCGGCTAAC 1620  
TTCCTTATTC TCGATGAGCC GACCAATCAC CTCGATATGC GCTCGAAGGA TGTACTGAAA 1680  
20 GAGGCGATCA AGAAGCTTCA TGGGACTGTC ATCGTAGTAT CTCACGACCG TGAGTTCCTC 1740  
GATGGGCTTG TCAGCAAGGT GTATGAATTT GCAGATGGAC AGGTGAACGA ACACCTCGGA 1800  
GGTATATACA ACTATCTCCG GACCCGCCGT ATGCAAGCGT TGACAGAGCT GGAGCGAACC 1860  
ACTACGATCG AAACAAAAAC CACACGGGAG GCTATACCTG AAACGGAAGC CAAAGCGGAC 1920  
TACCGTCGGC AAAAGGAGGT AGCCAAACAG CTGCGCACGT TGGAGCGAAC CGTAGCAACC 1980  
25 TGCGAGGAGC GGATCGGAAA ATTGGAGTCG GAATTACAGG CAATAGAGAT GCTACTGCAA 2040  
GATCCGAAAC ATGCGACTGA CGCGAATCTG TTCGAGCGAT ACGCCGGCAT GAAACAAGAA 2100  
CTCGAAAAGG CCATGGAGGA CTGGGAACAG GCTTCCGAAG CTTTATCCGA AGCCCAAGGA 2160

30 (2) INFORMATION FOR SEQ ID NO:15  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 1158 base pairs  
(B) TYPE: nucleic acid  
35 (C) STRANDEDNESS: double  
(D) TOPOLOGY: circular  
(ii) MOLECULE TYPE: DNA (genomic)  
(iii) HYPOTHETICAL: NO  
40 (iv) ANTI-SENSE: NO  
(vi) ORIGINAL SOURCE:  
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS  
45 (ix) FEATURE:  
(A) NAME/KEY: misc\_feature  
(B) LOCATION 1...1158  
50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:15

55 TATTGAAGC TATTAATACT ACAAATAGCC TTGATGAATT TCTTAAAAA AGAACCGTTT 60  
AAAATATTCT CTATGATTTA TCTGCTGTTA GATACAATAA CAAACCGTGC CGGTACAGAA 120  
CGCGCCGTGA TCAACTTGGC TAACAACCTG CATGCCAATG GTCATCGCGT ATCATTAGTC 180  
AGCGTTTGT ACAAAGAAGG AGAGCCTTCC TTCCAAGTAG AAAAAGGAAT AGAAGTACAC 240  
CATCTCGGAA TTAGGCTTTA TGGCAATGCA TTAGCCCGCA AAACAGTATA TTTCAAGGCT 300  
TATCGAAGGA TAAAGCCCT ATACAAGAAG CGTGAACCGG TTTTATGTAT AGGGACTAAT 360  
ATTTTATCA ATACAATTTT GTCTCAGATC AGTAACAGAG GCAGAAATATT TACGATCGGA 420  
TGCGAACATA TCTCTTATGA TATTGCCCGC CTTATTACAA AACGCATAAG GGGGTTTCTG 480  
60 TATTCAAGGC TTGATGCCGT TGTAGCACTG ACAAAGAGAG ATCAGCAATC GTTCGAGGCA 540  
ATCTTACGTG GACGCTCTAA AGCATATGTC ATACCCAATC AAGTTTCATT TACTACAGTC 600  
CAAAGAGATG CTACTACTCA CAAACAAATG TTGGCGATTG GCAGGCTTAC CTACCAGAAG 660  
GGTTTGAAT TCATGATAGA AGATGCATCA CGAGTGCTGC GAGAAAGGCC TGATTGGAAG 720  
CTTATCATAG TCGGAGATGG CGAAAATGAA TCGATGCTAC GTAAAGAAAT TGCATCTCGC 780  
65 AATATGGAAT CGCAAATAGA AATACATCCA TCTACACCGG AAATTGCGAA ATACTACGAA 840  
TCATCTGCTA TTTATCTAAT GACGTCCCGT TTCGAAGGAC TACCAATGAT ACTTCTCGAA 900  
GCAGAAAGCAT ATGCACTACC TATAATCTCA TACGATTGTC CGACCGGCCC GAGGGAACTG 960  
ATCGAAAACG GTCGCAATGG TTTCCCTTGTG CCAATGGAAG CACATGAAGA CTTCGCGGAT 1020  
70 AAGTTACGCT TATTGATGGA TGATGAAACT CTTCGTAAAG AAATGGGACA AGAATCAGAG 1080  
TTGATGSTCA AATCCTACTC TCCGGCAAAT ATCTATGAAT GTTGAAGAA ACTATTCTGC 1140  
GAAATCGGCT ACATGAAT 1158

75 (2) INFORMATION FOR SEQ ID NO:16

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- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 1965 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:  
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:  
(A) NAME/KEY: misc\_feature  
(B) LOCATION 1...1965
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:16

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ACAACGAAAG AAAACGAGAC AACAAACAAA AACGAATATA GAATTATGGG AAAAATCATT 60  
GGAATTGACT TAGGCACAAC GAACCTCTGT GTCTCTGTAT TGGAGGTAA CGAACCTATC 120  
GTTATTACAA ACAGTGAGGG CAAGCGCACA ACGCCCTCGG TAGTGGCTTT TGTGGATGGT 180  
GGCGAGCGTA AGGTGGGCGA TCCGGCCAAG CGTCAGGCCA TCACCAATCC GACCAAGACG 240  
ATATACTCTA TCAAACGCTT CATGGGCGAA ACTTACGATC AGGTTCCAG AGAAGTGGAG 300  
AGASTGCCAT TCAGGTAGT ACGTGGGGAC AATAATACTC CGCGCGTAGA TATAGACGGT 360  
CGTCTCTATA CGCGCAGGA AATTTCGGCC ATGATCCTTC AGAAGATGAA GAAGACGGCC 420  
GAAGACTACC TCGGTCAGGA AGTAACGGAG GCCGTGATCA CTGTGCCCGC ATACTTCAAC 480  
GACGCTCAAC GTGAGGCAAC GAAAGAAGCA GGAGAGATCG CCGGCCCTGAA AGTTCGCCGT 540  
ATTGTGAACG AGCCTACGGC AGCTTCTCTG GCCTACGGTC TGGACAAGTC CAATAAGGAT 600  
ATGAAGATCG CTGTCTTCGA CTGGGTGGC GGTACCTTCG ATATCTCTAT CTGGGAATTG 660  
GGCGACGGCG TTTCGGAAGT GAAATCGACC AACGGTGATA CGCACCTCGG AGGAGACGAC 720  
TTCGACCACG TGATCATTGA CTGGCTGGCA GAAGAGTTCA AGTCTCAGGA AGGTGTGGAT 780  
CTTCGCCAGG ATCTATGGC TATGCAGCGT CTGAAAGAAG CTGCCGAAA AGCCAAGATA 840  
GAGCTCTCCA GCACTTCATC TACGGAGATC AACCTCCCTT ATATCATGCC GGTGAACGGC 900  
ATCCCAAGC ACTTGGTGAT GACGCTTACA AGGGCTAAGT TCGAGCAGTT GGCCGATCGT 960  
CTGATTACAG CATGTGTGGC ACCCTGCGAA ACGGCCCTGA AAGATGCCG TATGTCACGT 1020  
GGCGATATCG ATGAAGTGAT TCTCGTAGGT GGTTCACAC GTATTCTGTC TATTCAGGAG 1080  
TTGGACGTTA CCCCCTTGTC GCTCGGTATC GAGACTATGG GAGGCGTGAT GACTCGCTTG 1140  
ATCCCAAGC ACTTGGTGAT GACGCTTACA AGGGCTAAGT TCGAGCAGTT GGCCGATCGT 1200  
GCTGTGGGTG CCGCTATTCA AGGCGGTGTT CTGACCGGTG AGGTAAAGGA TGTCTTGCTG 1260  
TTGGACGTTA CCCCCTTGTC GCTCGGTATC GAGACTATGG GAGGCGTGAT GACTCGCTTG 1320  
AATCAACCTT CCGTAGAGAT TCATGTACTT CAGGGTGAGC GTTCTTTGGC TAAGGACAAT 1380  
AAGAGCATCG GCCGTTTCAA CTGGSACGGT ATTGCTCCGG CGCCCCGTCA GACACCGCAG 1440  
ATCGAAGTAA CGTTTGACAT CGATGCCAAC GGTATCCTGA ATGTAACGGC TCATGACAAA 1500  
GCTACCGGCA AGAAGCAGAA TATCCGCATC GAAGCCTCCA GCGGTTTGTG CGATGATGAG 1560  
ATCAAGCGCA TGAAGGAAGA GCGCGAGGCC AATGCCGAAG CAGATAAGAA AGAGAAAGAA 1620  
CGTATCGACA AGATCAATCA GCGCGACAGC ATGATCTTCC AGACGGAAA GCAGTTGAAG 1680  
GAGTTGGGAG ACAAATTCCC GCGCGACAAG AAGGCTCCGA TCGATACCGC TCTCGACAAA 1740  
CTGAAAGAG CACACAAAGC ACAGGATGTA GCTGCTATCG ATACAGCCAT GGCCGAAGCT 1800  
CAAACCGCTC TTTCGCGAGC GGGCGAAGAG CTTTACAAGA ATGCCGGAGC AGCCCAAGGT 1860  
GGCGCACAA CCGGTCCGGA CTTCGGCGGT GCTCAAGGTC CCTCTGCCGG TGATCAGCCC 1920  
TCTGACGACA AGAACGTCAC AGACGTAGAC TTCGAGGAAG TGAAG 1965

- (2) INFORMATION FOR SEQ ID NO:17
- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 1401 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:  
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:  
(A) NAME/KEY: misc\_feature

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(B) LOCATION 1...1401

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17

5 AAGTGGGCAC GTACAACCTAC TTAAAGGATA TCGAACGCAA CAATCTATAA AACTATGCGC 60  
TACGACTTAG CTATCATCGG TGGAGGGCCG GCCGTTTATA CGGCTGCCGA ACGTGCTGCC 120  
AAAGGTGGCC TGAACACCTT CCTAATTGAG AAGAATGCTC TCGGTGGTGT ATGCCTCAAC 180  
GAAGGATGTA TACCGACCAA GACGCTACTC TACTCGGCCA AAGTGCTACA TCAAATTGCT 240  
ACGGCATCTA AATATGCAGT AAGTGGAAAG GCCGATGGAC TTGACCTCGG CAAGGTGATT 300  
10 GCCAGAAAAG GTAAAATCAT TCGCAAGCTG ACTGCAGGCA TCCGTTTCAG CCTGACAGAG 360  
GCCGGAGTAG AGATGGTGAC GGCAGAAAGT ACCGTAACGG GATGCGATGC AGACGGCATC 420  
ATCGGCATTA CTGCGGGCGA AGCACAGTAC AAAGCTGCCA ACCTGCTACT ATGTACCGGT 480  
TCGGAGACGT TTATTCCACC CATCCCCGGA GTGGAGCAGA CAGAGTATTG GACAAACCGT 540  
GAAGCTCTAC AGAACAAGA GATTCGACCC TCTCTCGTCA TCATCGGTGG TGGAGTGATC 600  
15 GGAATGGAGT TCGCTTCTTT CTCAACGGT ATCGGTACGC AAGTGCACGT GGTGGAGATG 660  
CTGCCGAAA TACTCAACGG TATCGATCCC GAACATGCAG CTATGCTACG CGCTCACTAT 720  
GAAAAAGTAG GAATCAAAAT CTACCTCGGG CACAAAGTAA CATCGGTTCG CAACGGAGCT 780  
GTACGGTAG AATACGAAGG AGAAAGCAA GAGATCGAAG GAGAACGTAT CCTGATGAGT 840  
20 GTGGGACGTC GCCCGGTGCT GCAAGGATTC GAGTCGCTCG GATTGGTGCT TGCCGGCAAA 900  
GGTGTAAGA CTAATGAGAG GATGCAAACT TCCCTGCCCA ATGTCTATGC TGCAGGTGAT 960  
ATTACAGGCT TCTCGCTTTT GGCACATACG SCTGTACGGG AAGCAGAGGT AGCAGTAGAT 1020  
CAGATTTTGG GCAAAACAGA CGAAACGATG AGCTACCGTG CCGTACCAGG TGTGGTGATC 1080  
ACCAATCCCG AGTCCGCCGG TGTGGGAGAG ACGGAAGAAT CGCTTCGCAA AGCAGGACGT 1140  
25 GCCTACACTG TTCGTCGCTT TCCTATGGCC TTCTCCGGTC GATTTGTAGC AGAAAACGAA 1200  
CAAGGCAATG GAGAGTGCAA ACTACTACTT GATGAAGAGA ACCGCTTGAT CGGAGCACAC 1260  
CTCATTTGCA ATCCGGCCGG CGAACTCATC GTAAACCGCTG CCATGGCCAT CGAGACCGGC 1320  
ATGACGGATC GACAAATCGA ACGAATCATA TTCCCTCATC CGACTGTAGG CGAAATCCTA 1380  
AAAGAAACTC TCGCCGGAGG T 1401

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(2) INFORMATION FOR SEQ ID NO:18

(i) SEQUENCE CHARACTERISTICS:  
35 (A) LENGTH: 2835 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: circular  
  
(ii) MOLECULE TYPE: DNA (genomic)  
40 (iii) HYPOTHETICAL: NO  
(iv) ANTI-SENSE: NO  
  
(vi) ORIGINAL SOURCE:  
45 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS  
  
(ix) FEATURE:  
(A) NAME/KEY: misc feature  
50 (B) LOCATION 1...2835

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18

55 CCTAAGATAC TTATGGAATT GAAAAGATT TTATCACTTG GTCTTCTGCT TGTGGGATTC 60  
ATTCGGATGA AGCTTTCTGC CCAACAGGCT CAGCCACTCC CTACAGATCC GGCTGTTCGT 120  
GTGGGTAAGT TGGACAACGG ATTGACTTAT TTCATCCGTC ACAACGAGAA CCCGAAAGAT 180  
CGTGCGGATT TCTTTATCGC ACAAAGGTA GGTCTCTATC TTGAAGAAGA TAGCCAGTCC 240  
GGTTTGGCTC ACTTCTTGGG ACACATGGCT TTCAACGGTA CGAAGAACTT CCCCAGTAAG 300  
60 AACTTGATCA ACTATCTCGA AACGATCGGT GTACGTTTCG GTCAGAACCT GAACGCTTCT 360  
ACCGGATTCG ACAAGACGGA ATATACGATA ATGGATGTGC CGACTACACG TCAGGGAATC 420  
ATCGACTCCT GCTTGCTTAT CCTGCATGAT TGGAGTAACA ATATTACCCT CGACGGGCAT 480  
GAGATCGACG AGGAGCGCGG TGTGATCCAG GAAGAGTGGC GTGCTCGTCG CGATGCCAAC 540  
CTTCGTATGT TCGAGGCTAT ACTTGCCAAG GCTATGCCGG GTAATAAATA TGCAGAACGC 600  
ATGCCCATCG GTCTGATGGA CGTCGTGCTC AACTTCAAGC ATGATGAGCT GCGCAACTAT 660  
65 TATAAGAAAT GGTATCGTCC CGACCTGCAA GGTCTGGTGA TCGTGGGAGA TATCGATGTG 720  
GACTATGTGG AGAACAAGAT CAAAGAACTC TTCAAGGACG TTCCTGCTCC CGTGAATCCA 780  
GCAGAGCGTA TCTATACGCC GGTAGAGGAC AACGATGAGC CTATCGTAGC CATTGCTACC 840  
GATGCTGAGG TCTATCCAC GCAGCTCTCC ATCAGCTTCA AGAGCGACCC CACTCCTCAA 900  
70 GAAGTGCGAG GATCGATATT CGGACTTGTG GAAGACTATA TGAAACAGGT GATCACTACA 960  
GCCGTGAATG AGCGTCTGTC CGAGATTAAT CACAAGCCTA ACGCTCCTTT CCTCAGTSCA 1020  
GGAGCTTTCT TCTCTAACTT CATGTACATC ACCCAGACTA AGGACGCATT CAATTTTGTG 1080  
GCCACGGTTC GTGAGGGTGA AGCGGAGAAA GCGATGAACG CATTGGTGGC AGAGATAGAA 1140  
AGCCTCCGTC AGTTCCGTAT CACCAAGAGC GAATACGATC GTGCACGCAC GAATGTGCTC 1200  
AAGCGATACG AGAATCAATA CAACGAAAGA GACAAGCGTA AGAACAATGC TTATGCCAAT 1260  
75 GAATACTCCA CCTACTTCAC CGATGGCGGC TATATCCCGG GTATTGAGGT GGAATATCAG 1320

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5 ACGGTGAATG CTTTGTCTCC TCAGGTTCCCT CTGGAAGCAT TCAATCAGGC TATTGCCCAA 1380  
 ATGATCGATC CGGTGAAGAA TGCTGTCTGT ACCCTCACCG GTCCTTCAAA GGCTGAAGCC 1440  
 AAGATTCCGA GCGAAGCAGA CTTCTCGCT GCTTTCAAAG CTGCTCGTCA GCAGAAAGTA 1500  
 GAAGCCAAGA AAGACGAAGT CTCCGACCAA AAATTGATGG AGAAAGCTCC TAAGGCCGGA 1560  
 AAGATCGTTT CCGAGAAGAA AGATCAGAAG TTCCGTACCA CGGAACCTAC CTTAGCAAT 1620  
 GGCATCAAAG TATACCTCAA GAAGACCGAT TTCAAATCAA ACGAAATCCT GATGAGTGCT 1680  
 CTCAGCCCCG GTGGTATCCT CTCCGGAAAG CATGCTCCCA ACCAATCTGT GATGAATTCG 1740  
 TTCTGAACG TGGGTGGCTT GGGCAACTTC GATGCTATCC AGCTGGATAA GGTGCTGACA 1800  
 10 GGTGCTCTG CTTCCGTATC TCCCTCTTTG TCTCTGCTCA GTGAAGGTCT TTCGGGCAAA 1860  
 ACGACTGTAG AAGATATGGA AACTTTCTTC CAGTTGATCT ATCTCCAAAT GACTGCTAAC 1920  
 CGCAAGGATC CCGAAGCGTT CAAGGCCACA CAGGAAAAGT TGTACAATAA CTTGAAAAAT 1980  
 CAGGAAGCCA ACCCGATGGC TCGGCTTATG GACTCTATCC GTCATACCAT GTACGGCGAT 2040  
 AATCCGATGA TGAACCCAT GAAAGCTGCT GACGTGGAGA AAGTAAATTA CGATCAGGTA 2100  
 ATGGCTTTCT ACAATGAGCG ATTGCTGAT GCCGGCGACT TTATGTTCTT CTTTATCGGT 2160  
 15 AATCTGGATG AAGCCAAGAT GAAGCCATTG ATCGAAACTT ATCTTGCTTC ATTGCCAAC 2220  
 CTCAAGCGTG GCGATAAGAT GAATAAGGCT CAGGTACCGG CTGCCCGTTC GGGAAAGATC 2280  
 GATTGCAAGT TCGAGAAGGA AATGGATACT CCTTCGACTA CTATATTCTGA TGTCTGTCTC 2340  
 GGAAATGTGG AATATACGCT CAAGAACAGT CTCTGCTGG AAGTCTTCTC AGCCGTAATG 2400  
 20 GATCAGGTGT ACACGGCTAC CGTTCGCGAG AAGGAAGGCG GTGCATACAG TGTGGCTGCA 2460  
 TTCGGCGGTG TCGAGCAATA TCCTCAGCCC AAGGCTCTGA TGCAGATCTA TTTCCCCACG 2520  
 GATCCTGCTC GTGCCGAGGA AATGAATGCT ATCGTTTTTG CTGAGTTGGA GAAGCTTGCC 2580  
 AAGGAGGCG CCAATGTGGA ATACTTTAAG AAGACTATCG AAAACCTGAA TAAGCAGCAC 2640  
 AAAGAAAGTC TCGGTGAGAA TCGTTTCTGG CTGGAAGCCA TGAAGGCGTC TTTCTTCGAA 2700  
 25 GGAAATGACT TCATCACAGA CTACGAATCC GTACTGAACG GTCTTACTCC TGCTGAATTG 2760  
 CAAAAGTTG CCGCAGACCT CTTGAAGCAG CAGAATCGGG TTGTTGTCAT GATGGCTCCT 2820  
 GTTGCAAAGG CTCAA 2835

30 (2) INFORMATION FOR SEQ ID NO:19  
 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 2058 base pairs  
 (B) TYPE: nucleic acid  
 35 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular  
 (ii) MOLECULE TYPE: DNA (genomic)  
 (iii) HYPOTHETICAL: NO  
 40 (iv) ANTI-SENSE: NO  
 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS  
 45 (ix) FEATURE:  
 (A) NAME/KEY: misc feature  
 (B) LOCATION 1...2058  
 50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:19

TACACTATGA GTAAGAAAGG AACAAATCGGG GTAACGAGCG ACAATATATT CCCCCTCATC 60  
 AAAAAATTCC TGTACAGCGA CCATGAGATA TTCCTGCGTG AGATCGTCTC CAATGCCGTG 120  
 55 GATGCTACGC AGAAGCTGAA AACGCTTACA TCCGTGCGCG AATTCAAAGG CGAGACGGGT 180  
 GACCTCCGCG TAACGGTCAG CGTGGATGAA GTGGCAGCA CGATCACGGT CAGCGACCGC 240  
 GCGTAGGGA TGACCGAAGA GGAGGTGGAG AAGTACATCA ATCAGATTGC TTTCTCCAGT 300  
 GCGGAAGAGT TTCTTGAAAA GTACAAAGAC GACAAGGCCG CCATTATCGG CCACTTCGGA 360  
 CTCGGATTTT ACTCGGCTTT CATGTTGTCC GAGCGAGTGG ACGTGATCAC GCGCTCTTTC 420  
 60 CGAGAAGATG CTACGCGCGT GAAATGGAGC TCGGACGGAT CGCCGAATA CACGCTCGAA 480  
 CCTGCGGACA AGGCTGACCG TGGCACCGAC ATCGTGATGC ACATCGATGA GGAGAATAGC 540  
 GAGTTCTCTA AAAAAGAAAA GATAGAGGGG CTCCTCGGCA AATACTGTAA GTTCTTACC 600  
 GTGCCGATCA TTTTCGGCAA GAAGCAGGAA TGGAAAGACG GCAAGATGCA AGATACGGAC 660  
 GAGGACAATC AGATCAACGA CACACATCCT GCCTGGACCA AAAAGCCTGC CGACCTCAAG 720  
 65 GACGAAGACT ATAAGGAATT TTACCGTTCG CTCTATCCCA TGTCCGAAGA GCCTCTCTTC 780  
 TGGATCCACC TCAATGTGGA CTATCCGTTT AATCTGACAG GTATCCTCTA TTTCCCGAAG 840  
 ATCAAAAACA ACTTGGATCT GCAGCGCAAC AAGATTGAGC TCTACTGCAA TCAGGTTTAC 900  
 GTCACCGATG AAGTACAGGG TATCGTGCCG GACTTCCTCA CCTCTCTGCA CGGGGTCATC 960  
 GATTGCGCGG ATATTCCCT CAACGTATCG CGCTCCTATC TGCAGAGCGA TGCCAATGTG 1020  
 70 AAGAAGATCT CGTCTCATAT CACCAAGAAG GTGGCAGACC GTCTGGAAGA AATTTTCAAA 1080  
 AACGACCGCC CCACATTCTGA GGAGAAATGG GATAGTCTGA AGCTCTCTCGT CGAATACGGT 1140  
 ATGCTGACGG ATGAGAAGTT CTATGAGCGT GCAGCCAAAT TCTTCTTTT CACCGATATG 1200  
 GACGGACACA AGTACACGTT CGACGAATAC CGAAGCGTCG TCGAAGGTGT ACAGACGGAT 1260  
 AAGGACGGAC AGGTAGTGTA TCTCTATGCT ACGGACAAGC ATGGACAGTA CAGCCACGTG 1320  
 75 AAACGTGCAT CCGACAAAG CTACAGCGTG ATGCTGTTGG ATGGTCAGTT GGATCCGCAT 1380  
 ATCGTGAGCC TGCTGGAGCA AAAGTTGGAG AAGACACACT TTGTCCGTGT CGATAGCGAT 1440



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ACGATCAACA	ATCTGATCCG	CAAGGAGGAA	AGAGCCGAAG	TGAAACTGTC	CGATACGGAG	1500
CGCGCCACTC	TCGTGAAGCT	GTTCGAAGCA	CGCCTGCCAC	GGGACGAGAA	GAAGCACTTC	1560
AATGTAGCTT	TCGAATCGCT	CGGAGCCGAA	GGTGAAGCCA	TCCTTATCAC	ACAAGCCGAA	1620
TTCATGCGCC	GTATGCGCGA	TATGGCACAG	CTGCAGCCGG	GAATGAGCTT	CTACGGCGAA	1680
CTCCCCGATT	CGTACAATCT	GGTACTTAAT	ACCGATCATC	CGCTCATCGA	CAGGGTACTC	1740
TCCGGTGAGA	AAGAATCGGT	AGAGCCTTCG	CTCACAGAGC	TTAGAGCGAA	AATCGCCGAG	1800
CTGAAAGCGS	AAGAGGCCAA	GCTGCTCGAT	GAGGAAAAAG	GGAAGAAACC	GGAGGAAATC	1860
CCTGTTGCCA	CGAAGGAAGC	CAAGGAGAAC	AACGCCGTCG	AACAGGCCAA	AACCGAAGGC	1920
AGTATCAACG	ATCAACTGAC	CAAATATGCT	CAGGACAACG	AGCTGATAGG	TCAGCTCATC	1980
GACTTGCTC	TGCTCGGAAG	CGGATTGCTG	ACGGGAGAGG	CTTTGGCCGA	ATTCATTTCG	2040
CGCAGCCAGC	GTCTTCTC					2058

## (2) INFORMATION FOR SEQ ID NO:20

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1446 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: circular

## (ii) MOLECULE TYPE: DNA (genomic)

## (iii) HYPOTHETICAL: NO

## (iv) ANTI-SENSE: NO

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature  
(B) LOCATION 1...1446

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:20

60  
120  
180  
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600  
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780  
840  
900  
960  
1020  
1080  
1140  
1200  
1260  
1320  
1380  
1440  
1446

GACATTCGAC	AGAAAAGACC	GTGCTTCAAC	GCCAAATTGT	ACTTTTACCG	TGCAATGGAA
AAACTGATCG	ATATTTTGGT	CGTAGACGAT	GATGTGGCAG	TCTGTGCCGC	ACTGCGTCTG
GTGCTCAAGC	GAGCGGGCTA	TAATCCCCTT	ATAGCCAACA	GTCCCGACGA	AGCTTTGTCC
ATAATGCGGA	ATCCTGATGG	CGGCTGTAAG	CCGGCTGTGA	TTCTGATGGA	TATGAATTTT
TCCCTTTTCA	CCTCCGGCAG	GGAAGGATTG	GAAGTACTGG	AGAAGATGCA	GATATTCACT
TCTTGCCCTG	TCATACTGAT	GACGGCTTGG	GCTTCGATTG	CACTGGCAGT	GGAGGGAATG
AGGCTTGSAG	CTTTCGACTT	CATAGGCAAG	CCATGGGACA	ACGATCGGCT	CCTTCGTACC
ATAGATACGG	CCTTGCATCT	GGCTGCTCCC	TCAGCTGTGG	CGAATCCATC	GGAACAGTCT
GACAGAGATA	CAGCCCCGTC	GCCGAAAGCT	ACAGTCCAAG	AGAATGACCC	CTGTGCCCAT
ATCATAGGCC	GGAGCGATGC	CATCTGTAAG	ATCAAGGAAC	GGATACGCCG	CATAGCTCCC
ACCCATGCCT	CTGTGCTGAT	CACGGGCGAG	AGCGGTACGG	GCAAAGAGTT	GATAGCCGAA
GCTCTGCACC	GTGGGAGCAA	ACGAGCCTCA	GCCCCATTTC	TCAAGGTCAA	TTTGGGTGGG
ATTCCCGAAA	GTTTGTTCGA	AAGTGAGCTG	TTTCGGACATA	AGAAAGGAGC	TTTTACCAAT
GCTTTTTCGG	ACAGGAAAGG	ACGGTTCGAG	CTGGCTGATG	GCGGCACGAT	CTTTCTGGAC
GAAATAGGCG	AACTACCGGT	CGGCAACCAA	GTAAACTGCT	TGCGAGTGTG	ACAGGAACAG
ACATTCGAGC	CGTTGGGCGA	GAGCGTCTCC	CACCGAGTGG	ACATCCGTGT	GGTATCGGCT
ACGAATGCTT	CCTTGGAGCG	AATGGTAGCC	GAAGGACGTT	TCAGAGAGGA	CCTCTACTAT
CGAATCAACC	TGATACATCT	GCATCTGCCT	CCGCTGCGTG	AGCGTCAGGA	GGATATACAG
CTGCTGGTGG	AAGCCTTCAG	TGAAGCCTTT	GCCCAATCGA	ACGGATTGCC	CCATGCCGTT
TGGAGTGCAG	AAGCTATGCG	ACGTATCTGT	GCCATGCCCC	TACCGGGCAA	TGTACGCGAA
CTGAAAAACG	TAGTGGAGCG	TACGCTATTG	CTCTCGGGAT	CGAGAGAAAT	CAGTGCCCGG
GATGTGGCTG	ACTTCGGTTC	GCAGGTGACG	GCAGCAGACC	ACTCCGACGA	ACGGGCTTTG
ACCGACATGG	AGGAAGCTGC	TATCCGAGAG	ACGCTGACTA	AATACAACGG	CAACGTTAGT
CGTCTGTCAC	GAGCCTTGGG	ATTGAGCCGG	GCAGCTCTTT	ACCGGCGAAT	GGAGAAATAC
GGACTG					

## (2) INFORMATION FOR SEQ ID NO:21

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 789 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: circular

## (ii) MOLECULE TYPE: DNA (genomic)

## (iii) HYPOTHETICAL: NO

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(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc\_feature

(B) LOCATION 1...789

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21

```
AGATCTCTGC AATCATTTC AATAAAAAA CACTCAAGTA TGCTTAAGAT AAAGAACCTC 60
CACGCCACAG TACAGGGCAA AGAGATATTG AAAGGAATCA ATCTGGAGAT CAATGCCGGA 120
GAGATTTCATG CTATCATGGG GCCGAACGGA TCGGGGAAAA GTACGCTCTC TTCCGTTTTG 180
15 GTGGGACATC CCTCCTTTGA AGTCACGGAA GGAGAGGTGA CATTCAATGG AATCGACCTG 240
CTCGAACTCG AACCGGAAGA ACGTGCACAC CTCGGACTCT TTCTCAGTTT CCAATATCCG 300
GTCGAGATCC CGGGCGTCAG CATGGTGAAT TTCATGAGGG CAGCTGTCAA TGAACATAGG 360
AAAGCGATCG GAGCAGAACC CGTATCGGCA AGCGACTTCC TCAAGATGAT GCGAGAGAAG 420
CGTGCCATTG TGGAGCTGGA CAACAAATTG GCCAGCCGTT CTGTGAACGA AGGCTTCTCC 480
20 GGTGGAGAAA AAAAGAGGAA CGAAATCTTC CAAATGGCTA TGCTCGAACC CAAGCTGGCT 540
ATTTTGGACG AAACCGATAG CGGGCTCGAT ATCGACGCTC TCCGCATCGT AGCAGGCGGG 600
GTAAACCGAC TCCGCTCTCC GGAGAATGCT GCTATTGTGA TCACACACTA TCAGCGTTTG 660
CTCGAGTACA TCAAGCCGGA CTTCTGTACAC GTCCTTTACA AGGGGCGCAT CGTCAAGTCG 720
GGAGGAGCCG AGCTGGCTCT CACGCTCGAA GAAAAAGGCT ACGACTGGAT CAAGGAAGAG 780
25 ATAGGAGAA
```

(2) INFORMATION FOR SEQ ID NO:22

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1386 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc\_feature

(B) LOCATION 1...1386

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22

```
AGCATGGCTA AGGAGAAAAC GATCTACGTC TGCCGTTCGT GCGGAACCAA ATACGCCAAA 60
TGGCAAGGCA ACTGCAATGC CTGTGGAGAG TGGAACTGCA TTGATGAGGA GAAGGTGCCG 120
GCACCCGCAT CGGGCAAGCA TGCAGCCAAG AGTTTATGCT CTCGGGAGCA GGACAACCGG 180
55 CCAAGACTCT TACAGGATGT GGAGTCCGGC GATGAAGAGC GTATTCGCCT CGGCGATGAA 240
GAGTTCGACC GCGTACTGGG TGGAGGAATT GTCAAAGGAG CATTGTCTCT GCTTGGCGGG 300
GAGCCGGGAA TCGGTAAGTC CACGCTTATC CTCCAGACGG TGCTGCGTCT GCCGCACTG 360
CGCACGCTCT ATGTGTCGGG CGAAGAAAGT GCCCGACAAC TGAAGATGCG CGCCGAACGA 420
CTGGGGCAAG CCATGAATGG GTGCTACGTA TACTGCGAAA CGAATATAGA GAGGATACTC 480
TCCCGTGCAG AAGAACTCAC ACCCGATCTC CTCGTGATAG ACTCTATACA GACGCTCTAT 540
60 ACGGAGGAAA TGGAAAGCTC GGCCGGCAGC GTGGGGCAGA TCCGCGAATG TGCCGCCCTA 600
CTGCTCAAT ACTGCAAGAC TACGGGTATC CCCGTCAATG TCATCGGACA CATCAACCAA 660
GAGGATGACA TAGCCGGACC GAAGGTGCTG GAGCATATAG TGGATACGGT GCTTCTCTTC 720
GACGGGGATA AGCATCATCT CTACCGGATA CTCGAGGAC AGAAGAACCG CTATGGCAGT 780
ACTTCCGAGC TGGGGATATA CGAGATGCGG CAGGACGGTC TGCGTGGCGT GGAGAATCCG 840
65 AGCGAACATC TCATCACACG CAATAGGGAA GACCTCAGTG GCATAGCCAT AGCCGTAGCG 900
ATGGAGGGCA TTCGCCCAGT ACTCATCGAA GCGCAGGCTT TGGTCAGCTC GGCCATTTAT 960
GCCAATCCGC AGCGTTCGGC CACGGGCTTC GATATTCGGC GGATGAACAT GCTCTTAGCC 1020
GTACTGGAGA AACGTGCCGG CTTCAGGCTC ATACAGAAGG ATGTGTTTCT GAACATTGCC 1080
70 GGAGGTATCA AAATAGCCGA TCCGGCTACG GATCTGGCCG TTATCTCGSC AGTGCTGGCG 1140
TCGAGTCTGG ACATCGTTAT CCCGCCGGCC GTATGCATGA CGGGCGAGGT CCGACTCTCC 1200
GGAGAGATAC GTCCCGTGAG CCGCATCGAG CAGCGCATAA CGGAAGCGCG TCGCATAGGG 1260
TTCAAAGAGA TATTGGTACC GGCCGATAAT TTCCGGCAGG AGGATGCCGG CCGCTTCGGT 1320
ATTCCGGCTG TGCCGGTCAG AAAGGTGGAG GAAGCCTTCC GCCATCTGTT CTCGAAAGGA 1380
75 AGAGAA
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## (2) INFORMATION FOR SEQ ID NO:23

- 5 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 1119 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: circular
- 10 (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- 15 (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:  
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- 20 (ix) FEATURE:  
(A) NAME/KEY: misc\_feature  
(B) LOCATION 1...1119
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:23

25 GGGTCTTGTG GAAGTAGCCC AGCAATTGGC CGATCAGGGT GTTCGCGTTG TGATCGCCGG 60  
ATTGGACATG GACTTTTCGAC GTCAGCCTTT CGGACCTATG CCGGGCTTGT GTGCCATAGC 120  
CGACTCCGTG ACCAAGTTTC ATGCCGTGTG TGTGGAATGC GGCCGATTGG CCAGCTATTC 180  
TTTCCGTCGT GTCCAAGGCG ATCAGCAAGT GATGCTGGGC GAACTGAACG AATACAGTCC 240  
CCTCTGCAGA ACCTGCTACA GGAAATGCAG TTCTCCCCCA CAAACAGAAG AAATCCATTC 300  
30 GACAATATGA ATAGCAGACA TCTGACAATC ACAATCATTG CCGGCCTCTC CCTCTTTGTA 360  
CTGACATTGG GCGGCTGCTC CGTAGCCCAA CAAGATACGC AGTGGACTCT CGGCGGAAAG 420  
CTCTTTACTT CGGCGTGGAT ACAACGTTCG GCCGAATATC AAGCGCTTTG CATTCAAGCA 480  
TACAACATCG CTACGGAAAG AGTGGACGCT CTACCGGCAG AACGTAAACA AGGAGATAGG 540  
CCTTATGCCA TCGTAACGGA CATAGACGAA ACCATTTTGG ACAATACGCC TAACTCCGTG 600  
35 TATCAGGCTC TCAGGGGCAA GGATTATGAT GAAGAGACTT GGGGGAAATG GTGTGCACAG 660  
GCCGATGCCG ACACACTGGC AGGAGCTTTG TCTTTCTTCC TCCATGCAGC GAACAAGGGG 720  
ATCGAGGTCT TTTACGTAC CAACCGCAGA GACAATCTGC GCGAAGCAAC TCTTCAGAAC 780  
CTTCAGCGTT ACGGATTCCC CTTTGCCGAT GAAGAACATT TGCTTACGAC CCATGGGCCA 840  
TCCGACAAAG AACCCCGTCG GCTCAAATA CAAGAACAGT ATGAAATAGT ATTGCTCATA 900  
40 GGAGACAAC TGGGCGACTT CCACCACTTC TTCAATACGA AAGAAGAGTC CGGACGCAAA 960  
CAGGCTCTGG GCCTGACAGC CGGGGAGTTT GGCCGGCACT TCATCATGCT GCCCAATCCC 1020  
AACTACGGAT CTTGGGAACC GGCATGGTAC GGCGGGAAGT ATCCGCCACT GCCCGAAAGA 1080  
GACAAAGCAC TTAAACAAC TCACTCACAG AACAGCAGA 1119

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## (2) INFORMATION FOR SEQ ID NO:24

- 50 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 1278 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: circular
- 55 (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- 60 (vi) ORIGINAL SOURCE:  
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:  
(A) NAME/KEY: misc\_feature  
65 (B) LOCATION 1...1278
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:24

70 CGTTGGGGTT TTTCTAATTT TGTGGCCATG AGCACCAATA TAGATGTACA ACAGATCAAA 60  
CAGCGTTTCG GCATCATCGG TAGCAGTCCG CTGATGGAAC ATGCCATACG AGTGGCAGCA 120  
CAGGTGGCTC CTACCGACAT GTCCGTCTCT GTGACGGGGG AGAGCGGTTT GGGGAAAGAG 180  
TTCTTCCAC AGATAATCCA CTACTACAGC GCCCGGAAAC ATCATAGCTA CATTGCAGTC 240  
AATTGCGGAG CCATCCCCGA AGGAACCATC GATTCCGAGC TGTTCCGACA CCGCAAAGGT 300  
TCCTTTACCG GAGCCGTATC GGATCGCAAG GGGTACTTCG AAGAAGCATC CGGCGGCACG 360  
75 ATCTTTCTGG ACGAAGTGGG CGAACTGCCT TTGCCACGCG AGGCGAGGCT GCTGAGGGT 420

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5	CTGGAGACGG	GCGAGTTCAT	CCCCGTAGGA	GCCAGCCAGT	CGCAGAAGAC	GGATGTCCGT	480
	ATCGTAGCGG	CGACGAATGT	GAACCTCAAG	GAGGCGGTAG	CGAACGGGAA	GTTCCGGGAA	540
	GACCTCTTCT	TCCGGCTCAA	TACGGTACCG	ATCGAGGTGC	CTGCGCTGCG	TATGCGACCG	600
	GACGACGTGC	CCTTGCTTTT	TCGCCGATTC	GCCGCCGACA	GCGCCGAGAA	GTATCGGATG	660
	CCTCCGCTGC	GCCTATCGGA	CGAAGCCCGT	ACCATATTAA	TGCGTTACCG	CTGGCCCGGC	720
	AATGTGCGAG	AGCTGCGCAA	TATAACCGAC	AGGCTGAGCA	TCCTGGAGGA	GGAGCGGACG	780
	GTATCGGCAG	AGACCATCAC	TCGCTACCTG	GACGCTGAGG	GGATGCAAGA	CCTCCACCCC	840
	GTCTGTATCC	GACGGAACGA	AACGACCGAA	GCGGACAAAC	AAATCCCCCA	TTACGAGCGC	900
	GAAATCATCT	ACCAGGTGCT	ATACGATATG	AAGAAAGAGA	TAGCCGATTT	GAAGGGGATG	960
10	ATGAACCGCC	TGGCGCACCA	CGAACAGCCC	TCATGGCCTG	TAGGGTCGGA	CGTCTGGGSC	1020
	AACGACGACA	AGCGCACCGC	AGATCCGAAG	TGGGGCGTCA	GCACGCACAA	GGCCCCCATC	1080
	GCGAACGCGG	CAGAACCCGT	GGAGCCGATA	CAGGAAGCCA	GCGAATACAC	CGAGGATCCG	1140
	GTTCGCTGG	AGGAGGTAGA	GAAGAAAATG	ATTTCCCTTG	CATTGGAACG	CCACGGCGGA	1200
15	AGGCGCAAGC	AGACAGCCGA	GGAAGTGAAG	ATTTCCGAGC	GGACACTATA	CCGTAAAATC	1260
	AAGGAGTATG	GACTGGAA					1278

## (2) INFORMATION FOR SEQ ID NO:25

- 20 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1959 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular
- 25 (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- 30 (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: FORYPHYROMONAS GINGIVALIS
- 35 (ix) FEATURE:  
 (A) NAME/KEY: misc feature  
 (B) LOCATION 1...1959
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:25

40	AAAAATCTTC	CGAGGTACGC	TCCGGCATTT	GGCAGAAATC	GTAAAAGGGA	ACAACCTGAC	60
	CCTGACAACG	ATGATAGTCG	TGGGAGAAGC	CATAGACAAT	CGGGAAGGGC	TGTCACGGTT	120
	GTATGCCGAC	GAATTCAAAC	ACCTCTTCCG	CACATGATCC	TACTCTTCGG	CGGTACTACG	180
	GAAGGCCGTG	CCGCAGCTCG	CGTGCTGGAT	GAAGCGGGAA	GTCCGTTTTT	CTACTCCACC	240
45	AAAGGCAATC	TGCAAGAGAT	CCAGAGTAGC	CACGGCCATC	GTCTGACAGG	AGCCATGACG	300
	GTGCGCGACA	TGGTTTCGTT	TTGTCCGAAA	GAAGAGATCC	GACTGATCGT	GGACGCCGCT	360
	CATCCTTTCC	CCGAAGAATT	GCACGCTTCA	GTGGCAGAAG	CCTCTGAACA	AACAGGTATC	420
	CCCGTAGTAA	GATACGAGAG	ACAATACCCCT	CCACGCGAAG	AAGGTATCGT	CTGGTGTGCA	480
	AACTACGATA	CGGCTGCCGA	GCGSATGCCT	GCGGATGGCG	TGCAGCGTCT	GCTGATGCTC	540
50	ACAGGAGTGA	ATACGATCCC	CAAGCTGGCT	GCTTTCTGGA	AAGAGCGCAC	CACCTTTTGC	600
	CGCATATTGA	AGCGAGACGA	ATCGGTTGCT	TTGGCAGAGA	AGAACGGGCT	TCCTGCGGAG	660
	CGCATCGTTT	TCTTCGAACC	GCATGCGGAC	GAGGAGCTGA	TGCAAGCCGT	TCGCCCCGAT	720
	GCCATTATCA	CAAAAGAAAG	CGGAGAGAGC	GGTTACTTCC	GAGAAAAGAT	AGAAGCTGCC	780
	CGACGGATGG	GCATCCGTAT	ATATGCCGTC	GTACGTCCCC	CTTTGCCTCC	TTCAATTCATT	840
55	CCCGTAGGCG	GGCCTGTCCG	TTTGAGACGG	GCGGTAGAAC	GCCTCGTGCC	GGGATTCTTT	900
	TCACTCCGAA	GCGGATTCAC	TACCGGCACC	ACAGCTACCG	CTGCAGTAGT	AGCAGCCATG	960
	TACCGATTGA	TGGGGCTTGG	CTCTCTCGCC	GAAGCTCCCG	TAGAATTGCC	TTCCGGCGAA	1020
	ATAGTCAGTC	TGCCCCATAGC	GGAAATTCGA	GAGGAAGAAG	ATGCTGTCTG	ATCCGCAGTC	1080
	CTGAAAAGATG	CAGGTGATGA	TCCGATGTG	ACCAATGGCA	TGGCGGTATG	CGCTACGATC	1140
60	AGGCTCAATC	CCGAACATGA	GGAACTCCCG	TTCTGCGAGG	GTGAAGGGGT	GGGGGTAGTG	1200
	ACGCTCCCGG	GCCTCGSTCT	GGAGGTCCGA	GGTCCGGCTA	TCAACCTCGT	ACCTCGACGA	1260
	ATGATGACAG	CAGAGGTACG	CCGACTCTAT	GCGCAGGGAG	GTGTGGATAT	TACGATTAGC	1320
	GTACCCGAAG	GCGGAGAGGC	TGCTACCCAG	ACATTCAATC	CCCGACTCGG	CATACGGGAC	1380
	GSCATCTCTA	TTATCGGAAC	ATCGGGAGTC	GTGAAACCTT	TTTCGGCCGA	AGCGTTCGTT	1440
65	GGTGCCATCC	GTAAGCAAGT	GGGTATTGCC	ACCGCCTTGG	GAGCCAATCA	TATCGTCCTC	1500
	AATTCCGGAG	CCAAGAGTGA	GCGTTATGTA	AAAGGAGCCT	ATCCGGCACT	CATTCCACAG	1560
	GCCTTTGTGC	AGTATGGCAA	TTTCGTCCGC	GAATCACTCA	GTGTGTGAGC	TTCTTCCCTC	1620
	TCTGTCCGTT	CGGTAACGGT	AGGAATCATG	CTCGGCAAAAG	CAGTGAAACT	CGCCGAAGGC	1680
70	TATCTGATA	CGCACAGTAA	AAAGGTAGTG	ATGAATCGGG	ATTTCTTGCA	CGAACTGGCT	1740
	CGTCAGGCAG	GTTGTTCCGA	AGACATCCAT	GCCATAATAG	ACAGCCTGAA	TTTGCTCGST	1800
	GAGCTATGGA	CTATGCCGAG	TGCGSAGGAC	AGCGATCGAC	TGCTACGAAA	GATTGCCGAA	1860
	CGATCTTGGG	AAACTTGGCG	CCCATCGGTA	CCATCGGCCG	AATTAGAACT	CCTGCTGATC	1920
75	GATGAGTCCG	GAGCGATTCC	TTTTCGTATC	GGTGGAGAA			1959

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## (2) INFORMATION FOR SEQ ID NO:26

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 1353 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:  
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:  
(A) NAME/KEY: misc\_feature  
(B) LOCATION 1...1353

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:26

CAACAAAGAC CACATAGAAT TATTATGTTG AGGACTTTCC GAATCGGTGG TATTCACCCC 60  
CCCGAAAACA AGTTGTGGGC AGGCAAGCCC GTAGAGGTGT TGCCTATCCC CTCACAGGTA 120  
GTCATCCCTC TTGGTCAGCA CATCGGTGCA CGGGCAACTG CCACGGTCAA GAAAGGGGAT 180  
GAAGTTAAGG TCGGGACTAT CATTGCTCAG GCCGGAGGAT TCGTATCAGC TAATATCCAC 240  
TCATCTGTGT CGGGTAAGGT GCTGAAGATC GATAACGTAT ACGACTCAAG CGGCTATCCC 300  
AAGCCCGCAG TCTTCATTAG CGTAGAAGGT GACGAATGGG AAGAGGGCAT CGATCGCTCA 360  
CCAGCCATCG TCAAAGAATG CAATCTGGAT GCAAAAGAAA TCGTAGCCAA AATTCTTGCA 420  
GCCGGTATTG TGGGTCTTGG CGGTGCTACC TTCCCTACCC ATGTGAAGCT GTCCCTCCT 480  
CCGGGCAACA AAGCTGAGAT CCTGATCATC AACGCCGTAG AGTGCGAGCC TTATCTGACG 540  
AGCGACCATG TCCTTATGCT GGAGCACGGC GAAGAGATCA TGATCGGCGT GAGTATCCTG 600  
ATGAAAGCCA TTCAGGTAAA CAAGGCCGTC ATCGGAGTTG AGAATAATAA GAAAGATGCT 660  
ATTGCTCACC TCACCAAAC GGCCTACTGCA TATCCGGGCA TAGAGGTAAT GCCGTGGAAG 720  
GTGCAATATC CTCAAGGCGG TGAGAAGCAG CTGATCGATG CAGTGATCCG CAAGCAGGTA 780  
AAAAGCGGTG CCTTGCCTAT CAGCACAGGT GCCGTAGTAC AAAACGTGGG TACGGTATTC 840  
GCCGTGTACG AAGCACTACA GAAGAACAAG CCTCTGGTCG AGCGCATCGT GACGGTTACA 900  
GGAAAAAATC TGTCCTCGTC GTCTAACCTC CTCGTTCTGTA TAGGTACTCC TATTGCGGCT 960  
TTGATCGAAG CAGCAGGTGG CTTGCCGGAG AATACGGGCA AGATCATCGG CGGAGGTCCG 1020  
ATGATGGGAC GCGCTCTGCT GTCACCGGAT GTGCCTGTGA CCAAAGGCAG CTCGGAGTA 1080  
TTGATTCTCG ATAGAGAAGA GGCAGTTCGC AAGCCTATGC GCGACTGTAT CCGATGCGCC 1140  
AAGTGGGTGC GAGTGTGTCC GATGGGACTC AATCCGGCTT TCCTTATGCG CGACACCTTA 1200  
TATAAGAGCT GGGAAACAGC GGA AAAAGGC AACGTGGTTG ACTGTATCGA ATGCGGTTTCG 1260  
TGCAGCTTCA CCTGTCCGGC CAACCGTCCT CTGCTGGATT ATATCCGCCA AGCCAAGAAG 1320  
ACTGTGATGG GTATCCAAAG AGCACGTAAG CAA 1353

## (2) INFORMATION FOR SEQ ID NO:27

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 1467 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:  
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:  
(A) NAME/KEY: misc\_feature  
(B) LOCATION 1...1467

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:27

ATGAAGTCTC AAAAGAAAGA GGCTTTTAAT ATGAAAAGAA TACAATAAC TCTTATCGCT 60  
CTCTTCGCGC CTGTTGCCGG TTTGGTTCGCT CAAAATGCTT ACGAGGGAGT AATTTTCATAT 120  
AAAATTTTCG TGGACAAAAC CGGAAACAAG GTTGTACTGA ATGGTGGCGC AGATATGAGT 180  
AATTTAAAGC TCAAGAGCAC TCAGATGATC ATTGTTACGC CTATTCTTCG TTCAGAAGAT 240

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5 GGTACCAGCC GGGTGGAAAT TCCTTCGGTA GTCATTACAG GCCGCAATAG AACAAAAGCT 300  
 CTCAAGCGTG AAATCGCATT TAGTTCGGCT TTGCCCAAG CAAAACATGC AGCTCAATAC 360  
 ATTCGCCGCTG ATAATGGGAA GAGCGAGCAG TTTGCTTTTA CAGGAGAACA TGCTTATGCA 420  
 TCATGGATGA TGGATGCCAA GTTTGTGGTT CGTGAGGAGG TACGAGGTG TGCTAAATGC 480  
 CCTGTAGGTG TCTCGAGTAA TATTGTTCCT TTTGATCCAC TCTTCAATCC GGCAGAGGCT 540  
 CCTTATTGTG TGGCACACAT TACTCCGGCA GAAGAAGTGG AAAACACAGCG AGAGTCCAGC 600  
 TTCGATGCTT ATATCAACTT CAAAGTCAAT AAGGCAGATG TCCTTCCTGA GTATCGCAAC 660  
 AATAAGGCGG AGTTAGAGAA AATCAAAGAA TTTGTAAGCA CCGTTAAGGC TAATCCAAAC 720  
 TATTCGGTCA ATAAATGAT CATCGAAGGG TTTGCTTCTC CCGAGGCTTC AATAGCCCAC 780  
 10 AATAAGGCTT TGTCGGAGCG CCGTGCTAAA AGACTCGCGG AAGAATTGGT GCGTAAGTAT 840  
 GGCAAAACAT TGCCGAATAT AACCCTGAA TCGGCGGGTG AAGATTGGAA GGGGCTGAAA 900  
 CTGGCTATCG AAAAGAGTGA TATAGCCGAT CGTGACCGCG TATTGGAGAT AATCAACTCC 960  
 GATAAATATG CCGATGATGA TGCACGTGAA CAGGCTCTGA AGCAACTTC GTCTTATCGT 1020  
 TATATCTTGG ATCAGATCTA TCCGAATTTG CGTCGCAATA CGATAACCAT GGGGTATATC 1080  
 15 GTTCGTGATT ATACCTCTGA AGAAGCTCGT GAAATCATTA AGACTGCTCC GAAAGAAGCTT 1140  
 AGTAGGCGG AAATGTACCG TGTGGCAATG TCTTATCCTG AGGGGCACCA AGAGCGTTTG 1200  
 TTTGCTCTGA ATACGACCCT TAAGTATTTT CCTGAAAGTG TAACGGGGCCG AATCAATTTG 1260  
 GCTGTAGCCG CTTTTAATGG TGGAGACGTT CAACAGGCAA TTGCTCTGTT GAGTCCGATT 1320  
 CAGACAGAAA AGGGGTGAAG CAATATCCTT GGAGCTGCTT ATGCTCGTAC GGGAGATTTT 1380  
 20 GCTCGTGCCG AAACCTTCTT CCGTAAGGCC GTTGCAAGAG GAGATGCAAA TGCGCAGCGC 1440  
 AACCTCGATA TGCTGCTTGG CAAAAAG 1467

## (2) INFORMATION FOR SEQ ID NO:28

25

## (i) SEQUENCE CHARACTERISTICS:

30

- (A) LENGTH: 1152 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

## (ii) MOLECULE TYPE: DNA (genomic)

35

## (iii) HYPOTHETICAL: NO

## (iv) ANTI-SENSE: NO

## (vi) ORIGINAL SOURCE:

40

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...1152

45

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:28

50 GACATGGCAG AAAAAAGAGA CTATTACGAA GTCCTCGGTG TATCGAAGAA TGCCACCGAC 60  
 GATGAAGTGA AAAAAGCATA TCGCAAGAAG GCTATCCAAT ACCATCCTGA TAAGAACCCC 120  
 GGTGACAAGG AGGCCGAAGA GCACTTCAAA GAGGTAGCTG AAGCCTACGA CGTATTGAGC 180  
 GATCCGCAGA AGCCGAGTCA ATATGACCCG TTCGGCCATG CCGGATTGGG CGGAGCTGCC 240  
 GGTGGAGGTT TCAGCGGAGG CGGTATSTCC ATGGAGGATA TTTTCAGTCG CTTCGGTGAT 300  
 CTATTCGGTG GGTTCGGCGG TTTCGGCGGA TTCTCCGATA TGGGCGGTGG CAGTCGCAGA 360  
 CGTGTTCCGA GAGGGTCTGA CCTGCGAGTA CGAGTGAAGC TTTCTTTGGC CGATATAAGT 420  
 55 AAAGGTGTGG AGAAGAAAGT GAAGGTAAAA AAGCAGGTAG TGTGCAGCAA ATGTCTGTGG 480  
 GATGGCACGG AAGAAGCCAA TGGCAAGACT ACCTGCCAGA CCTGCCATGG AACCGGCGTG 540  
 GTTACACGTG TGAGCAACAC TTTCTTTGGG GCCATGCAGA CCCAGAGCAC TTGTCCCACT 600  
 TGCCACGGAG AGGGTGAGAT CATCACGAAG CCATGCTCCA AGTGTAAAGG CGAAGGTGTG 660  
 GAGATCGGCG AAGAGGTGAT CTCATTCAC ACCTCTCCG GTGTAGCCGA AGGAATGCAA 720  
 ATGTCCGTGA ACGGCAAGGG AAATGCCGCG CCCCGAGGAG GCGTGAATGG CGACTTGATA 780  
 60 GTCGTGATCG CCGAGGAACC GGATCCGAAT CTGATCCGCA ATGGCAACGA TCTGATATAC 840  
 AATCTGCTTA TATCCGTTCC GTTGGCTATA AAAGGAGSTA GTGTGGAAAT GCCGACGATA 900  
 GACGGACGAG CCAAGATCCG CATCGAGGCG GGGACACAAC CCGSCAAGAT GCTGCGTTTG 960  
 CGCAATAAGG GGTGCCCCAG CGTAAACGGC TATGGCATGG GAGACCAACT GGTGAATGTC 1020  
 AATGTCTATA TCCCGAATC GATCGATGCC AAAGATGAGC AGGCTATCGC AGCGATGGAA 1080  
 65 AACTCGGACA GCTTCAAACC TACCGATGCT GCTCGTAAGG ATATAGACAA GAAATACAGA 1140  
 GAGATGCTGG AT 1152

## (2) INFORMATION FOR SEQ ID NO:29

70

## (i) SEQUENCE CHARACTERISTICS:

75

- (A) LENGTH: 927 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

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(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:  
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:  
(A) NAME/KEY: misc feature  
(B) LOCATION 1...927

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29

CGATTTCGATT	CAACAACATA	TGTCTCACAA	ATTAATTTAA	GAACAGAGAT	GAACAACTG	60
ATTTTAGCGA	CTTTGGGACT	TATGGCCATT	GCCATGCTCT	CATGTTCAAG	CAACAACAAG	120
GATTTGGAGA	ACAAAGGGGA	GGCTACTCTT	TTGGTAACGT	TTGGTAGCTC	CTATAAAGCT	180
CCACGCGAAA	CCTATGCGAA	GATTGAGAAG	ACTTTGCGG	CAGCTTATCC	CGATCAAAGG	240
ATAAGCTGGA	CATACACGTC	TTCTATTATC	CGAAAGAAAC	TGGCTCAGCA	GGGTATTTAT	300
ATCGATGCTC	CGGATGAGGC	TTTGGAGAAA	TTGGCTCGTC	TGGGTTATAA	GAAGATCAAT	360
GTACAGAGTC	TTTATGTGAT	TCCCAGCCGA	GAATATGATG	AGATGATCGA	CTTTGTCAAT	420
AAGTTTAAGG	CAGCACATAG	TGATATTACT	GTGAAGGTAG	GGGCTCCGCT	TTTCGATACC	480
GATGAAGATA	TGCGCGAGGT	GGCAGAGATC	TTGCACAAGC	GTTTTCAGCA	AACGATAGAG	540
AAAGGTGAAG	CTATTGTATT	CATGGGACAC	GGCACCAGC	ATGCTGCCAA	TSACAGGTAT	600
GCCCGTATCA	ATAAGATCAT	GAAGAACTAT	AGCAAGTTCA	TGATCGTCGG	AACCGTCGAG	660
TCCGATCCCT	CTATCAATGA	TGTTATTGCC	GAAGTGAAG	AAACCGGTGC	CACGGCCGTA	720
ACAATGATGC	CGCTGATGAG	TGTGGCAGGC	GACCATGCTA	CGAATGATAT	GGCCGGAGAT	780
GAGGACGATA	GCTGGAAGAC	GTGCTGACC	AATGCCGCT	ACACAGTTTC	TATAGACAAG	840
CTGGACAAAT	GCAATTTCTC	AGCTCTTGGG	GATATAGAAG	AGATCCGGAA	TATCTGGCTC	900
AAGCATATGA	AAGCCACCTC	TGCTCGC				927

(2) INFORMATION FOR SEQ ID NO:30

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 1473 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:  
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:  
(A) NAME/KEY: misc feature  
(B) LOCATION 1...1473

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30

CGGAGAGATG	CGCGGAGGCA	ACTGGTACGC	CGTAGGAGGA	AAGAGCTATC	TGGCACAGCA	60
AATACCGCAT	GCCGGAGGAG	AGTATTTCCCT	GAAAGACGAT	CAGCGATCCG	GTGGTGTTC	120
CCTCGACTTC	GAGACGGTCT	ACAGCCGATC	CGATTCGGCT	CGCTACTGGC	GAATCCTCAA	180
CAGCTATCCC	GGGGAGTTCG	GTTACGAAGC	TTTGAAAGCC	GAAGACAGCC	GATATGCCGA	240
TTTCAGGGCA	TTCAAGGAAA	AAGGCGTGAT	ATACTGCAAC	CTGAGGGAAA	CAGCCTTCTA	300
CGAACTCATG	CCCATGCATC	CCGATTGGGT	GCTGGCCGAT	CTTATCGCTA	TCTTGCACCC	360
CGGACTACTT	CCCGACCACC	AACCCCATTT	CTATTATTTC	CTCCAATGAC	ATCCGTCAGC	420
CACCTACGTA	CAATTTCTGT	CGCAGGTATC	CTGGCTGCGC	TGGGAGGGGC	TGTACTCATT	480
CTCTTCGGGG	TTAATCTCTT	CCTCGGCTCG	GTGGCTATTC	CGATGAGCGA	GATCTTCCGA	540
CATCTTTTTT	CAGATCGTCC	CGAAGGAGGA	GAAGCACTCG	TGCACTACAA	TATCCTATGG	600
AAATCCCGCC	TGCCCCGAAGC	CCTCACGGCT	GCTTTTGCCG	GCGCAGGTTT	ATCCGTTAST	660
GGCTTGCAGA	TGCAGACCGT	CTTTCGCAAT	CCTTTGCGCG	GTCCGTCCGT	TCTCGGCATC	720
AGCTCCGGTG	CCAGTTTGGG	TGTTGCTTTG	GTCGTTCTGC	TGAGCGGGTC	GCTGGGAGGA	780
GTGGCATTTGA	GTAGCCTGGG	TTATATGGGC	GAGGTGGCCA	TGAATATAGC	CGCTGCCGTA	840
GGCTCGCTGG	CAGTAATGGG	GCTGATCGTT	TTTGTCAACA	CCAAGGTGCG	CAGCCACGTT	900
ACGCTGCTCA	TTATCGGCGT	TATGATCGGA	TATGTAGCCA	CTGCCGTCAT	CGGGGTATTC	960
AAGTTTTCCT	GTATCGAAGA	AGATATTCGG	GATACGTAA	TTTGGGGGTT	GGGCAGCTTT	1020
TCCCGTGCCA	CGGATTCGCA	ACTGAGTTTC	TTTGCCATTC	TGATGTTGAT	CTTTATTCCG	1080

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5 GCGGGTATGC TCCTTGTCAA GCAGTTGAAT CTCTTATTGC TGGGAGAAAG CTACGCACGT 1140  
AATCTGGGAC TGAATACTCG TCGGGCACGG CTGCTCGTGA TCTCTTCCGC CGGTTTGCTC 1200  
ATCGCTACCG TCACGGCCTA TTGGGGTCCC ATCGGGCTTT TGGGGATGGC TGTGCCACAC 1260  
TTGGCACGGG TTATCTTTCA CACATCGGAT CATCGGATCC TGATGCCTGC TACCTGTTTG 1320  
ATTGGAAGTG CTCTGGCTCT TTTCTGCAAT ATCATTGCTC GTATGCCGGG GTTTGAGGGG 1380  
GCTTTGCCCG TCAATTCCGT AACGGCTTGG GTGGGAGCAC CTATTATCGT CACCGTTTTG 1440  
TTCCGGCGCA GACGCTTCAA GGAAGAAACC GAC 1473

## 10 (2) INFORMATION FOR SEQ ID NO:31

## (i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 2289 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: circular

## (ii) MOLECULE TYPE: DNA (genomic)

## 20 (iii) HYPOTHETICAL: NO

## (iv) ANTI-SENSE: NO

## (vi) ORIGINAL SOURCE:

- 25 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

## (ix) FEATURE:

- 30 (A) NAME/KEY: misc feature  
(B) LOCATION 1...2289

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:31

35 CATTTTTAG TAACGATTAT GCGGACAAAA ACTATCTTTT TTGCGATTAT CTCTTTTATT 60  
GCTCTATTGT CGTCTTCTCT GTCGGCTCAG AGCAAAGCCG TTTTAACCGG TAGTGTGTCG 120  
GATGCCGAAA CCGGAGAGCC TCTTGCCGGT GCTCGAATCG AAGTCAAACA CACCAACATA 180  
GTAGCCGGTG CCGATGCCGG CCGACATTTC GAGATCAAGA ACCTGCCGGC AGGGCAGCAT 240  
ACTATTATAT GTTCGTTGGG GGGGTATGGA CAGAAAGAGG AGGTGGTTGC CATCGAAGCC 300  
GGACAGACCA AAACGATCTC TTTTGCAATG CGACTGCGAA CGAACAACCT GGAGGAAGTC 360  
GTCGTTACCG GTACCGGTAC ACGTTACCGC TTGGTTCGATG CTCCTGTGGC AACCGAAGTC 420  
40 CTTACCGCTA AGGACATAGC CTCTTCTCG GCTCCTACTT CCGAGGCCTT ATTGCAGGGG 480  
CTGAGTCCGT CTTTTGACTT CGGCCCAAT CTGATGGGCT CTTCATGCA GCTGAACGGC 540  
CTTAGCAGTA AGTATATCCT CATCCTTATC GATGGTAAGC GTGTGTACGG CGATGTAGGC 600  
GGTCAGGCCG ATTTGAGTCG TATTTCTCCT GATCAGATCG AACGGATCGA ACTGGTGAAA 660  
45 GTTGCTTCGA GTTCGCTCTA CGGATCCGAT GCCATCGCCG GGGTAATCAA TGTGATCACA 720  
AAAAAGATA CGAATCGACT GAGTGCATAT ACGTCACATC GCATATCGAA GTACAACGAT 780  
CGGCAACCA ATACTTCGCT CGATATAAAC ATCGGTAAGT TCAGTAGCAA TACCAACTAT 840  
TCTTCTTACC ATACGGATGG CTGGCAGAAT AGTCCGTTCG AAATAAAAAA GAAAAAAGGA 900  
TCCGGCGAAC CGGTCTTGA GGAACGTAT AAGAAAACCT TTCGTGCACA GGAAATCAG 960  
GGTGTAAGCC AATCGCTTTC CTATTATGCA ACTAACAATC TTAGCTTCAG CGGAAATGTG 1020  
50 CAGTACAATA AACGTGATG CTTCACCTCG ACTTTTCCG AAAAGAAGGC CTATGACATG 1080  
GATTATCGTG CTTTGACGGC TTCACTCGGT ACGAATATC TTTTCCCAA TGGTCTGCAT 1140  
ACGCTTTCTT TCGATGCCGT CTACGATCGC TTCCGTTTCG GATATTTGTA TCATGACAAG 1200  
GACAGCAGTG AGAGCCTGAT CAACAACCAA GGTCAGACCG AGCAACCCAC ATTCTTTCCG 1260  
GGTCAGCTAC GCAATAAAAA CGATCAGATC CGATACAGCG CAGAGGCTCG CGGTGTATTT 1320  
55 ACCTGCCCTT ATGCGCAGAA ACTGACCGGC GGTGTTGAGT ATTTCCGTGA GGAATTGATC 1380  
TCTCCCTATA ATTTGATTAC CGACAAGGCA GATGCTTCCA CGCTCTCTGC TTATGTACAA 1440  
GATGAATGGA AACCGCTCGA TTGGTTCAAT ATGACAGCGG GTTTCGTCT GGTACACCAT 1500  
CAGGAGTTCG GTACACGAAT GACGCCTAAG GTATCCATAC TCGCCAAGTA TGGGCCGCTG 1560  
AATTTCCGCG CTACGTATGC TAACGGCTAT AAGACTCCCA CGCTGAAAGA GCTTTTGTGA 1620  
60 CGGAACGAAC TCACCACTAT GGGTTCGCAC AATCTCTATC TCGGCAATGC GGATCTTAAG 1680  
CCACAGATGT CGGATTATTA TGCTTTGGGC TTGGAGTACA ATCAAGGCCC TATCTCGTTC 1740  
ASTGCAACGG TTTATGACAA TGAACCTCGC AATCTGATCT CTTTATGGA TATACCGACC 1800  
TCACCCGAGC ACGAAGCTCA GGAATCAAG AAAACCAAGC AGTATGCCAA CATAGGAAAA 1860  
GCTCGCAGCC GCGGCCTTGA TGTCCTATGT GATGCCTCTA TCGGTTGGGG TATCAAGTTA 1920  
75 GGAGCCGGAT ACAGCCTCGT GGAAGCTAAG AATCTCCAGA CGGATGAGTG GCTGGAAGGA 1980  
GCTGCACGTC ATCGTGCCAA TGTGCACGCC GATTGGGTTC ACTACTGGGG TCAGTATAGA 2040  
CTTGGCGTGA GCCTTTTCGG CCGTATTACG AGCGAGCGTT ACTACAAAGA CGGCAATGCT 2100  
CCGACTATA CCTTGTGGCG ACTGCCACA TCGCATCGTT TCGCTCATTT CCGCCACATC 2160  
ATCCTGGATG GAACGCTCGG TATAGACAAC CTGTTTGACT ACGTGGATGA TCGTCTATG 2220  
70 GGTGTCAATT ATGCTACCGT AACGCCGGGA CGTACTTTCT TTGCTCAAAT AGCGATTCTGA 2280  
TTCAACAAC 2289

## 75 (2) INFORMATION FOR SEQ ID NO:32



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5      (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 1095 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: double
          (D) TOPOLOGY: circular

      (ii) MOLECULE TYPE: DNA (genomic)

10     (iii) HYPOTHETICAL: NO

      (iv) ANTI-SENSE: NO

      (vi) ORIGINAL SOURCE:
          (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

      (ix) FEATURE:
          (A) NAME/KEY: misc_feature
          (B) LOCATION 1...1095

20     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:32

TGCTGCGCAA GGCTTCGGGA CACCTCTCCC CGGAAGAAAGT CGTTTCGGAA TGATACCGTT      60
TTTCTCTATT TCGTTATTCA TCTGATCAAA CATATTATCA TTATGACGGA CAACAAACAA      120
CGTAATATCG TATTCCCGGC GTTTCCTCTC TTGCTGGGAG TCATCGCAGT GGTGACGATC      180
GTTGGTTTTT TCATGCTCAG ACCGGCCGAG GAGATTATCC AAGGACAGAT AGAAGTGACC      240
GAATACCGAG TGTCACAGCA AGTGCCCGGG CGCATCAAGG AACTTAGGGT ATCCGAGGGA      300
CAGCAGGTGC AAGCCGGGCA TACCCTCGCT GTCATCGAAG CCCCCGACGT AGCGGCTAAG      360
ATGGAGCAGG CAAAGGCTGC CGAAGCAGTC GCACAGGCTC AGAACGCCAA GGCTCTCAAA      420
GGAGCACGCA GCGAACAGAT ACAGGCAGCC TATGAGATGT GGCAGAAAGC TCAGGCCGGC      480
GTAGCCATAG CGACCAAGAC ACACCAGCGC GTSCAGAACC TCTATGACCA GGGAGTGGTA      540
CCGGCTCAGA AGTTGGACGA AGCCACTGCC CAGCGCGATG CGGCCATCGC TACGCAAAAA      600
GCGGCCGAAG CCCAGTACAA TATGGCTCGC AACGGTGCCG AACGCGAAGA CAAGCTGGCA      660
GCTTCTGCCC TCGTCGATAG AGCGAGAGGA GCGCTCGCCG AGGTGGAGTC GTACATCAAC      720
GAAACCTACC TCATCGCCCC ACGGGCAGGC GAAGTGTGCG AGATATTCCC CAAAGCCGGC      780
GAACTCGTAG GTACCGGCGC ACCTATCATG AATATCGCCG AGATGGGCGA TATGTGGGCC      840
AGCTTTGCCC TTCGTGAGGA TTTCCTCAGC AGCATGACCA TGGGAGCCGT TCTGGAGACT      900
GTGGTGCCGG CTCGTGAATGA AGAAAAAGTA CGCTTCAAGA TCACATTCAAT CAAGAACATG      960
GGTACCTATG CTGCCTGGAA AGCGACCAAG ACAACAGGGC AGTACGACCT GAAGACCTTC      1020
GAGGTAAAGG CCACCTTTGC GGATAAAGAC AAGGCACAAA AGCTACGCCC GGGTATGTCC      1080
GTGATCATAC GCAAG
1095

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(2) INFORMATION FOR SEQ ID NO:33

45      (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 960 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: double
          (D) TOPOLOGY: circular

50      (ii) MOLECULE TYPE: DNA (genomic)

      (iii) HYPOTHETICAL: NO

55      (iv) ANTI-SENSE: NO

      (vi) ORIGINAL SOURCE:
          (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

60      (ix) FEATURE:
          (A) NAME/KEY: misc_feature
          (B) LOCATION 1...960

      (xi) SEQUENCE DESCRIPTION: SEQ ID NO:33

CGGCAATCCT CTCTGATCG AAGAAGCTTC CAAACGTC TGAATAAATA TCATTCTCAA      60
AGCGTTTAS AGGTCGGCAA AATTGGGATT GTGATTATCT TTGCGCCCAT AGTACGGAAT      120
GTACATCAAC AACCCCTTT TTTAAGCCAT AAATCAATTA TGCGTATTGT CAGTAATTTT      180
TTGTTCTCT CTTTTTCGGT TTGCTTTTT GCATCATGCC GTTCCCAGCG AGAAAAGGTC      240
GTTTACCTGC AAGATATCCA AACTTTTAAT CGGGAGATTA TCGCTAAACC ATATGACGTA      300
AAAATTGAGA AGGACGATGT GCTGAACATC CTTGTCAACA GAGAGACCC GGAGCTTTCA      360
ACGCCCTACA ACCAAGTGTT GACCACTCGT GCACTGGCCC GCAACGGCTA TGGAACGAAC      420
TCGAACGAAG GCTTCCTGCT CGATTGAAA GGGTACATCA ATTATCCTAT TTTAGGCCAG      480
ATCTATGTAG AGGGCCTTAC TCGTACCGAA CTGGAGAAGG AGATACAGAA GAGGATTATT      540
TCCAGTGGAT TTATCAAGGA TCGTACGGTA ACGGTGCAGC TTCAAAATTT CAAGGTGTCG      600

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22 / 490

5 GTTTTGGGAG AGGTGAATCA TCCGGGTTTCG ATGTCGGTAA AAGGAGAGCG AATAACTCTT 660  
 TTGGAAGCGA TCGGAATGGC CGGAGACCTG ACAATCTATG GTCGCCGCGA TCGGGTTTTT 720  
 GTGATTAGAG AAACCGATGG GCATCGCGAG GTTTTCCAGA CGGATCTCAG AAAGGCCGAC 780  
 TTGCTCGCAA GCCCGTGTA CTATCTGCAT CAGAACGACG TCATCTATGT GGAGCCGAAC 840  
 GACAAGAAAA CACAGATGAG CGAGATCAAC CAGAATAATA ACGTAAACGT ATGGCTGAGT 900  
 GTTACCTCCA CTTTGGTATC CATTTCCACG CTGACGATTA CGATAATAGA TAAGACCAAA 960

## (2) INFORMATION FOR SEQ ID NO:34

10

## (i) SEQUENCE CHARACTERISTICS:

15

(A) LENGTH: 1746 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

20

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

25

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc feature

(B) LOCATION 1...1746

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34

35 TCAAAAATAG TACTACGAAA GTTTTGTACC TTAGCGCGCA TGAAAAAGAC CAATCTGTTT 60  
 TTAATCTCTGC TGGTGATCTT TATCACCGGT AGTTTATGA CTGCCTGTGC ACAGAAGTCC 120  
 AAGACGAACA AACTCACCGA AGAAGATCGG AGCCGCAATG AGTATGTACA GTCGATGGAT 180  
 GTGCTTAGCA ATATTATCGG TAACGTCAGG CTGTATTTTG TCGATACCAT AAGTATCAAA 240  
 CATATGACTC GGGGTGGTAT AGATGCGATG TTGGGCGGGC TTGACCCCTA TACCGAATAC 300  
 ATTCTTACG AGGAAATGGA TGAAGTAAA TTGATGACTA CGGGAGAGTA TGCCGGAGTC 360  
 GGAGCTATCA TATCGCAGCG CCCGGATAGT GCTGTGATTA TCCAGAGACC TATGGAAGGT 420  
 ATGCCCGCAG ACGAAGCAGG ATTGATAGCA GCGACCGCA TCCTGACTAT CGATGGGAAA 480  
 40 GACTTCCGCA AATCCACCAC ACCGAAAGTA AGCCAAGCAC TGAAAGGGAT AGCCGGTACT 540  
 GTTGCAAAGG TGACAGTAAT GCGCTATGGC GAAACCAAAC CTCGTACTTT TTCCGTGAAA 600  
 CGTCAAAAAG TGATTATGAA TTCCGTCCTT TACAGCGGAA TGCTCGATGG CTCGATAGGA 660  
 TATATCCGCT TGAACAACCT TACGGACAAA AGTGCAGAAG AGGTGCGCAC GGCTTGTGTG 720  
 GATCTTCGTG ACAAAACAAG AGCGAAAGGT CTCATTTTGG ATTTAAGAGG CAATGGTGGC 780  
 45 GGACTGATGC AGGCTGCTAT CGAGATAGTC AATCTGTTTG TCCCTAAGGG CAAAGAGGTG 840  
 GTAACGACCA AAGGTGCGAT TGCAGAGTCG GCGTCCGTAT TTCGCACATT GACTGAACCG 900  
 ATCGACACGA AACTCCCGAT AGTAGTCCCTG ATCGATGGAC AATCGGCATC TTCTCGGAG 960  
 ATTGTAGCCG GAGCACTGCA GGATATGGAC AGGGCTGTAC TGATGGGACA AAAGAGCTAT 1020  
 GGCAAAAGGG TTGTACAAAC GACTCGTCAG CTACCATACA ACGGCGTGAT CAAATTGACT 1080  
 50 ACGGCCAAGT ACTACATCCC AAGCGGACGT TGTATTCAGC GTTTGGACTA CAGCCGCACC 1140  
 AATCGGACAG GTATGGCAAC GGCCATTCTT GACAGTCTGC ACAAATCTT TTACTGCT 1200  
 GCCCGAAGAC GTGTAGAAGA TGCAGGAGGA ATCTGCTG ACATCGAGGT CAAACAAGAT 1260  
 ACAGCTGCCA CATTACTTTA TTATATGGCC ATCAATAATG ACGTTTTTCA TTTCGTCACA 1320  
 55 GGTATGTGTC TCAAGCATAA AACGATTGCC AAGCCGGAGS ATTTTTCAT AACGAACGAG 1380  
 GACTATGCAG CTTTCTGCAA GATGATGGAA GAAAAGAAAT TTGACTATGA TCGCCAGAGT 1440  
 GGCAAGATGC TTGACAAACT GGAGGAACTG GCTAAGATAG AAGGCTACCT GCCGGAAGCC 1500  
 AACTCGGAGC TTAAAGCACT ACGCGAAAAG CTAAACCCA ACCTGTCGCG TGATCTGCTA 1560  
 CGATTCAAAA AGGAGATAAC AACTATCTC AACAATGAGA TTGCTACTCG CTATTATTAT 1620  
 60 GAGCGAGGCA GTATCCGCA GAGTTTGCCG GAAGATAAGS TAGTCAAAGA AGCTATTAG 1680  
 CTGCTGAAG ACCATCCGGA ACAAAATCGA CAGATCCTTG CAGCTCCGAA AGCAGAGAAT 1740  
 AAAGGG 1746

## (2) INFORMATION FOR SEQ ID NO:35

65

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2955 base pairs

(B) TYPE: nucleic acid

70

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

75

(iii) HYPOTHETICAL: NO

23 / 490

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc\_feature

(B) LOCATION: 1...2955

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35

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GTAAACAGACA AAATGCAAAA CAAAGGATTT GTGATTGTTA TCACATCGGC TCTGGCCATC 60  
ATCTGTGCGT TTTACCTGTC ATTCTCTTTC GTTACGAACC GTTACGAAAA GAAGGCTAAG 120  
GCGATGGGCG ATGTTGCCGG AATGGCCTAT CTGATTCCA TGTCGAATGA GAAGSTCTGG 180  
TTCCGGCTACA CGCTGAAAGA AGCTCAAGCC CAGCAAATTG GTCTTGGCCT GACTTAAAG 240  
GGGGGTATGA ACGTTATCTT GAAACTTAAC GCAAGCGATC TGCTTCGTAA CCTCTCTAAC 300  
AAAAGTTTGG ATCCCAACTT CAACAAAGCT CTGGAGAATG CTGCCAAGAG CACGGAGCAA 360  
TCCGACTTCA TCGATATTTT CGTGAAGGAA TATCGCAAGC TCGATCCCAA CGGTGCTTG 420  
GCCGTATCTT TCGTTTCGGG TGACCTTCGC GACCAGATTA CCGCAAAGTC TACGSATGCA 480  
GACGTAGTGC GTCTGCTCAA AGAAAAATAT AATAGTGCTG TAGAAGCTTC GTTCAATGTG 540  
CTCCGTGCTC GTATCGATGC TTTCCGGTGTG GTTGACCTA ATTTGCAGCG ATTGGAAGGG 600  
CAAGGGACSTA TCCTTGTGCA ACTCCCCGGA GTGAAAGACC CTGAGCGTGT TCGTACCCTT 660  
TTGCAACGCA GTGCCAACCT ACAGTTCTGG CGTACATACA AATTCGAAGA GGTGAGCGGA 720  
GACTTGATCG CTGCCAATGA TCGTCTGAGC GAATTGGCTA TGAACAACAC GGATGCTACC 780  
CCGGAAACAG AGCCTGCAAC TACTGACTCT GTAGCTGCAA CAGCCGATTC TGCTGCTGTA 840  
CAAGTGTAG CTGATTCTGC TACTGTAGCA CAAAAAGAGG CCAAGGATGC TACTCGTAAA 900  
GACGCACTCT TCTCTCTGCT TACTCCCCTG AATCGTGGCG GTGCAGTAGT GGGTGTGGCT 960  
CGTCTGTCTA ATATGGCTCA GATATCTGAA ATGCTCCAGC AAGCTCAGCA TCTGAAGGTT 1020  
ACACGTGAAG ATGTGCTTTT CCTCTGGGGT GCTAAAGCAA TCGAAGACCC CGAAACCCAA 1080  
AAGGAGACCG ACCTCTACGA ACTCTATGCT ATTCTGATCA ATCGTACGGG AGATCCTGAT 1140  
TTGGGAGGTG ATGTAGTGAC TTTCCGCCAG AGTGATATCC AAAATGACTT CGGTGCTTCC 1200  
GAACCGATCG TTTGATGAC GATGAATGAA GAAGGTGCTC GTAAATGGGC GCGTATCACA 1260  
AAGGATAACG TGGGACGGGC AATCGCTATC GTTTTGGATG GTGTGGTTTA TTCTGCTCCG 1320  
AACGTGAATG ATGAGATCAC GGGCGGTGCG TCTCAGATCT CCGGGCACTT CACCGTGGAG 1380  
GAGGCGGTG ACCTTGCCAA CGTACTCAAC TCCGGTAAAA TGGATGCTAC GGTAAGCATC 1440  
GAACAGGAAA ACGTGATTGG TCTACGCTG GGTGCCGAGT CCATTAAAGC CGGATTCTTG 1500  
TCGTTCTGCT TCGCTTTGGT TATCCTGATG TGTACATGT GTCTGGCTTA CGGTTTCTTG 1560  
CCGGGTCTTA TCGCAACGG CGCATTGATT GTAAACAGCT TCTTCACATT GGGCGTATTG 1620  
GCTTCTTTCC ATGCCGTGCT GACCCCTCG GGTATCGCAG GTTTGGTGCT GACGCTGGGT 1680  
ATGGCTGTGG ATGCCAACGT ACTTATCTTC GAGCGTATCA AAGAAGAGCT TCGTGCCGGT 1740  
AAGACTCCGA TTCGTGCCGT TACGGATGGT TATGGCAACG CTTCTCTGCT CATCTTCGAC 1800  
TCGAACGTTA CGACTATTAT TACCGGTATC ATCCTATTC TCTACGGGAC GGGGCCGATT 1860  
CGCGGTTTTG CCACTACGTT GATTATCGGT CTTATCGCTT CTTTCATTAC GGCTGTCTTC 1920  
TTGACTCGTA TCGTCTTCGA GAAACTGGCG AAAAAAGGTC GTTTGGATAA GATTACATTC 1980  
ACTACGAGCA TTAATCGCAA TCTCCTTGT AATCCCTCAT ACAACATCTT GGGAAGCGC 2040  
AAGACCGGCT TTATCATTCG GGTGATTATC ATCGTTTTGG GACTTATAGC TTCAATTTACA 2100  
ATCGGTCTCA ATAGGGGTAT TGAATCTCC GGAGGACGTA ACTACGTAGT TAAATTCGAC 2160  
CAGCCTGTAT CTTCGGAAGC CGTTCGTTCG GCCTTGTCTT CTCCCTGCA GGAAGAGGTA 2220  
TTGGTTACCT CCAATCGGTAC TGAAGGGACA GAGGTGCGTA TATCTACGAA CTATAAGATC 2280  
CAGGAGGAAA GCGAAGAAAC TGAAGCAGAG ATTACTGACA AATTGTATCA GAGCCTGAAA 2340  
GGTTTCTACA CCGAGCAGCC TACTGCTGAT CAGTTCTTGG ACAATATCAT TAGCTCTCAG 2400  
AAAGTAAGTC CCAATATGTC GAGTGACATC ACGAGAGGTG CTATTTGGGC TGTGCTGTTA 2460  
TCGATGATCT TCAATGGCCAT TTATATTCTG ATTCGCTTCC GTGACATTTT TTTCTCTGCC 2520  
GGGGTATTCT TATCTGTGGC CGCTACTACA TTCTGCATTA TTGCTCTGTA TGGTGTGCTG 2580  
TGGAAGATTG TGCCCTTCAC CATGGAGATC GATCAGAACT TCATCGCTGC TATTCTGGCT 2640  
ATCATCGGTT ACTCGCTCAA TGACACCGTG GTTGTATTTC ACCGTATCCG AGAGACGATG 2700  
AAATTGTACC CCAACAGAGA TCGCTATCAG GTGATCAACG ATGCCCTTAA TTCAACATG 2760  
GGTCGAACAT TAAATACGTC TTTGACTACG TTTATCGTTA TGTGGTAAT CTCATCTTT 2820  
GGAGGTGCTA CGATGCGTAG TTTACGTTT TCGATCCTGC TCGGTATCGT TATCGGTACA 2880  
TACTCTACGC TCTTTGTTGC TACACCCCTT GCCTACGAGA TCCAAAAGCG CAAGCTCAAC 2940  
AAAGCAGCTA AGAAA 2955

(2) INFORMATION FOR SEQ ID NO:36

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 3138 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

24 / 490

- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:  
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:  
(A) NAME/KEY: misc\_feature  
(B) LOCATION 1...3138
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:36

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GACTTCCCTT GGTTAGGGT AAAACCGGAG AAGAAAAGAA AACACATAA CAGTAATAAT 60  
TTTAAGTTTA ACGCAAAAGA AAAGTCTATG AAAAGAATGA CGCTATTCTT CCTTTGCTTG 120  
CTGACGAGCA TTGGGTGGGC TATGGCCCAG AATAGAACCG TGAAGGGTAC AGTTATCTCC 180  
TCCGAGGATA ATGAGCCCCT GATCGGCGCG AATGTCGTGG TTGTGCGAAA CACCACTATC 240  
GGTGCTGCAA CCGACTTGGA TGGCAACTTC ACGCTTAGCG TGCCTGCCAA TGCCAAAATG 300  
TTGAGAGTGT CCTATTCCGG TATGACTACC AAAGAGGTCT CCATCGCTAA TGTGATGAAG 360  
ATCGTACTGT ATCCGGACTC TAAGSTTCTG GAGCAGGTAG TTGTATTGGG TTACGGTACG 420  
GGACAGAAAC TCAGCACTGT TTCCGGTTCT GTGGCCAAAG TGTCCAGCGA AAAGCTCGCG 480  
GAAAAGCCCG TTGCCAATAT CATGGATGCC CTCCAAGSTC AGGTAGCCGG TATGCAGGTT 540  
ATGACTACAT CCGGTGACCC TACTGCCGTC GCTTCTGTGG AGATCCATGG TACAGGGTCTG 600  
TTGGGGGCAA GCTCTGCCAC ATTGTATATC GTGGATGGTA TGCAAACTTC TTTGGATGTT 660  
GTGGGTACGA TGAATCCGAA TGATTTTGAA TCTATGTCCG TTTTGAAAGA TGCTTCTGCA 720  
ACATCTATTT ATGGAGCTCG TGCTGCAAAAC GGAGTCTGTT TCATTCAAAC GAAGAAAGGT 780  
AAAATGAGCG AGAGAGGTCT TATTACCTTT AATGCCAGTT ACGGGATTTT TCAAATCCTG 840  
AATACTAAGC CCCTTGATTA TATGATGACT GGAGATGAAT TGCTGGATTT TCAGGTGAAG 900  
GCAGSTTTTT GGGGGAACAA TCAAACCGTT CAGAAGSTTA AAGATATGAT CCTTGCCGGA 960  
GCTGAAGATT TGTATGGCAA TTATGATTCT TTGAAAGATG AGTATGGTAA GACATTGTTT 1020  
CCAGTGGATT TTAATCATGA TGCAGACTGG CTCAAGGCTT TGTTTAAAC AGCACCACCC 1080  
AGTCAAGGTG ATATTTCTTT CTCCGGAGGG TCTCAGGGAA CTTCATATTA TGCTCTATA 1140  
GGCTACTTCG ATCAGGAAGG TATGGCTCGT GAACCGGCAA ATTTAAGCG CTATAGTGGC 1200  
CGGCTCAACT TCGAAAGTCG TATCAATGAA TGGCTGAAAG TTGGTGCAAA TTTGTCTGGT 1260  
GGCATAGCGA ATAGACGATC TGCCGACTAT TTTGGAAGT ATTATATGGG GTCAGGTACT 1320  
TTCCGTGTGT TAACGATGCC TCGTTATTAT AACCTTTTGT ATGTGAATGG GGATTTAGCA 1380  
GATGTCTATT ACATGTATGG AGCTACCAGA CCTTCTATGA CAGAACCCTA CTTCGCAAAA 1440  
ATGAGACCGT TCAGTTCCGA ATCACATCAG GCCAATGTAA ATGGTTTCGC CCAGATTACT 1500  
CCGATCAAAG GCCTTACTTT AAAGGCACAG GCTGGTGTG ATATTACTAA TACTCGCACT 1560  
TCTTCTAAGA GAATGCCCAA TAATCCGTAT GATTCTACTC CTCTTGGGGA AAGAAGAGAA 1620  
AGAGCTTATC GAGATGTTAG CAAGTCTTTT ACAAATACGG CTGAATATAA GTTTTCAATT 1680  
ATGAAAAAAC ATGATCTTAC AGCATGTGAT GGGCATGAAT ATATTGAATA TGAAGGGGAT 1740  
GTTATTTGGG CATCTCTAA AGGATTTGAA AGTGATAAGT TGATGTTACT GAGCCAGGGA 1800  
AAAACCGGAA ATAGTTTGTC TTTGCCGTAA CACAGAGTCG CTGAATATGC CTATTTGTCT 1860  
TTCTTTAGTC GTTTTAATTA CGGTTTGGAC AAATGGATGT ATATAGATTT CTCTGTTCTG 1920  
AATGACCAAT CCTCTCGATT CGGATCCAAT AATAGAAGCG CGTGGTTCTA TTCTGTCTGG 1980  
GGAATGTTTG ACATATATAA TAAATTCATT CAAGAAAGTA ATTGGCTCAG TGATCTTCGA 2040  
CTCGTTACTG TGAACAATTA TACTGAAGAT GCTATGGGCG TTAGCATTTT TACAGCAGGC 2100  
AATCCCGACC TCTCGTGGGA AAAGCAGTCT CAGTTCAACT TCGGTTTGGC TGCAGGGGCT 2160  
TTCAATAATC GCTTATCTGC AGAGGTAGAT TTCTATGTCC GCACTACGAA TGATATGTTG 2220  
ATTGATGTCC CGATGCCTTA TATCAGTGGT TTCTTCTCAC AGTATCAGAA TGTAGGCTCT 2280  
ATGAAAAATA CGGGTGTAGA CCTTCTCTTT AAGGGGACGA TCTACCAAAA TAAGGACTGG 2340  
AATGTATATG CTTCTGCGAA TTCAACTAC AATAGACAGG AAATAACAAA GCTTTTCTTC 2400  
GGTCTCAATA AGTACATGTT GCCTAATACC GGTACTATAT GGGAAATTGG GTACCCCAAT 2460  
TCGTCTTATA TGGCTGAATA TGCTGGAATC GACAAAAAAA CCGGTAAGCA GTTGTGGTAT 2520  
GTTCTGGTC AAGTCGATGC GGATGGTAAT AAAGTTACAA CAAGCCAGTA CTCAGCTGAC 2580  
TTGGAGACAC GAATTGATAA GTCTGTTACT CCTCCTATTA CAGGTGGTTT CTCCTTAGGT 2640  
GCTTCTTGGG AAGGACTTTT TTTAGATGCT GATTTTGCTT ACATCGTTGG TAAATGGATG 2700  
ATCAATAATG ACCGTTACTT TACAGAGAAT GCAGGTGGAT TGATGCAATT AAATAAAGAT 2760  
AAAATGCTAT TGAATGCCTG GACAGAGGAT AATAAAGAAA CAGATGTTCC AAAATTGGGA 2820  
CAGTCTCCTC AGTTTGATAC GCATTGTGTT GAGAATGCTT CTTTCTCTCG TTTGAAGAAT 2880  
CTCAAACTCA CCTATGTAAT CCCCATAAGT CTTTTGCTG GGCAGAAATG GATTGGTGGG 2940  
GCTCGTGTCT ATTTGATGGC GCGCAATCTG TTAAGTGTTA CGAAGTATAA AGGCTTTGAC 3000  
CCTGAAGCAG GGGGGAATGT GGGAAAAAAT CAATATCCTA ATTCTAAGCA GTACGTTGCG 3060  
GGTATTCAGT TGTCTTTT 3120  
3138

(2) INFORMATION FOR SEQ ID NO:37

- 70 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 2607 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: circular
- 75 (ii) MOLECULE TYPE: DNA (genomic)

25 / 490

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:  
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:  
(A) NAME/KEY: misc\_feature  
(B) LOCATION 1...2607

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37

15	TGGCATAGGA ATATTTTTAT CTTTGCGAGT ACATTTAGCC CGAAAAATAT GCTCCCACTG	60
	CCATACCGTT ATGCAAAAAC CGAGCACCTT TTTCTCGCAA AAGGATACTG CAAGAATCCA	120
	ATAACAAACA TAATTATCCT ATTTATGAAG AAAAAGAATT TTTTGCTTCT TGGCATTTTC	180
	GTGCTTTTGC TGACTTTTCAT CGGCAGCATG CAGGCACAAC AGGCCAAAGA TTATTTCAAC	240
20	TTTGACGAAC GGGGCGAGGC CTACTTCTCA TTCAAAGTGC CTGATAGGGC CGTTCTACAA	300
	GAGCTGGCTC TGATCATGTC CATCGACGAG TTTGACCCCG TAACCAATGA AGCCATGCCC	360
	TATGCCAGCG AAGAGGAGTT CGAGGCATTG CTGCGCTATG GGCTCAAGCC TACATTCTTG	420
	ACTCCTCCAT CCATGCAGCG CGCTGTCGAG ATGTTGCGACT ACCGCTCAGG AGAAAAATAC	480
	GAATGGGAATG CTTACCCAC CTATGAAGCC TATATCAGCA TGATGGAAGA GTTCCAAACA	540
	AAGTATCCAT CACTTTGTAC TACTTCCGTC ATTGGCAAGT CCGTAAAGGA TCGTAAACTG	600
25	ATGATTTTGA AGCTGACGTC CTCTGCCAAT ACAGGGAAAA AGCCTCGCGT GCTCTATACT	660
	TCTACGATGC ACGGAGACGA AACGACCGGA TATGTGGTAC TGCTCCGACT CAAAGACCAT	720
	CTGCTGTGCA ACTACGAATC CGATCCGAGG ATTAAGAACA TTCTGGATAA AACGGAAGTA	780
	TGGATCTGCC CTTTGACCAA TCCGGACGGA GCATACAGAG CCGGAAACCA CACCGTACAA	840
	GGAGCTACTC GGTACAATGC CAACAATGTC GATTGGAACC GTAACCTCAA GGATGATGTA	900
30	GCCGCTGATC ACCCGATGG AAAACCTTGG CAGCCGGAGG CAACTGCATT CATGGATTG	960
	GAAGGAAACA CCTCTTTCGT GCTCGGTGCC AATATACATG GAGGAACAGA GGTGGTGAAC	1020
	TATCCATGGG ATAATAAAAA AGAAAGACAT GCAGACGATG AGTGGTACAA ACTGATCAGT	1080
	CGCAACTACG CAGCCGCTTG TCAGAGTATT TCCGCCAGCT ACATGACCTC CGAAACCAAT	1140
	TCCGGGAATCA TCAACGGTTC AGACTGGTAT GTAAATCCGG GAAGTCTGCA GGACAATGCA	1200
35	AATTATTTC AATCGTCTCG AGAAATTACC CTTGAAATCA GCAACACGAA GTTGGTGCCG	1260
	GCCTCTCAAC TTCCAAAGTA TTGGAATCTG AACAAAGAAT CTCTGCTTGC TCTGATCGAA	1320
	GAATCCTTAT ACGGCATCCA TGGTACAGTG ACTTCCGCTG CGAACGGACA GCCTCTCAAA	1380
	TGCCAGATCT TGATAGAAAA CCATGACAAG CGCAACTCCG ATGTTTACTC CGATGCTACC	1440
40	ACAGGCTACT ACGTACGTCC TATCAAAGCC GGCACCTATA CGGTGAAATA CAAAGCCGAG	1500
	GGTTATCCTG AGGCAACTCG TACCATTAGG ATCAAGGACA AAGAAACCGT CATCATGGAC	1560
	ATTGCATTGG GCAACTCGGT TCCTCTGCCT GTACCCGATT TCACAGCTTC TCCTATGACC	1620
	ATCTCAGTAG GCGAAAGCGT CCAATTCCAA GATCAAACGA CAAATAACCC CACGAATTGG	1680
	GAGTGGACGT TCGAAGGCGG ACAGCCTGCC ATGAGTACAG AGCAGAATCC GCTCGTATCC	1740
	TATAGTCATC CCGGTCAGTA CGACGTTACG CTCAAAGTGT GGAATGCAAG TGGTTCCAAC	1800
45	ACGATPACGA AAGAAAAATT CATCACTGTC AATGCCGTTA TGCTGTAGC TGAATTTCGT	1860
	GGTACCCCGA CGGCAATAGA AGAGGGCCAG ACGGTATCTT TCCAAAACCA ATCCACCAAT	1920
	GCCACCAACT ACGTATGGAT ATTCGATGGC GGCACCTCCG CTACCACTGA AGACGAAAAC	1980
	CCGACTGTGC TTTACAGCAA AGCCGGCCAA TACGATGTCA CGCTCAAGGC GATCACTGCT	2040
	TCCGGTGAAA CCGTGAAGAC GAAAGAAAAA TACATCACTG TCAAGAAAGC TCCGTCCTCT	2100
50	GCTCCGCTAG CCGACTTCGA AGGAACACCT CGAAAAGTAA AGAAAGGCGA GACAGTTACT	2160
	TTCAAAGACT TGTCTACGAA CAATCCGACT TCATGGCTTT GGGTGTTCGA AGGCGGCTCT	2220
	CCTGCCACCA GCACGGAGCA AAACCCGGTG GTCACTTACA ATGAAACAGG CAAGTACGAT	2280
	GTCCAGCTGA CTGCCACCAA CGAGGGCGGA AGCAATGTGA AGAAAGCAGA AGACTACATT	2340
	GAGGTATCC TCGATGACAG TGTCGAGGAC ATAGTGGCAC AGACGGGTAT CGTCATTCTGT	2400
55	CCGCAAAACG GAACGAAGCA GATCCTCATA GAAGCCAACG CTGCTATCAA AGCGATCGTT	2460
	CTCTATGACA TCAATGGACG GGTCGTACTC AAAACTACTC CGAATCAGCT CCGCTCGACC	2520
	GTAGATCTTT CCATCCTGCC CGAAGGAATC TACACCATCA ATATCAAAC GGAATAATCC	2580
	GCTCGCACGG AAAAGATCCA TATCGGG	2607

(2) INFORMATION FOR SEQ ID NO:38

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 318 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc feature  
(B) LOCATION 1...318

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38

CTTTCGTACA	GTGGAGAGAG	CGATGCAAAA	GAGTCTGATC	AGAATTGCCG	GAAATGTACC	60
TTCATCGGCT	TTGAAAAACG	AGTAAATACG	ATGCGACTGA	TCAAGGCTTT	TCTCGTGCAA	120
CTCTTACTGC	TCCCCATTTT	CTTCTACAAG	CGGTTTATAT	CGCCGCTTAC	ACCGCCTTCA	180
TGCCGGTTTA	CCCCCTCATG	TTCGTCCTAT	GCCATCGAAG	CCTTACGTAA	ATATGGCCCG	240
GGCAAAGGAC	TATTGCTGAG	CATCAAGCGT	ATTCTCCGCT	GTCACCCGTG	GGGTGGAAGT	300
GGCTATGACC	CCGTTCCG					318

(2) INFORMATION FOR SEQ ID NO:39

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2583 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc feature  
(B) LOCATION 1...2583

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39

TTAGAGATGG	CATACGACTT	TACACAAACA	TTCCGCAACA	GCCTGGAGTA	CAGCTATCAG	60
GAAGCAACCC	GTCTCGGCGT	CGTAGCCGTG	ACGCAAGATA	TGCTCGTACT	CGGTATCATT	120
CGCGACGGAG	ACATGGCGC	GATCGACATC	ATGCGGCACT	ATGGGATCAA	CTTGTACGAA	180
CTCAAACGCT	TGATCGAGTT	GGAAGCCATC	GCCGAGAGTT	TGCCTGCTTC	GCCTGAGGGA	240
TCGCCCATCT	TCACCCCTTC	GGCTCGGGAG	GCTATCGATG	ATGCCACAGA	CATCTGTGCC	300
GACATGGAGG	ACGAGGCCGT	CAGCCCGGTC	CATCTGTTGC	TGAGTATCCT	CAACTCGACA	360
CAGGAGAGCT	TAGTACAAAA	GATATTTATG	AAACAAGGTA	TAAAAATCGA	CACCATCCCTG	420
TCGGATTACT	TCGGACAGCG	CAACCCCTCC	GAAGGGAAGT	CTCCCTCCGA	AATGGAGATC	480
CTCGACGGGT	ACCAAGACAA	CGACTTCGAC	GACGAAGAGG	ACGAATCCTC	TCCGCCTTCC	540
GGGAATAGCG	GGACAGGCGG	AGGCTCCGGC	GACGCCCCCG	AACAGAATAC	CGGCGGAGGC	600
GATACTACCA	CCACGACACG	GAGTGGAGGC	GACACGCCCTG	CACCTGGACAC	CTTCGGCACC	660
GACATCACTG	CCATGGCGGC	AGCAGGCAAG	CTCGACCCGG	TAGTGGGTCG	GGAGCAGGAG	720
ATCGAAAGGG	TGATACAGAT	ACTCAGCCGG	CGCAAAAAGA	ACAATCCGGT	GCTCATCGGG	780
GAACCCGGTG	TAGGCAAGAG	TGCCATCGTG	GAAGGACTGG	CCGAACGCAT	CGTGAACAGG	840
AAGGTGAGCC	GTATTCTTTT	CGACAAGCGG	ATCATCAGCC	TCGATTTGGC	TCAGATGGTA	900
GCCGGCACCA	AATATCGCGG	ACAGTTCGAA	GAGCGGTGTA	AAGCCGTGCT	CGATGAGCTG	960
AAGAAGAATC	CGCAGATCAT	CCTCTTCATC	GACGAGATAC	ATACCATCGT	GGGAGCAGGC	1020
TCTGCAGCCG	GATCGATGGA	TACGGCCAAT	ATGCTCAAAC	CCGCTCTTGC	CCGTGGACAG	1080
GTACAGTGCA	TCGGAGCCAC	TACGCTGGAT	GAGTATCGTA	AGAACATAGA	AAAGGACGGA	1140
GCACTCGAAC	GCGGCTTCCA	GAAGGTGCCG	ATAGCCCCCT	CGACTGCAGA	AGAAACGCTG	1200
ACCATCCTGC	AAAACATCAA	AGAGAAATAC	GAGGACTATC	ACGGTGATCG	CTATACGGAC	1260
GAAGCGATCA	AAGCGGCAGT	GGAAGTACCC	GATCGCTATG	TATCCGATCG	TTTCTTCCCA	1320
GATAAGGGCGA	TAGATGCCAT	GGACGAGGCC	GGCGCGAGCG	TCCATATCAC	CAATGTGGTG	1380
GCTCCGAAAG	AAATCGAGAT	ACTGGAGGCC	GAATTGGCAT	CGGTGCGAGA	GAACAAGCTC	1440
TCGGCCGTAA	AGGCTCAGAA	CTACGAACTG	GCTGCCTCCT	TCCGCGATCA	GGAGCGGCGC	1500
ACTCAGCAGC	AGATAGCGGA	AGAGAAGAAA	AAATGSSAAG	AGCAGATGTC	CAAGCACCCG	1560
GAGACGGTGG	ACGAGAATGT	AGTGGCGCAT	GTAGTGGCGT	TGATGACAGG	CGTTCCGGCT	1620
GAGCGGCTGA	GCACGGGCGA	AGGCGAACGT	CTGCGCAQGA	TGGCAGATGA	TCTCAAGACC	1680
AAAGTAGTAG	GTCAGGACAC	AGCCATCGAA	AAGATGGTGC	ATGCCATCCA	GCGCAATCGT	1740
CTGGGACTTC	GCAATGAAAA	GAAACCGATC	GGTTCTTTCC	TTTTCCTCGG	CCCCACGGGG	1800
GTAGGCAAGA	CCTATTGGGC	CAAGAAGCTC	GCCGAATACC	TGTTTCGAGGA	TGAGAATGCC	1860
ATGATCAGGG	TGGATATGAG	CGAGTATATG	GAGAAGTTCT	CCGTTTCGCG	TCTCGTGGGT	1920
GCCCCCTCCG	GATATGTGGG	CTATGAAGAA	GGCGGCCAAC	TGACGGAGCG	CGTAAGACGC	1980
AAACCTTATT	CCGTGGTTCT	CTTGGATGAG	ATCGAAAAGG	CGCATGCCGA	TGTCTTCAAT	2040
CTGCTCTTAC	AGGTGATGGA	CGAAGGTCAG	CTGACCGACA	GCTCGGGACG	GCGCGTGAAT	2100
TTCAAGAACA	CCGTGATCAT	CATCACCTCC	AACGTGGGTA	CACGCCAGCT	CAAAGACTTC	2160

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5 GGGCAGGGTA TCGGGTTCGG TTCGGAAAAA GACGAGGAAG CGAACAAGGA GCATAGCCGT 2220  
TCCGTGATCC AAAAAGCTCT GAACAAGACG TTCAGCCCCG AATTTCTCAA CCGTTTGGAC 2280  
GATATCATCC TCTTCGACCA ACTGGGCAAG ACGGAGATTG GCCGGATGGT GGACATAGAG 2340  
CTTAAAGCCG TCTTGGCGCG CATCCATCGT GCCGGATACG ACCTCGTCCT TACCGATGAA 2400  
GCCAAGGATG TGATAGCGAC GAAGGGATAC GACCTCCaAT ACGGAGCACG ACCGCTCAAG 2460  
CGCACACTCC AGAACGAAGT GGAGGATCGC CTCACGGATC TTATCCTCTC CGGACAGATC 2520  
GAGAAAGGGC AGACGCTTAC GCTCTCTGCT CGCGATGGCG AGATCATCGT ACAAGAACAA 2580  
GCA 2583

10

(2) INFORMATION FOR SEQ ID NO:40

15 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 1368 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: circular

20 (ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

25 (vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

30 (A) NAME/KEY: misc\_feature  
(B) LOCATION 1...1368

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40

35 AGAGGAGGAC AAATCCGCCG ACACCATACC GATTCGTCAA GGGGATCGGA CAGCAAAGCC 60  
TGCCGCTTCT CCTTTCATGC CGAGACCATC GGTTTCTCCA ACCACCAAAG AGCAAAAATG 120  
AATTACCTGT ACATACTGAT TACACTTTTA CTCTCCGGCT TTTTTCCTGG TGCTGAGATT 180  
GCTTTCCTTT CTTCGGACAA ACTGCGTCTT GAGTTGGACA GGAATAGAGG CGATCTCACA 240  
GGCAGAGCGT TAAACTTGCT GTATCGACAT CCGGACCAAC TGGTGACTAC TCTCCTTGTTG 300  
GGTAATAATA TCGTTTTGGT AGTCTATGGT CTGCTGATGG CGGGATTGCT GGCCGCACCT 360  
TTGGCGCAAT GGATTGATAA CGATGCTATG ATCGTCGTTT TCCAATCTGT CTTATCCACT 420  
ATCATCATAC TGTTTACCGG GGAATTTCTA CCCAAAGCCA TTTTCAAGAC CAATGCCAAT 480  
ATGATGATGA GGGTATTTCG CCTCCCTATC GTAGCGATCT ATTATCTGCT TTATCCTCTG 540  
TCTAAACTCT TCACCGGTTT ATCTCGCTCT TTTATTCTGT TGGTGGACAA GAATTATGTG 600  
CCTACAACAG TAGGGTTGGG GCGCGTAGAT CTGATCATT ATTTGGCAGA AAATATGTCC 660  
45 GGAGAAAACG AACAGAACGA CTGACTACC GAAGTGAATA TCATCCAGAA TCGCTGGAT 720  
TTTTCCGTA TTCAGGTGCG AGACTGCATG ATCCACGCA ATGAGATGAT AGCATGTGAG 780  
TTGCAAACGG ATATTGAAGT ACTCAAAACG ACTTTTATCG ATACCGGTTT GTCCAAGATC 840  
ATTATCTACA GACAGAACAT AGATGACGTA GTAGGATATA TCCATTGAG CGAAATGTTT 900  
CGTGGGCAAG ACTGGCAAAA ACGTATCAAT ACTACTGTAT TCGTACCCGA AAGCATGTAT 960  
50 GCCAATAAAC TGATGCGACT ACTCATGCAG CGCAAGAAAA GCATTGCCAT CGTCATCGAT 1020  
GAACTTGAG GTACGGCCGG AATGGTCACA TTAGAGGATT TGGTAGAAGA GATTTTCGGT 1080  
GACATTGAGG ACGAACACGA CACTCGCAAG ATCATAGCCA AACAGCTCGG CCCTCATACC 1140  
TATCTGGTCA GTGGTCGTAT GGAAATAGAT GATGTGAACG AACGTTTGG GTTGTCCTTG 1200  
CCTGAGCTG ACGACTACCT TACCGTGGCC GGATTTATCC TGAATAGCCA TCAAAATATC 1260  
55 CCACAGGCCA ATGAGGTCGT GGAGATTGCT CTTATACTT TTACCATTC CAGATCTTCT 1320  
TCCACCAAGA TCGAAGTGGT GAAATGTCC ATCGACGACC AATCGAAC 1368

60 (2) INFORMATION FOR SEQ ID NO:41

65 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 897 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

70 (iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

75 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:  
(A) NAME/KEY: misc feature  
(B) LOCATION 1...897

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:41

TTAAAAAAGG AGATAACTAT GAAACAGAAC TACTTCAAAA GAGTCTGCTC ACTGCTTTGG 60  
CTGGTTTTAC CCATGCTTAT TATGCCATTG GAAGTAGCAG CTCAAGAGAT TATCCGAAC 120  
GAAGAGGTGT TGGAAATCATT GACTTTCGTT GCACCGGTTG AGGAGACAGA CGCAATAGAG 180  
10 GCAGAGGTAG AAGCTCTGCA GGAGATAGTC GCTACTGAGG AGATTGCGGA GCAGGCTGTT 240  
CGTTCTTATA CCTACACGGT CTATCGTGAT GGCGTGAAGA TTGCTTCAGG ATTGACTGAG 300  
CCCACCTTTC TCGATGAAGA TGTTCCCTGCC GCGGAACATA CCTACTGCGT AGAAGTACAG 360  
TATCAGGGAG GCGTATCCGA CAAAGTATGC GTGGACGTAG AGGTGAAGGA CTCAAAACCG 420  
GTTACCAATC TCACCGGAAC TGCTTCCAAT GACGAAGTTT CTTTGGACTG GGACGGGTGTG 480  
15 GAAGAGAAAG CTGAAGAGCC GGCAAGTGT AAAGCAGTCA GCTACAACGT CTACAAGAAT 540  
GGAACCTTGA TCGGTAATAC AGCTGAAACT CATTATGTGG AGACCGGTGT AGCCAATGGT 600  
ACATACATCT ACGAAGTGGA AGTAAAGTAT CCTGACGGTG TATCTCCGAA GGTGGCTGTA 660  
ACCGTGACCG TGACCAACAG CTCATTGAGC AATGTAGATG GACAGGCTCC TTACACATTG 720  
CGAGTAGAAG GCAAGAAAGT TATTGCGGAA GCCCATGGTA TGATCACGCT CTACGACATC 780  
20 AACGGACGTA CCGTGGCCGT AGCCCGAAT CGATTGGAAT ACATGGCGCA AACCGGTTTC 840  
TATGCASTGC GCTTCGATGT GGGGAATAAA CACCATGTAT CGAAAATACA AGTAAGA 897

25 (2) INFORMATION FOR SEQ ID NO:42

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 1131 base pairs  
(B) TYPE: nucleic acid  
30 (C) STRANDEDNESS: double  
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

35 (iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

40 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc feature  
(B) LOCATION 1...1131

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:42

TTGTTTAATC ATAAAAATC ATGGTATGAA ACATTTCAT TTTATCTCGT TGTTTTCCGC 60  
TCTGGCTTTA TTCTTTTGTG TGAAAATACC CTTGCACAAC AAAAAACAGA GGAGTTTGCA 120  
50 CCTGTSTCGG ATTTACGTGC AGAAGCGTAC GGCTCTACCG TTTTCCTCCA CTGGACTCCG 180  
CCGTATGACA ATCCGATGAT TCCTCTAAGC GAGAGTTTGG AATCAGGTAT TCCAGCTATA 240  
TGGAAGACCA TTGACGCAGA TGGCGATGGC TATAATTGGA TGCATTTGAC CAATTTACAG 300  
GGACAGAGTG GTCTCTGTGT CTCTTCGGCT TCATACATAG GCGGCGTCGG AGCTTTGACT 360  
CCGGACAATT ATCTGATAAC ACCCGAATTA AAACCTACCCA CAGACGCGTT GGTGGAAATA 420  
55 ATCTATTGGG TATGTAATCA AGATCTCACT GCTCCATCGG AGCACTATGC CGTTTATTCC 480  
TCTTCTACAG GCAATAATGC TGCTGACTTT GTTAATCTCT TATATGAAGA GACTTTGACT 540  
GCCAAACGGA TACAATCCCC CGAGTTGATC CGCGGAAATC GGACACAAGG TGTTTGGTAT 600  
CAAAGAAAGG TGGTACTCCC TAACGATACT AAATATGTTG CTTTCCGCCA TTTTAATTCC 660  
ACGGATAAAT TCTGGCTCAA TTTGGATGAA GTATCTATCC TGTATACCCC TCTTCCCCGA 720  
60 AGAGCTCCGT GTCCGCATCC GGGTGGTTAC ACTTATTCTG TATTCCGTGA TGGACAAAAG 780  
ATAGCGAGTG GATTGTCGGC ATTGGCATAT ATCGATACGG ATGTACCGTA TGGGACTCAA 840  
GACTATTGTG TCCAAGTCAA TTATCTGCAA GGAGACTCGT ATAAAGCTG CAAAAATATA 900  
GTGGTGGCAA ATTCTGCAA CATCTATGGG GCGGATAAGC CTTTTCGTTT GACCGTGGTT 960  
GGCAAGACCA TTGTAGCGAG TGCTTTCAAA GGAGAGATCA CTCTTTATGA CATTCTGGGC 1020  
CGGCTGATAG CTTCCGGCTG CGATACGCTT AGGTACAAAG CGGAAATGG TTTTACCTC 1080  
65 ATTAATAATC AGGTAAACGG AACTGTCTAT ACTGAGAAAA TCCAAATCCA A 1131

(2) INFORMATION FOR SEQ ID NO:43

70 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 2547 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
75 (D) TOPOLOGY: circular



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(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

5 (iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:  
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

10 (ix) FEATURE:  
(A) NAME/KEY: misc feature  
(B) LOCATION 1...2547

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:43

TTCGGAATAT	CACCTTCAAT	GAAAAAAGT	TTTCTTTTAG	CCATAGTAAT	GCTCTTTGGC	60
ATTGCCATGC	AGGGACATTC	TGCTCCGGTT	ACGAAAGAGC	GAGCTTTGAG	TCTGGCTCGG	120
CTGGCTTTGC	GACAGGTATC	CTTGCGAATG	GGACAAACAG	CAGTATCTGA	CAAGATTTCC	180
ATCGATTACG	TTTATCGGCA	AGGAGATGCT	GAGAGGGGTA	TCACATCACA	AGAGGAAGGC	240
TCTCGTGCAT	ATTTTATGT	AGCTAATCGT	GGAAATAATG	AGGGCTATGC	TCTTGTAGCA	300
GCAGATGACA	GAATACCGAC	AATTTTAGCC	TATTCACCCA	TTGGCCGTTT	CGACATGGAC	360
AGTATGCCGG	ACAATCTTCG	CATGTGGCTA	CAAATTTACG	ATCAGGAAAT	AGGCCTGATA	420
CTTTCCGGAA	AAGCTCAGCT	CAATGAAGAG	ATATTACGTA	CCGAGGGCGT	ACCGGCTGAA	480
GTACATGCTC	TGATGGATAA	CGGTCATTTT	GCCAACGATC	CCATGCGATG	GAATCAAGGT	540
TACCCATGGA	ACCAATAGGA	ACCACTGCTT	CCTAATGGCA	ATCATGCCTA	TACCGGCTGT	600
GTTGCTACTG	CTGCAGCACA	AATCATGCGC	TACCATAGCT	GGCCGCTTCA	AGGTGAAGGC	660
TCTTTTCGAT	ATCATGCAGG	TTCATTAGTT	GGCAACTGGT	CCGGCACATT	TGGTGAAATG	720
TACGACTGGA	TCAATATGCC	CGGAAATCCC	GACCTTGATA	ATCTGACTCA	ATCTCAAGTG	780
GATGCCTACG	CCACACTGAT	GCGTGATGTG	AGTGCATCTG	TTTCGATGAG	TTTTTATGAA	840
AATGGAAGTG	GTACGTACAG	CGTTTATGTA	GTAGGAGCCT	TGCGAAACAA	CTTTGCTAC	900
AAGCGTTTAC	TGCAGCTACA	TGTACGCGCC	TTATATACCT	CACAGGAGTG	GCACGATATG	960
ATCCGCGGGG	AACCTGCCTC	CGGAAGGCCG	GTCTATTATG	CAGGGAATAA	CCAGAGCATA	1020
GGACATGCTT	TCSTTTGCGA	TGGTTATGCT	TCGGATGGTA	CTTTCCATTT	CAACTGGGGT	1080
TGGGGAGGTG	TTTCCAACGG	CTTCTACAAA	CTAACACTCC	TCTCGCCGAC	TTCTGTGGGT	1140
ATCGGAGGTG	AGGGAATAGG	TTTTTACCATT	TATCAAGAGA	TCATCACCGG	TATCGAACCG	1200
GCTAAGACTC	CCGCTGAAGC	CGGTACAGAT	GCCTTGCCGA	TCTTGGCACT	GAAAGACATA	1260
GAAGCCGAGT	ATAAAAGTGA	ATCCGGATTG	AACGTAGGGT	ATTCGATATA	TAATACAGGT	1320
GAAGAGCAAT	CAAATCTTGA	CCTCGGATAC	AGATTGAACA	AGGCTGACGG	AGAAGTCATA	1380
GAGGTGAAAA	CTTCATCTAT	CAATATCTCT	TGGTACGGAT	ACGGAGAGCA	TCCCGAGAGT	1440
TTCTCATTGG	CACCTAATCA	GTGTGCACAA	GGAATCAACA	CCATCACCCCT	ACTTTATCGT	1500
CGCACAGGCA	CCGAACAGTG	GGAGCCGGTA	CGGCATGCAC	AGGGAGGATA	TGTCAATAGC	1560
ATTAAAGTAA	ATACGACAGA	CCCGAACAAT	GTCTAGTCA	CGGTAGATAA	TAACGAAGGC	1620
AAGCTCAGTA	TGCTCCCAA	CAGCTTTGTC	GCAGATCTGA	ATTCTTATGA	ACATAGTACG	1680
ATTACAGTAC	AGTTCAATAG	CGACAGCCCT	GATGAGATCC	GTACACCCGT	AGCCTTTGCT	1740
CTATCTACAG	GAGCTACTGC	GGACGATGTA	ATATCTTTGG	GCTGGGTAAT	GGCTGAAGTT	1800
CCGGGCGGTA	GCAGCAACTA	TCCGTTGGTT	TGGTCTAAAG	ACGTTCTCAC	TCTCTCGGAA	1860
GGCGACTATA	CATTGTGGTA	TAGATTTTCC	ATCAACAACC	AAAAGGATGA	ATGGAAAAAG	1920
ATCGGAAGCG	TGTCAGTAAA	AACACCGACA	GAGTATACSC	ACCCCTTAT	CGAAGTGGGC	1980
CATAATCAAA	CTTCTACCTA	TACGCTGGAT	ATGGCACACA	ACAGAGTATT	GCCCGACTTT	2040
ACACTCAAAA	ATCTCGGATT	GCCTTTCAAT	GGTGAGTTGG	TTGTTGTTTT	CCGCCAAACA	2100
CAATCCTCAT	CGGGGTCTTT	ATGGGCAGCT	CAAGAAACAG	TACATATCAA	GCAAGGAGAA	2160
ACTTTGSTAT	ATAAACCTGT	TGTCGAAGGC	CCTATACCTG	ATGGATCCTA	TCGTGCGACC	2220
CTCCATGCA	TCGTAAACGG	ACAACAACAG	TTGTACCTCA	AGGGGAAAAG	GAATACACG	2280
GTGAAGATCG	TCAATGGTAC	AGCGGTAGAA	GCAATAGAAT	CGTCAGAAGA	GATCAGAGTA	2340
TTCCCTAATC	CGGCACGCGA	TTATGTGGAA	ATATCGGCAC	CTTGCAATCC	CCAAGAAACA	2400
TCTATCATTC	TTTTCGATCT	GTCAGGCAAG	ATTGTCATGA	AGAATAGTTT	ATCAGCGGGG	2460
CATGGCAGAA	TGGATGTCAG	CCGACTTCCT	AATGGGGCCT	ACATCCTTAA	GGTGGATGGA	2520
TATACGACGA	AAATAAATAT	AGTGACAC				2547

60 (2) INFORMATION FOR SEQ ID NO:44

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 885 base pairs  
65 (B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

70 (iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

75 (vi) ORIGINAL SOURCE:

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(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

5

(A) NAME/KEY: misc feature  
(B) LOCATION 1...885

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44

10 ACGAAGAAAA CACTGATGAA AAAGCTATTT CTCTCGCTCA CGAGTCTTGT AATGGTCTTC 60  
GCTGTGCAA GTTGCGATAT AATCGACAAG GATCAAACCC TCTTGCCGGC TCCGACCAAT 120  
GTGACACCCG ATAATCCGGA TGACAATCCT TCGGAGATCG ACATTACGCA GACGCACACA 180  
GAAAAATATG TTTTGGCTGA AGAATTTACC GGCCAAAAAT GTCTCAACTG TCCGAAAGGT 240  
CATCGCAAAAC TGGCGGCTCT CAAGGAGCAA TACGGTAAGA GATTGACTGT TGTCGGTATA 300  
CATGCCGGCC CTGGATCTCT CGTGCCACCT CTTTTCCGTA CAGAAGCCGG AGACGCATAT 360  
15 TATAGCAAST TCGCCAATAA TACCCCTCTC CCTGCGCTGA TGGTTTCGCG CAAAAAGTTC 420  
GGCTCTTCCT ACGTTTATGA TAAGAGCTAC AAAACGTGGG ACGTGCCAT TGCCGAGCAG 480  
ATGGAGCAAA AGGCGAAGAT CAATATCTTT GCCGTGGCCG AATACACCGA TACCCAAAAG 540  
ATCAAGGTGA CTGTAAAGGG TAAAATACTG GAGGGGAATA CACTCCCGAA GTCCATGGTT 600  
CAGGTGTATC TGTTGGAGGA TAAGCTGATC GCTCCGCAGG TGGATGGCAA TACGACAGTC 660  
20 GAGAATTACG AGCACAATCA CGTGTTCGCT GGAGCCGTTA ATGGTATTTG GGGCGAAGAA 720  
TTTGTGAATC TCAAAGATTA TTTGTATACT TACGCCGTTG AACCGCTCTC GGGTATGTCC 780  
TTCGTAGCCG AGAATTATTC GATTGTGGCT TTTGTATACG ATGTGCAGAC GTTCGAAGTG 840  
TATGACGTTG TGCATGTAAA GATCAATCCG CAATCCGATG GCAAA 885

25

(2) INFORMATION FOR SEQ ID NO:45

(i) SEQUENCE CHARACTERISTICS:

30

(A) LENGTH: 690 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

35

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

40

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

45

(A) NAME/KEY: misc feature  
(B) LOCATION 1...690

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45

50 ACGAATAAAA AAGAAGAGAC AATGAAGAAA TCAAGTGTAG TAGCCTCAST TTTGGCCGTG 60  
GCTCTCGTGT TCGCCGTTG CGGACTGAAC AATATGGCAA AAGGCGGCCT TATCGGCGCC 120  
GGAGTAGGAG GTGCCATTGG TGCCGGAGTA GGTAACGTAG CCGGAAATAC GGCTGTCGGT 180  
GCCATCGTCG GTACTGCACT CGGTGGAGCA GCCGGTGCTC TCATCGGAAA GAAGATGGAC 240  
AAGCAGAAAA AAGAACTGGA GGCCGAGTA CCCGATGCTA CGATTAGAC AGTAAATGAC 300  
55 GGAGAGGCTA TTCTGTTTAC TTTCGATAGC GGTATCCTCT TTGCGACGAA CTCCAGCACT 360  
CTGAGTCCCA ACTCAGCAC TGCGCTGACG AAGTTTGCTG CAAACATGAA CAAAAACCCC 420  
GACACGGATA TTCTGATCGT AGGCCATACG GACAATACCG GCTCCGACAA GATCAACGAT 480  
CCTCTGTCTG AGAGACGTGC AGCCAGCGTA TATTCTTTCC TGAATTCTCA GGGTGTGAGT 540  
ATGTCGCGCA TGGCAGCCGA AGGGCGTGGG AGCCATGAAC CGGTGTCAGA CAATAGCACA 600  
60 GTTGGCGGAC GTTCGGCCAA CCGCGGTGTG GAGGTTTATA TCTTGCCGAA TGCCAAGATG 660  
ATCGAACAAG CACAGCAAGG TACGCTGAAG 690

(2) INFORMATION FOR SEQ ID NO:46

65

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1026 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: circular

70

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

75

(iv) ANTI-SENSE: NO

31 / 490

(vi) ORIGINAL SOURCE:  
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

5 (ix) FEATURE:  
(A) NAME/KEY: misc\_feature  
(B) LOCATION 1...1026

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:46

AACAGGAACA	GAAATATGTC	GAAAAAATCG	ATCCTTCTGC	TTTGCTGTTC	GCTGTGCTTC	60
ATTTCTGCTA	CGAAGGCTGT	GACCCCGTC	AGAAATGTGC	GCAATAGCCA	AGTGAACAGC	120
AAAGCAAAGA	CCGAACGTAC	AAAGCCCTCG	GACTCTGTAC	GGTACATTAG	CAACATGATT	180
GCAGATCGGC	TGGAGTTCCG	CAACAAGATT	TCTTCCGAAA	AAGAGGTAAG	AAAAGCCGAA	240
15 TATGAAAATC	GGGTGGCGAT	GGAAGCACTC	AATTACCCCTG	CCATAGATTT	ATATGGTGAA	300
GATTCTTGGA	GCGAGTATGT	AAACCCCTTC	GTGGGTGCAG	GAACCGATGT	CGAAATTCCG	360
AATCCTATG	ACATTGATG	CTCTTCGTTC	GTGATGCCCG	TCGAAGATAA	GCAGGTCACC	420
TCTCAATTGG	GCTACCGTCG	GCGTTTCGGA	CGGATGCACT	ATGGTATTGA	TCTTTCAGTG	480
AATCGTGGCG	ATACGATACG	AGCAGCCTTT	GACGGGAAAG	TTCGTGTACG	CAGCTATGAA	540
20 GCGCGTGGCT	ATGGCTACTA	CATAGTCTTG	CGCCATCCGA	ACGGACTGGA	GACTGTGTAC	600
GSACACATGA	GTCCGCAATT	GGTAGACGAG	AATCAGATCG	TTCGAGCAGG	ACAACCGATC	660
GGATTAGGAG	GCAGCACGGG	TCGAAGCACG	GGTCCTCATC	TTCACTTCGA	GACCCGCTTC	720
ATGGGTATTC	CCATCAATCC	GAGTACCATT	ATAGACTTCG	ATAACGGAGT	GCCGCTCCGA	780
GACATTTACA	CATTCAAACG	AGGGAGCAAT	TCTCGCTATG	CAAAAGCCTC	TAAGACTTCT	840
25 TCTCGCTATG	CAAAAAAAGG	GAAGAAAGGC	AGACAAGCTT	CTTCTCCTAT	GACCTATAGA	900
ATCAAAAAAG	GCGATACTTT	GGAAACAATA	GCCAAAAGGC	ACGGCACTTC	TGTTTCAGAAA	960
CTCTGTGCTA	CCAATGGCAT	TGGCAAGAGT	AAAATTTTGA	CTCCGGGCAA	AGCCTTGAGG	1020
ATCAAA						1026

30 (2) INFORMATION FOR SEQ ID NO:47

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 477 base pairs  
35 (B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

40 (iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

45 (vi) ORIGINAL SOURCE:  
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:  
(A) NAME/KEY: misc\_feature  
50 (B) LOCATION 1...477

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47

CCGAGCAAAA	CGATAATTAA	GACAATGGCA	AAAATCAATT	TCTATGCTGA	AGGCGTCAGC	60
CTTCCTCGGA	TCAGAAGACG	GATCGTCGGT	AAGTGGATAG	CCGAAGTATG	CAGCCGATAT	120
GGGAAAACGG	TGGGAGAAAT	CTCCTATCTT	TTCTGTGATG	ACGAATATAT	CCTGAAAGCC	180
AATCAGGAAT	TTCTCGATCA	TGACTACTAC	ACCGACATCA	TCACCTTCGA	TTCTGCGGAA	240
GCGGATACGG	TGAATGGCGA	CCTGCTTATC	AGTCTCGATA	CCGTACGCTC	GAATGCCCGT	300
60 GCTCTTGATC	TTCGATACGA	AGACGAACTG	CATCGTGTCA	TTATCCACGG	CATACTGCAT	360
CTTTGCGGAT	TGAAAGACAA	GAGCAAAAAG	GATGAAGCCC	AAATGCGTGC	AGCCGAAGAG	420
AAAGCCCTTG	TCATGCTGCG	AGAAACCATC	GGATCGGAGC	TTTCCCTATT	GCATACA	477

65 (2) INFORMATION FOR SEQ ID NO:48

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 1185 base pairs  
70 (B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

75 (iii) HYPOTHETICAL: NO

32 / 490

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:  
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:  
(A) NAME/KEY: misc feature  
(B) LOCATION 1...1185

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48

AAAAAGTAAAA	CTATGAAGGT	AAAGTACTTA	ATGCTCACAT	TGGTTGGAGC	AATTGCACTG	60
AACGCAAGTG	CACAGGAGAA	TACTGTACCG	GCAACGGGTC	AGTTACCCGC	TAAGAATGTT	120
GCTTTTGCTC	GCAATAAAGC	AGGCAGCAAT	TGGTTTGTA	CACTGCAAGG	CGGTSTTGCA	180
GCGCAGTTCC	TCAATGACAA	CAACAACAAA	GACCTCATGG	ACCGCTTAGG	AGCCATAGGT	240
TCTCTTTCTG	TCGGAAAGTA	TCACAGCCCT	TTCTTTGCAA	CTCGTTTGCA	AATTAACGGA	300
GGTCAAGCCC	ACACTTTCCT	CGGAAAAAAT	GGCGAACAAG	AAATCAACAC	CAATTTTGGT	360
GCAGCTCACT	TCGACTTTAT	GTTTGATGTG	GTTAACTACT	TTGCACCATA	TCGCGAAAAAT	420
CGTTTCTTCC	ATTTAATTCC	ATGGGTAGGT	GTTGGCTACC	AACACAAAT	CATCGGTAGC	480
GAATGGAGCA	AAGACAATGT	GGAATCACTG	ACGGCGAATG	TAGGAGTTAT	GATGGCTTTC	540
AGATTAGGAA	AGCGAGTAGA	CTTTGTGATC	GAAGCACAAG	CAGCTCACTC	CAATCTCAAT	600
CTAAGTCGCG	CATACAATGC	CAAGAAAAC	CCCGTATTCC	AAGATCCCGC	AGGACGTTAT	660
TACAATGGAT	TCCAGGGGAT	GGCTACAGCA	GSTCTTAATT	TCCGCCTGGG	AGCCGTAGGC	720
TTCAATGCCA	TTGAHCCAAT	GGACTACGCA	CTTATCAATG	ATCTGAATGG	TCAGATTAAC	780
CGTTTGCACA	GCGAGGTCGA	AGAACTCTCA	AAACGTCCTG	TATCATGCCC	CGAATGTCCT	840
GAAGTAACCT	CTGTTACTAA	GACAGAAAA	ATACTGACGG	AAAAAGCTGT	ACTGTTCCGT	900
TTGCGACGCC	ACGTTGTGGA	CAAAGATCAA	TTGATCAACC	TGTATGACGT	AGCTCAGTTT	960
GTAAAAGAAA	CTAACGAGCC	GATTACCGTT	GTTGGTTATG	CTGATCCTAC	GGGTAATACT	1020
CAATACAACG	AGAAATTGTC	TGAGCGTCGG	GCTAAAGCCG	TTGTTGATGT	TCTGACAGGT	1080
AAATATGGTG	TGCCTTCCGA	ATTAATCTCT	GTAGAATGGA	AGGGCGACTC	TACGCAACCG	1140
TTTACGAAGA	AAGCTTGGA	TCGTGTTGTA	ATCGTTTCGT	CCAAG		1185

(2) INFORMATION FOR SEQ ID NO:49

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 1161 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:  
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:  
(A) NAME/KEY: misc feature  
(B) LOCATION 1...1161

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49

TATAAAATGA	CATACAGAAT	TATGAAAGCT	AAATCTTTAT	TATTAGCACT	TGCGGGTCTC	60
GCATGCACAT	TCAGTGCAAC	AGCCCAAGAA	GCTACTACAC	AGAACAAAGC	AGGGATGCAC	120
ACCGCATTCC	AACGTGATAA	GGCCTCCGAT	CATTGGTTCA	TTGACATTGC	AGGTGSAGCA	180
GGTATGGCTC	TCTCGGGATG	GAATAATGAT	GTAGACTTTG	TAGATCGTCT	AAGTATCGTT	240
CCTACTTTTC	GTATCGGTAA	ATGGCATGAG	CCTTATTTCC	GTAATCGTCT	CCAATTACAC	300
GGATTTCGACA	TCTATGGATT	CCCGCAAGGG	AGCAAGSASC	GTAACCACAA	TTACTTTTGA	360
AACGCCCCACC	TTGACTTCAT	GTTTCGATCTG	ACGAACATAT	TGCGGTGTATA	CGTCCCAAT	420
CGTGTCTTCC	ATATCATCCC	ATGGGCAGGT	ATAGGATTTG	GTTATAAATT	CCATAGCGAA	480
AACGCCAATG	GTGAAAAAGT	AGGAAGTAAA	GATGATATGA	CCGGAACAGT	TAATGTCGGT	540
TTGATGCTGA	AATTCCGCCT	ATCAAGAGTC	GTAGACTTCA	ATATTGAAGG	ACAAGCTTTT	600
GCCGGAAAGA	TGAACCTTTAT	CGGGACAAAG	AGAGGAAAAG	CAGACTTCCC	TGTAATGGCT	660
ACAGCAGSTC	TACCGTTCAA	CCTTGGAAG	ACAGAGTGGA	CAGAAATTGT	TCCTATGGAC	720
TATGCTTTGG	TCAATGACCT	GAACAACCAA	ATCAACTCAC	TTGCGGGTCA	AGTGGAAGAG	780
TTGAGCCGTC	GTCTGTGTTT	ATGCCCTGAA	TGCCCTGAGC	CTACACAGCC	TACAGTTACT	840
CGTGTAGTCG	TTGACAATGT	GGTTTACTTC	CGTATCAATA	GTGCAAAAGT	TGATCGTAAT	900
CAAGAAATCA	ATGTTTACAA	TACAGCTGAA	TATGCCAAGA	CCAACAACGC	ACCGATCAAG	960
GTAGTAGGTT	ACGCTGACGA	AAAAACCGGT	ACTGCGGCCT	ATAACATGAA	GCTTTCAGAG	1020
CGTCGTGCAA	AAGCGGTAGC	CAAGATGCTT	GAAAAGTATG	GTGTTTCTGC	GGATCGCATT	1080
ACAATTGAAT	GGAAGGGCTC	ATCAGAGCAA	ATCTATGAAG	AGAACGCTTG	GAATCGTATT	1140

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GTAGTAATGA CTGCAGCGGA A

1161

## (2) INFORMATION FOR SEQ ID NO:50

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 585 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: circular

## (ii) MOLECULE TYPE: DNA (genomic)

## (iii) HYPOTHETICAL: NO

## (iv) ANTI-SENSE: NO

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature  
(B) LOCATION 1...585

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:50

GTAATTGGCA	TCATTATGGA	ATTTTTCATG	TTATTCATAG	CGGCGGTTTT	CGTTAATAAC	60
GTCTGTCTGT	CGCAGTTCCT	CGSTATATGC	CCATTCTTAG	GCGTATCGAA	GAAGGTAGAC	120
ACCTCAATCG	GTATGGGTGC	AGCCGTGACA	TTCGTATTGG	CACTGGCTAC	CTTGGTTACC	180
TTCTGATTC	AGAASTTCGT	TTTGGATCGT	TTCGGATTGG	GCTTTATGCA	GACCATGCA	240
TTTATTTTGG	TCATTGCCGC	CTTGGTGCAG	ATGGTGGAGA	TCATACTCAA	GAAAGTATCT	300
CCTCCCCTCT	ATCAGGCACT	GGGTGTATTC	TTGCCCTTGA	TTACGACGAA	CTGCTGTGTG	360
CTCGGTGTGG	CTATTTTGGT	TATCCAGAAG	GATTATACCC	TGCTCCAGAG	CTTCGTCTAT	420
GCAATATCCA	CGGCTATCGG	TTTCACCTTG	GCAATGGTTA	CTTTCGCAGG	TATTCGAGAG	480
CAACTCGATA	TGACCAATCT	CCCCAAAGCT	ATGAAGGGAA	TACCTTCGGC	ACTCTTGGCT	540
GCCGGTATAT	TGGCTATGGC	TTTCATGGGC	TTCAGCGGTA	TCGCC		585

## (2) INFORMATION FOR SEQ ID NO:51

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2628 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: circular

## (ii) MOLECULE TYPE: DNA (genomic)

## (iii) HYPOTHETICAL: NO

## (iv) ANTI-SENSE: NO

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature  
(B) LOCATION 1...2628

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:51

TACCGATCTT	ATCGTGGGAT	AGGGAGTGGG	ACACACTCTC	CTAACCTCAA	AAACCGACTA	60
AAAAGGATCG	GAATAAGGAT	ACCGAACAGA	CACTATATCC	ATATCAAGCC	AATCAAACCA	120
AAAAATAAAA	TGAAACAAC	AAACATTATC	AGCTTCATCA	TTGCTTTCCT	ATTCTTAGGA	180
ACGAGCGCAT	CGGCTCAGCA	ATCGGGCGGA	TCCGTTACAG	GTACCGTAGT	GGACAAAAGC	240
TCAAAGAAGC	CTATCGCATA	CGTACAAGTA	TTCGTCAAAG	GAACCACTCT	CGGAACCTCC	300
ACGGATGCAA	ACGGAAACTA	CTCGATCAAG	GGAAATCCCTT	CGGGTAATCA	AACATATCGTA	360
GCCCCGACTCA	TGGGTTACTC	CACTTGCGAA	GAAAAAGTAC	ATATAGAAAA	GGGTGGTTCC	420
CGCCACGTAG	ACCTCTATCT	GACCGAAGAG	ATTCTCTCTC	TCGATGGGGT	AGTGGTATCT	480
GCCAAATAGAA	ACGAGACTTT	CCGCCGTCAA	GCACCCCTCGT	TGGTAACGGT	ACTGTCCCGG	540
GAACATTTTCC	TCAAAAACCAA	CTCTACCAAC	CTGAGTCAGG	GACTTAASTT	CCAGCCCGGT	600
CTGCGCGTGG	AGGACAACCTG	TCAGAACTGC	GGTTTCAACC	AAGTTCGTAT	CAATGGACTC	660
GAAGGAGCCT	ATTCCGAAAT	TCTTATCGAC	AGCCATCCCA	TCTTCAGTTC	GCTTGCCGGT	720
GTCTATGGCT	TGGAGCAGAT	GCCTGCCAAT	ATGATCGAAC	GTGTAGAAGT	AATTCGCGGT	780
GGAGGTTCGG	CTCTGTTCGG	CTCTAATGCT	GTGGGAGGCG	TTATCAACGT	AATTACGAAA	840

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	GAACCGCTTC	GCAATTCGGC	CGAGATCAGC	CATTCTACGA	TGACCTTCGA	CCACGCGAAA	900
	GGGTGGGGGA	GCTTCCAAAA	TACGACCCAG	TTCAACGGTT	CTATGCTGAC	GGAAGACCGC	960
	AAAGCCGGTG	TCATGGTATT	CGGCCAACAC	AACCTACCGTC	CCGGACAGGA	TATAGACCGC	1020
5	GACAACTTTA	CCGAACTACC	CAATCTGCGC	AACCGCTCGC	TCGGTTTCCG	CTCATACTAT	1080
	AAGACCGGTC	TCTACAGCAA	AGCAACCCCTC	GAATATCACA	GCATGCAGGA	GTACCGTCGT	1140
	GGTGGCGACA	GACTGGACAA	TCCTCCTTTC	GAAGCCCAGA	TAGCGGAATA	TCTCCAGCAC	1200
	TATATCAATG	GCGGAAGTTT	CAAATTCGAT	CAGGGCTTCA	GCGGTGGCAA	GGATTCTTTC	1260
	AGTCTGTATG	CTTCAGCACA	AGACGTTTCAG	CGTCTGTAGCT	ACTACGGGGG	TGGCGACTAT	1320
	ACCGAAAATC	TGCTGAACGG	AGCAGTTCAG	AGTGAAGCA	CCGAATCGGA	CGAATACAAC	1380
10	GATGCTTTCA	CGGCTCTTAC	TTCTACGGG	ACTACCAAGG	GATTCGATT	GCAAGGAGGA	1440
	GGTATGTACC	GTATACCTT	CGGAGAAAAC	TGGGACTTTA	CCGGCGGACT	CGAATATATC	1500
	TACGGCCAAAC	TCGATGACAG	AAGCGGCTAC	AGACCGAGCA	AAATAGATCA	GAATACCTCT	1560
	ACTTTTAGTC	AGTAGACCA	GCTCGAATAT	AAGACGGAGA	AGTTAAGTGC	CCTTATCGGA	1620
	GCACGTATCG	ACTATGTTCT	CCTCAATCAG	GATGGCAAAC	GCTATATCGA	TCCGCTCTTC	1680
15	ATTTTCAGTC	CTAGAGCCAA	CGTACGATAC	AATCCCAATA	AGAATCTCAG	CTTCCGACTC	1740
	TCATACAGCG	AAGGATTCCG	CGCTCCTCAG	TATTTTCGATG	AAGATCTGCA	CGTAGAGTTG	1800
	GCGGTGGTA	CTCTATCAG	CGGTGTCTT	TCCCCCAATC	TGAAAGAAGA	ACGTTTACGA	1860
	AGCATCAGTG	CTTCTTTTGA	TTATTACCAC	AGAGCCGACG	AATGGCAATT	CAATATCATG	1920
20	GGAGAAGCT	TCGCCACCTT	TATCAGCAAT	CAGTTCAAAC	CATCCGATAA	GGTCGAAACC	1980
	ACGAGCGATG	GCAAAGAAATG	GATCATTCGT	ACCATCTACA	ACGACAAGGA	TGGAGTATCG	2040
	AAGGTATATG	GTGTGAATCT	GGAGGGAAGA	ATCGCCTACA	ACAAATCGTT	CGACCTCCAG	2100
	CTCGGCGGTA	CATGECAGAG	AAGCCGCTAC	GGAAGCATCT	ATACCGCTGT	GGAAGCGGAC	2160
	AAAACAACGG	GACAAGCCGA	GATCTCTGTG	AAAGACTATG	TACGCACTCC	GAATCTGTAC	2220
	GGCTATTTCC	TTGCTACGGT	ACGTCTCTACC	GAGCACTTCG	CCATCAATCT	CTCCGGTACA	2280
25	TTACAGGGCA	AAATGGATGT	AGTACACGAA	GCCTATGAAG	GCGATATTCC	CGCAGAACAC	2340
	ATAGCTCCGG	ACGGATCGTT	CGACTTTGAA	ATGAATGGTC	AGCAATTCAA	AGGTTTGGCC	2400
	GAAGGTCATG	CCAAGCTCGT	CAAGACTCCG	GCCTTCGCCG	ATATAGACCT	CAAGCTGAGC	2460
	CACGACTTCC	ACCTTGCTTC	CATATGACC	TTGGAATTGA	ATGCCGGAAT	ACAGAACATA	2520
30	TTCAACAGCT	ATCAGAAAGA	CACGGACAAG	GGACCGGGTA	GAGCTTCTAC	TTACGTATAC	2580
	GGTCTATG	AGCCAGAAAG	GATTTTCGTC	GGTACAAAGA	TCAATTTTC		2628

## (2) INFORMATION FOR SEQ ID NO:52

- 35 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 2697 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular
- 40 (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- 45 (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- 50 (ix) FEATURE:  
 (A) NAME/KEY: misc feature  
 (B) LOCATION 1...2697
- 55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:52

	ATATTGAATC	ATTTGAGAAA	GACTATGTAC	AAAAAGATTA	TGCGCGTAGC	AGCTCTCTTC	60
	TGCGCCAGCA	TAGGGATCCT	GAAAGGACAG	TCCTCGGATC	TGACCCCTCA	GGATACTATA	120
	TATAGCCCTG	AAATATCCTA	TGCCAAGCCT	ATTCATAAGA	CCATAGCATC	TATTTGAGATC	180
	GAGGGAATGA	GGTCTTTTCA	TGACTTTGTC	TGCGCAATC	TTTCAGGCTT	GGCTGTAGGT	240
60	GATGAAGTCC	TGATTCTTGG	AGATGCCATG	TCTGCTGCCG	TGAATAGAA	TATGCGTCAG	300
	GGCTACTTCT	CAAATGTGCG	AATCATCGCG	GATAAATATG	TCGGCAATAA	AGTCTATCTG	360
	AAAATCATTG	TCACTGAACG	TCCTCGCATC	AGTAAGGTTA	CTTTTAGCGG	GGTAAAGAAG	420
	TCTGAGAGAG	AAGATCTTGA	AATGAAAATC	GGTCTTCGCG	AGGGGATTCA	GATGACCAGA	480
	AATAATGAAG	ACAAGGTCAG	GCAAAATCGTA	CAGAAGTATT	TTAGTGAGAA	AGGTTATCGC	540
65	GATGCCASCA	TACGGATAAC	GCAGGAACCG	GATCTTTCCA	AAGATGGCTT	TGTCAATGTG	600
	CTTATCTCGA	TTGAGAAGAA	AAGCAAAACC	AAGGTGAATG	AAATTTATTT	TTCCGGCAAC	660
	AAGGCCCTTA	GCAATCATAA	GCTAAGAATG	GCGATGAAGA	ACACCAATGC	CAAAATTCAGT	720
	CTTAGAAAGC	ATATTTCGTC	ATCTTTCTTG	AAACTTTTAA	GTAATCATAA	GTTTGTGGAA	780
	GAGAGCTACC	GTGAAGATTT	GGTCCGATTG	ATAGAGAAGT	ATCAGGAATA	TGGATATCGT	840
70	GATGCTGAAA	TACTGACCGA	CAGTGTCTGT	AAGSCTCCTG	ACGGCAAAAG	AGTGGATATT	900
	TATCTCAACA	TGGAAGAGGG	GCAGAAGTAT	TATATTAAGS	ATGTCAACTT	TGTGGGCAAT	960
	TCACAAATATC	CATCGGAGTA	TTTGGAAACGA	GTGCTCGGAA	TAAAAATCCG	AGATGTGTAC	1020
	AATCAGAGAC	GATTGGCTAA	GCGTCTCAAT	GAAGATGAAG	ATGCTGTGGG	GAACCTGTAC	1080
	TATAACAATG	GCTATATTTT	TGCGTGGGTC	GATCCCCTGG	AAACAAATGT	AGTGGGGGAT	1140
75	TCTGTTTCGC	TTGATATTTC	TATAGCGGAG	GGGAAGCAGG	CCAATATCAA	TAAGGTGATC	1200

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5 ATCAAAGGAA ATACTGTCGT GTACGAAGAC GTAGTACGCC GAGAGCTTTA CACAAAGCCC 1260  
 GGCCAGCTCT TTAGTCGCGA GGATATCATT AACTCTATTC GTCTCATCAA TCAGCTTGGG 1320  
 CATTTTCGATG CCGAAAAATC TATTCCTCGT CCGATTCCCA ATCCCGAAAC AGGAACAGTG 1380  
 GATATAGAST ATGATTTGGT GCCGCGTAGC AGTGACCAAT TGGAGCTTTC TGTCGGTTGG 1440  
 AGTCAGTCCG GACTTCTGTT CCGAGGAGCC ATTAAATTCA CGAACTTCTC TGTCGGCAAC 1500  
 TTGCTCCATC CCTCGATGTA TAAGAAAGGG ATCATTCCGC AAGGGGATGG GCAAACACTA 1560  
 TCACTGAGTG CTCAGACCAA TGGAAAGTAC TATCAGCAGT ATAGTGTAC ATTTATGGAT 1620  
 CCATGGTTTG GGGGCAAGCG GCCGGATATG TTCAGCTTCA GTGCATTCTA TTCCAAGACT 1680  
 10 ACGGCGATTG ACTCCAAGTT CTACAATAGC AATGCCGGCA ACTACTATAA TGCCTACTAT 1740  
 AATAGCTACT ACAACAATA TAATAGTTAT TACAACGGTA TGTCGAACTA TACCGGCGAC 1800  
 CTCTATACTC AGGCCAGCGA TCCGGATCGT TCGCTTCAGA TGTTAGGTAC TTCGATCGGT 1860  
 TACGGTAAGC GTTTGACTTG GCCGGACAAT TGGTTCCAGA TTTATACTTC TCTGAACACT 1920  
 ACCTACTATA GACTGCGAAA TTGGAGCTAC AATACCTTCC AAAATTTCCA TCATGGCTCG 1980  
 GCTAATGATC TCAACTTGA GCTGCGTCTC TCTCGTACTT CCATCGATAA TCCTATTTAT 2040  
 15 ACCAGAAGCG GATCGGATTT CATGGTTTCT GTTGCTGCTA CTCTTCCCTA TTCTTTGTGG 2100  
 GACAATCATG ACTATGCCAG CCAGAACCCT AGCGTAAGCG ATCGTTACAG ATTTATCGAG 2160  
 TATCACAAGT GGAAGTTTAG AGGACGAGTT TTTACTCCAT TGCTCAATCC TGCTACGCAT 2220  
 AAATATACAC CGGTGCTCAT GAGTCGAGTG GAAGGAGCAG TTCTTGGTTC GTATAATTCC 2280  
 AATAAGAAAT CTCCTTTCCG TACTTTCTAT ATGGGAGSTG ATGGTATGTC CAGCTATTAT 2340  
 20 GGTGGCTACA TGAATGAGAC TATAGGTTTG CGTGGTTATA AGAACGGATC TATTGCCGGT 2400  
 AATAACTACG ACTATGCATA TGCTTATATG CGGCTTACGA TGGAACTACG TTTCCCGATT 2460  
 CTGTTTGAAA ACTCATTCAA TGCGTGGCTC TTAGCTTTTG CCGAAGCAGG CAATGCGTGG 2520  
 CGCAGTATCG ACAATTATAA TCCCTTTAAC CTGAAGCGAT CGGCCGGTGT AGGATTGCGT 2580  
 25 GTAACGTTAC CGATGGTCGG AATGCTCGGT ATCGATTGGG GATATGGCTT TGACCGTCCG 2640  
 GACAATTCTC TACAGCGAGG AGGAAGCAAT GTCCACTTGG TGCTCGGACA GGAGTTC 2697

## (2) INFORMATION FOR SEQ ID NO:53

- 30 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 531 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 35 (D) TOPOLOGY: circular  
 (ii) MOLECULE TYPE: DNA (genomic)  
 (iii) HYPOTHETICAL: NO  
 40 (iv) ANTI-SENSE: NO  
 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS  
 45 (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...531  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:53

50 CAAATAAACA TGAATGGCGA TATGAAACGG TTTTGTATTT TGATCGGCTT TGCACTGGCG 60  
 GTAGCTTTCT CCGGTTTTTC CCAAAAGTTC GCTTTGGTAG ATATGGAATA TATCCTCAGG 120  
 AATATTCCTG ACTATGAGAT GATGAACGAA CAGCTGGAAC AGGTGTCCAA GAAATGGCAA 180  
 AATGAAATCG AAGCTCTCGA AAATGAAGCC CAATCTATGT ATAAGAAGTA TCAGAGCGAT 240  
 55 CTCGTATTCT TGTCTGCTGC ACAGAAGAAA ACCCAAGAAG AGGCTATCGT AAAGAAAGAG 300  
 CAGCAAGCAT CCGAGCTCAA GCGGAAGTAT TTCGGCCCGG AGGGGGAGCT GTATAAGAAA 360  
 CGCTCCGATC TGATGAAGCC TATTCAGGAT GAGATTGSA ATGCTATCAA AGAGATTGCC 420  
 AAGCGTAACA ACTATCAGAT GGTGCTTGAT AGAGGTACGT CCGGAATTAT CTTTGCCAGT 480  
 60 CCGTCTATTG ACATTAGCGA CCTTGTAAGT AGCAAGATGG GCTTTAGCAA G 531

## (2) INFORMATION FOR SEQ ID NO:54

- 65 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 510 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular  
 70 (ii) MOLECULE TYPE: DNA (genomic)  
 (iii) HYPOTHETICAL: NO  
 (iv) ANTI-SENSE: NO  
 75

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(vi) ORIGINAL SOURCE:  
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

5 (ix) FEATURE:  
(A) NAME/KEY: misc\_feature  
(B) LOCATION 1...510

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54

10 CGAATAAATA AACAAACACGA AATGAAGAAA TTTTCTCTCA TGCTTCTGAT GGCTCTTCCT 60  
TTGAGCCTCT TGGCACAATA GGTGGCAGTG GTAAACACTG AGGAGATCAT TTCCAAAATG 120  
CCGGAACAAG TAGCTGCTAC CAAACAGCTC AACGAATTGG CCGAAAAGTA TCGCCTTGAT 180  
CTCAAGAGTA TGGACGATGA GTTTGCCAAA AAGACAGAAG AATTTGTAAA GGAAAAAGAC 240  
TCTCTACTGG AGAACATCCG CAATCGTCGT CAGCAGGAAC TTCAGGATAT TCAAACTCGT 300  
15 TATCAGCAGT CATACCAAAC GATGCAGGAG GATTTGCAAA AGCGCCAACA ACAGCTTTT 360  
GCTCCTATCC AACAAAAGGT GGCTGATGCC ATCAAGAAAAG TGGGTGACGA AGAAAAGTGT 420  
GCCTACATCA TGGAGGCCGG TATGATGCTT TACACCGGAG CTAAGTCTAT TGACTTGACC 480  
GCAAAGGTAA AAGCGAAACT CGGAATCAAG 510

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(2) INFORMATION FOR SEQ ID NO:55

(i) SEQUENCE CHARACTERISTICS:  
25 (A) LENGTH: 2484 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: circular

30 (ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

35 (vi) ORIGINAL SOURCE:  
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:  
40 (A) NAME/KEY: misc\_feature  
(B) LOCATION 1...2484

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55

45 ATCATGAAGG AAGCTATTCC CCGAAAGAAC AAGTATATAA AGCTCAACGG TATATACAGA 60  
TTGTCAATCA TTCTGCTATG CTGCTGCTA TGCTCTCAGG CAGCTATGGC ACAAGGCGTC 120  
AGGGTATCGG GCTATGTGCT CGACCGTGGG GAAAAGCCGA TCCCGTTCGC CGGAGTCAAA 180  
GTGCGTGGTA CGGGACAGG CGCAACGACG AATCTGAAAG GATACTACGA GTTTCGGATG 240  
AAGGCCACGA CGGACAGCAT CACGATCGAG TTCAGCTCCA TGGGGTACCA AGGGGTAAGT 300  
CGCAGCTTTC CGTCTCTGAC CAAGGACACT CGGCTGAATG TTCGTTTGGC AGAGGCCGAG 360  
50 ATGGAGCTTT CGAGCGTGAC GGTACAGGCC ACAAACGCA GACTCAACAC GATGGAGCGC 420  
GTCAATACCC GAGACCTTCG TGTCATGCA GGGCCTACGG GAGGGGTGGA ATCGCTCATC 480  
AGTACCTACG CAGGAGTAAC GCAGAACAAT GAACTAAGCT CGCAATACTC GGTTCGCGGA 540  
GGAAGCTACG ATGAGAAATAT GGTCTATGTA AACGGAGTGG AGGTTTATCG CCCGCTGCTG 600  
55 GTTCGCTCTG CACAGCAGGA AGGTCTGAGC TTCGTCAATC CGGATCTGAC ACAATCCGTA 660  
CAGTTCTCCG CCGGAGGGTT CACGGCCGAC TATGGCGACA AGATGTCTCT CGTACTGGAT 720  
ATTCGCTACA AGCAACCGCA GGAGAAGGAA GGAGCGGTAC TCCTCGGGAT GCTACAATCG 780  
AGTGCCTACT ATGGCAGCAG TGCCGGAGCC TTCAGCCAAA TCACGGGTGT ACGCTACAAG 840  
AGTGCCAAAT CGCTCTTGGG CACTACGGAC ACGAAAGCCG AATACGATCC GATCTATGCG 900  
GACGGACAGA CATTCTATGAC GTACCGTTTC AGCCCCAAGC TGTCGGTTAG TTTCTCGGGC 960  
60 AATATTTTCG AACTCGCTA CAAGTTTGTG CTCAGACCC GTGAGACGAG CTTTCGGTACA 1020  
CTGAGCGATG CCAAAAAGTT GAAGATCTTT TTCGACGGTC AGGAACAAGA TCGTTTCTCTG 1080  
ACCTACTTCG GTGCCTTCAG CATGAACCTC GTGCCGAGC ACAAACAGCG GCATACGGTT 1140  
ACGCTTTTCG CCTTCAACAG TAACGAACGG GAGACCTACG ATATTCAGGG AGAATACTTT 1200  
CTGAACGATG TGCAGCTGGG GCGGACGCGA ACTGCTTCGA TGGCTTCGGG CTCAGAGAAC 1260  
65 TCCAACGGCT TGGGCATCGG GCGCAATCAC GAGCATGCGC GCAACAGGCT GAGCTACCGC 1320  
GTGCTGAACA TGGGTTACAG AGGGGAGATG AAGCTGAACG AGAAGCATCG CCTGCAAGCC 1380  
GGCGTATCGG CACAGATGGA GAAATAGCC GACCATATCA GCGAATGGGA ACGGAGGGAT 1440  
TCGGTAGGAT ACAACCTACC TCACTCGGAG ACCGTATTGC TSATGTACAA TAACCTATAT 1500  
GCCGATACGC AGATGAGGGG AACGCGCTTG TCGGCATTCC TACAGGATCG ATTCAACTTC 1560  
70 AGCATGGGAG GAGGTACATT TTCTCTCATT CCGGGTATCA GAGCTTCGTG GTGGAGCTTC 1620  
AACAAAGGAT TGCTCGTCAG CCCACGTATC AGCGTGGGTT ATTCTCCCGA AAGCAACCCG 1680  
GCTTTGGTAC TGCGTGCAGC CGCCGGACTT TATTATCAGG CACCGTTTTA CAAAGAGCTA 1740  
AGGCAGACGC ATAAGGATGC CGAAGGCAAT AAGTGGGTTG TCCTCAACGA GAAGATCCGC 1800  
TCTCAGGGAG CTTTTCACAT TCTCGCAGGA GCAGACTATA CCTCGAAAT GGGGGGGCGA 1860  
75 AAATACAAGT TTACGGCAGA GGCTTACTAC AAGAGCCTGT TCAACATCAA CCCGTATATA 1920



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5 ATAGAGAACG TGAAGATCCG CTATCTGGGC GAAAACATCG GTTCGGGTTA TGCTGCGGGT 1980  
 ATCGATCTCA AGCTCTTCGG CGAACTGGTA CCCGGAGTGG ATTCGTGGCT GACGGCTTCC 2040  
 ATTATAAAAG CCCGTCAGAA ACTGGATGGC TACGGTTCTT TACCACTGAT GAACGCACCC 2100  
 ACTTACAATT TCTCCTTCTT CCTTCAGGAG TACGTGCCGG GCAATAAACG CATCACAGCC 2160  
 ACCCTGCGGG CTGCACTAAG CGGAGGATTG CCCAGCTCA ATCCGAGCAA AGGGCTTAGC 2220  
 TCGCCGGCCT TTACCGCACC GGCCTATAAG CGTGTCCATC TGGGGGTAAT GTACAAATGG 2280  
 CTCGACCCGG ATGACTCCTT TGCCGGCCGA AGCAAATGGC TAATGGGAGT AAAAGGGGCC 2340  
 TACATAGGGG CTGACCTCTT CAATCTGTTC GACATGACCA ACCTCAATTC TTACTACTGG 2400  
 10 GTGTGCGATG CCTACCAACA GCAATACGCC GTACCGAACT ACCTGACACG CCGCCAATTC 2460  
 AACCTGCGTC TCCTCGTCGA ATTC 2484

## (2) INFORMATION FOR SEQ ID NO:56

15 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 2037 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRAINEDNESS: double  
 (D) TOPOLOGY: circular  
 20 (ii) MOLECULE TYPE: DNA (genomic)  
 (iii) HYPOTHETICAL: NO  
 25 (iv) ANTI-SENSE: NO  
 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS  
 30 (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...2037  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:56

35 CCTATCCCTT TTCTTCTTAA TATGTACAGC GGACATCATA AAATCCATTA TCCTTTTCTT 60  
 ATCCTGTTGG TATGCCCTTG TTTTGCTGCC TGCAAGAGCG TGAAGTTGAA AGATGCGGAG 120  
 AAGGCACATG ATCGCCCAAGA GTATACCAAG GCTGCCGATA TGTACAATAC ATTATACAGG 180  
 CGTACCCGAC GAAAGCAGGT GGAGATGAAA GCTTATACGG CTTCCTCGATC CGGTGAAAAC 240  
 40 TATCGTGCCG CCGGCAGACA AGCCAAAGCT TTGGCTGGCT ATCTGAATGC CAGACGCTAC 300  
 GGGTATCCGG ATTCTGTGGT ACTGCTCCGT TTGGCAGAGA CTATCAGCA AGGAGGTAAC 360  
 TATAAGGAAG CCGAGGTACT CTTCCTGGGA TATCTGGAAG CTATCCGAA AAGTTATTTT 420  
 GCAGCTATCG GTTTGGAGGG GTGTCTCTTT GCCCGCCAGC AAAAGGAATA TCCTACACGT 480  
 TACCGGATAC GCGAGCTGC CGAGTGAAT TCGGCACGGG GCGACTTCGG CCGGCCTAT 540  
 45 GCACCCGATG CTTCGGCTCT CTATTTTACA TCGAGCAGAA GCAAAGACGA CGGTTTGAT 600  
 AATAGCAGCA TAACGGGACT GAAACCCAAC GACATTTATA TCATCAAACG AGATGCACAA 660  
 GGACGATGGG GACGTCCCGA TAGCGTGTCC GGAGGAATCA AACTCCATG GGATGAAGGC 720  
 GTGCCAACGA TCACGCCCGA TGGTAGTACC ATATATTATA CGTGGCGCA GCAAGGAGCC 780  
 GATTACGACC GTACGGTACA GATCTATTCC GCGCTCGGA GCGGAGAAGG CGGTTGAGG 840  
 50 AACGGTTGCG TCGTGGACAT TATGCGCGAT TCGCTCCGTA TGGCTGCTCA TCCCTCTATG 900  
 TCGGCATCCG GCGATTACCT GTATTTCTGC AGCAATATAG GCGGTAGCTA TGGCGGCAAG 960  
 GATATTTATC GTGTCAAGGT GTCGGATCGT TCTTATGGTT CACCGGAGAA TTTGGGGCCT 1020  
 GATATCAATA CGCCGGGGGA CGAAATGTTT CCCTTCATAG ATGGGGATAG TACCCTTTTC 1080  
 55 TTGCTTTCGG ACGGACACGC CGGTCTGGGA GGACTGGATA TTTTCAAAGC CAGCTGGAC 1140  
 TCTACCGGCC AATGGCATGT AGTCAATATG GGACAACCGG TCAATTCCTC TGCCGATGAT 1200  
 TTTCGGCTTG CTGTGGAGCC TAAAGGCAAA AACAAAGAAG AAGCTTTGCC GGACAACGGA 1260  
 GTCAAAGGTG TATTTTGTTC CAACCGAGGC GATGCACGCG GATGGCCGCA CCTCTTCCAT 1320  
 TTGCAACTGC CGGCTATCTA CACCGAGATT CAAGGTTATG TGATGGACAG AGAAGAAAAT 1380  
 CCCATAGCCG GAGCCACTGT CAGGATCGTA GGCGAACGCG GCCCGTAGG ACAGGGATTC 1440  
 60 GTGACTACTC GTGACGATGG CTCCTATAAG ATGAGCGTGC AGGGCGATAC TCGCTATGTA 1500  
 ATGCTTCCG GAGCATCGGG TTATTTGAAT CAGTACGTAG AACTCAAGAC CGATACCGCC 1560  
 AAGCAGAGTG AGACCTACTA TGTGGACTTT TTCCTTGCA TCGGTGAGAA AGCCGAGGGC 1620  
 TTGCAAAATA TTTTCTATGA TTTGATAAAA GCTACTCTTC GCCCCGAAAG CATGAAGAGC 1680  
 TTGGACGAAC TGATTCTGAT CCTCACGGAC AATCCGCGTA TTCGGATCGA ATTGGSTTCG 1740  
 65 CATGCCGACA GGAAGGCCCC CGATGCTTAC AACCTCGGAC TATCTGACCG CAGAGCCAAA 1800  
 TCCGTGGTGG ATTACCTCAC GAGTCGTGGC ATAGCGGCCG ACAGGCTTAC GTGGAAGGC 1860  
 TACGCTAAGT CTGTCCCAA GACGGTGACA GCCAAAATG CCGAACGGCA CGATTTCTCTG 1920  
 AAGGAAGSCG ATGTGCTCAC CGAGGAATTC GTAGCACCTT TGACCGAGGA GCAGCACTCA 1980  
 70 GTCTGCGACC AACTGAACCG TCGTACCGAG TTCCTGTGTA TCGAAGAAGA GTTGCCT 2037

## (2) INFORMATION FOR SEQ ID NO:57

75 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 2316 base pairs

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(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: circular

- 5 (ii) MOLECULE TYPE: DNA (genomic)  
(iii) HYPOTHETICAL: NO  
(iv) ANTI-SENSE: NO  
10 (vi) ORIGINAL SOURCE:  
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS  
(ix) FEATURE:  
15 (A) NAME/KEY: misc\_feature  
(B) LOCATION 1...2316

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57

20 CCTGCACAGC CGAAAACATA TTGCATACGA TACTTTCGGA GAGAGGTATC TCCGAGGAGG 60  
CAAACAGAAA GGACATTGTA TGCGGACAAG ATGCGCCGGC ATATCGTCAA GTGCTGTCCC 120  
TCTGCCCTCCA TACTCTTGCA AGAATACTCC ACAACAGAAT TATTCAATCA TCACTTTAAC 180  
ATATCAATAA TTATGAAAAA GTTTTCTTTC GCGCTACTAT CGATTGGTAT TTCAGCGCAG 240  
GCTTTTGCCA AGACGGACAA CGTCCCGACA GATTGCGTAC GAGTACACAA TCTTCAGACC 300  
25 GTACAGGTCT ATTCTACAGC CACGGCCGTA CCTCTGAAAA AGATACCGGC CAAGATGGAA 360  
CTCATCTCAT CGCGCAACAT CAAGCACTCC GGCTTTAACA ACATGACCGA CATCCTCAAG 420  
ACGCAAGATT CGCTCGATGT CATACAATAC CCGGGCTTTPA GTTCGAACAT CGGTATCCGC 480  
GTGTTCAAGC CCTCCGGCAA GTATGTAACC GTATTGGTAA ACGGCATCCC TCGGGGAACG 540  
GACAATATCT CTACGCTCAA CACGAGCAAC ATCGAACAAA TCGAGATCCT CAAAGGCCCG 600  
30 TTCTCTTCCA TCTACGCGAC CAATGCCATG GCGGTGTGG TGAACATCAT CACCCACAAA 660  
TCCAAGGACA AGATCCATGG CAACGTTTCT CTCTTCGGCG GTAGTACCA GACCATGGCC 720  
GGATCATTTA ACTTGGGTGG CCGCTTCGAG GATATTTTCT CATTGATCT TAGTCTGGGC 780  
TTGGACAAGC AGAACAGGA CTATAAGACC GGATCAACA ATTTCCTATC CCTGAGCAAA 840  
CTGGAAGAAG CTATAGTAGA TGTAAATGCT ACCAAAAACA AGAAATGAA GGGGAGCGAC 900  
35 TATACTGTAG CAACGGGACG TCTGCGTTTC GGTATCGACT TCACGCCCCG ATGGTCGCTG 960  
AATCTGTATC AAAACGTATT CCTCGGAGAT GCGATCCCCG TAGGAGGATC TATATGGGGC 1020  
CTGTACGGAG AATCCAAAAA AAATCTGAAT CGTTCTTCGA CCTCTTCGA GCTGCTCGGC 1080  
AAACATGGCT GCCACACGCT TCAATTCTCC CCCTACTTCA ACATAGAGAA ATCGGAGAAC 1140  
TATAACAATG CCGATCCAC CGGTTTCATC AACTACAAAA GCGACTACTA CACCTATGGT 1200  
40 GCCCTACTCC AGGACAAGAT TTCTTTGGA GGACAAAATA TCGTACTCGG TGTGACAGC 1260  
CGAAACATGA CGATGGAGTC AGAAAGATTG GAGCAGGCAG GAGTGAATAC AAAGCCATAC 1320  
AACCCCGGAT ATGCCACGAA CAATATCGGT TTGTTCGGAC AGGCCAATTT CTACCTGCTG 1380  
AACGATGCTC TATCGATATC TGCCGGTGCA CGTGCCGACT TCATGTTCTT TGACCTGAAA 1440  
GCGAACGAGT ATCTCAACAA TGAAGCCAAA CAGGAAACTC ATAACGTAAT CAATCCGAAT 1500  
45 GTCGGAATCA AATATGAGTT TGTGAAAGGC CTTACAGCTC ATGGTACATT CGGTAGTGCA 1560  
TTCAGTGCTC CCGATGCTTT CCAAAAAGCA GGCCAATACG TAGGCCCGTT CGGCACGACC 1620  
ATAGGCAATC CTGACCTGAA ACCCGAAAAG TCCATGACCT GGGACTTCGG TATCGGATAC 1680  
AGCAATGCAC GCTGCGGGAT CCAAGCCGAC GTAACCTTAA CCTATTTCCA CACCGACCAC 1740  
AAAGATGCTA TCTTGCCAG CCCTGACTAT GCTAATAATA TCACCACATA CATCAATGCC 1800  
50 GACAAGGCTC GTATGAGCGG TATCGAGGCC CTTTGTCTT ATGACTTCGG CAGCCTCTTT 1860  
GCCAACAAAT TCTCTCTCCG CGCATTTGCG AATGCCACGA TCATGCTCAA TTCCGAGATG 1920  
AAGAAAAGCC AGACCGATGC CCCTGGAGC GAAATGTACT ACGTTCGCAA GCAGAACATC 1980  
ACCTTCGGTA TCGAATATCG TGGCAAAGAA GGACTTGAAG TGATGCTCAA CGGTGCTTC 2040  
ATGGGACGCA GGATCGAGCA AAACCTGGTAT GCTTACTACC CCGAAGTTCG CCGGAACTC 2100  
55 CAGCAACTGC TTGCAGCAGA AGAGCCTGAA TTGGCTGCTC AGGGACTGCT CCGTCATCCG 2160  
CAAGCAATGG TGTTCATGCT CTCTGCTTAC TACCACATGA ACAAGTATCT CACCTTCGGT 2220  
GTGAACCTGA ACAACATCTT GGATGAGCTT TATACGGAGA AAGACGGCTA CCACATGCCC 2280  
GGACGTAACA TCATGGGTAA GGTATGGTC AACTTC 2316

- 60 (2) INFORMATION FOR SEQ ID NO:58

(i) SEQUENCE CHARACTERISTICS:  
65 (A) LENGTH: 1452 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: circular

- 70 (ii) MOLECULE TYPE: DNA (genomic)  
(iii) HYPOTHETICAL: NO  
(iv) ANTI-SENSE: NO

- 75 (vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc\_feature

(B) LOCATION 1...1452

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58

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GGCCGGGCGCT CTTCCCTTA CAGGCAAATG GATGGCATA TAAACGATGA ATATAGACAA 60  
GCATCTATGA ACAGGTTTTT AAATCATTGG CCCTGCATCC TCGTGGGGTT TGTACTCTGG 120  
TTTGTATCGG CGAGTCGGAC TGTGGCACAA AACGCCCTCC AAACGACGGT ATCGTACGAT 180  
ACGGATACCG CCGTACTCTC CGAAGCCGAT GTGCTTCGGA TCGCTCTTAG TGAGAATGCC 240  
ACAGTGAAAG TGGCCGATAT GGATGTGCGC AAACAGGAAT ATGCACGTAG GGCAGCACGT 300  
GCCGATCTCT TCCCGAAAGT AGACCTCAAT GGCCTTTACA GCCATACGCT AAAGAAGCAG 360  
GTCTTATATA TAGATATGCC CGGTTTCAGC AGTAGCGAAG GTATCGAAAT GGGGCGTACA 420  
CACAAACGCG AAGGAGGGGT GAACGTCTCC ATGCCATTGG TGTCCGCACA GCTTTGGAAA 480  
AGCATTGCCA TGACCGGAGA ACAGCTCGAT CTGGCTCTGG AGAAAGCTCG CAGCTCCCGA 540  
ATCGATTTGG TGGCAGAGGT GAAGAAGGCT TACCTCAGTG TATTGTTGGC CGAGGACTCT 600  
TATGGCGTAT TCAAGCGCAG CTATGACAAT GCTCTGGCCA ATTATAAGAA CATATCCGAC 660  
AAGTTCGATC GTGGACTTGT GGCCGAGTAT GATAAGATTC GAGCCCATGT ACAGGTACGC 720  
AACATCGAGC CTAACCTCTT GCAAGCGCAG AACTCCGTAG CCCTTGCTCT CTGGCAGCTC 780  
AAGGTCTCTA TGAGCATGGA AGTGGAAACT CCGATCAGAC TCTCCGGTTC ATTGTCCGAC 840  
TATAAAGAAC AAGTCTATAC CGGCTATTTT GCCGCCGATA CGCTTATTTT CAACAACCTC 900  
TCCCTGCGTC AGCTCGATAT ACAGCGTCGT CTGGCTGTCA GTGCAGACAA GCTGAACAA 960  
TACAGCTTCC TGCCACACT CAATCTGGGA GGGCAGTACA CCTATTCGCT CAACAGCAAC 1020  
GACATCAAAAT TCTGGGGCGA GGGACAACGC TGGACGCCCT TCTCCACCAT ATCGCTCAGC 1080  
CTGTACATTC CTATATTCAA TGGAGGCAAA CGTCTGTACA ACGTGAAGCA AAGTGCCTTA 1140  
TCGATCCGTC AGATCGATCT GCAACGACGC CACATAGAGC AATCCATCCG AATGGGAATC 1200  
AAGAACCAAA ATGACCGTCT GCGTACCTGT ATGCAGAGAT TTGTGGCCTC GGAAGAGGCT 1260  
GTCCGAAGTG CAGAAAAGGG CTATCAGATA GCAGAGAAAC GCTATCAGAC AGGCGAAGGC 1320  
ACTCTCGTCG AGCTCAACGA TGCCGATGTG GCTCTTTTGC AGGCTCGACT CAATTATAAT 1380  
CAGGCCATAT TCGACTTTAT GACCGCAAAG GCCGAATTGG ACAAGATGAA CGGCATGGGG 1440  
ATCCCGAAC AA 1452

(2) INFORMATION FOR SEQ ID NO:59

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1620 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc\_feature

(B) LOCATION 1...1620

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59

60  
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TTTCATAACT TTGACTTCCT AACGGTATA AAATGTTTTT CGATGGCAAA TAATACTCTT 60  
TTGGCGAAGA CTCGACGTTA TGTCTGCCTT GTCGGTTTCT GTTGGCTCAT GGCGATGATG 120  
CACCTCTCTG GGCAGGAAGT CACTATGTGG GGGGACAGCC ATGGAGTGGC GCCGAACCAA 180  
GTGCGCCGAA CGCTGGTGAA GGTAGCCTTA AGTGAATCCC TTCTCCGGG TGCAAAACAG 240  
ATTCGTATCG GATTCTCTCT TCCGAAAGAA ACGGAGGAAA AAGTCACCGC CCTATATCTC 300  
CTTGTGAGTG ATTCTTTAGC GGTGCGCGAC TTGCCGGACT ACAAGGGGCG AGTCTCTTAC 360  
GATAGCTTCC CGATCTCAAA GGAAGATCGT ACCACAGCCC TTTCTGCGGA TTCGGTAGCC 420  
GGACGCCGCT TCTTTTATTT GGCTGCGGAT ATAGGGCCTG TTGCTCTTTT TTCCCGATCC 480  
GATACGCTGA CTGCCCGTGT GGAAGAGGTG GCTGTGATG GCCGCCCTTT GCCGTTGAAA 540  
GAGCTGTGCG CTGCCTCCCG TCGTCTGTAT AGGGGGTATG AGGCCCTCTT TGTACCCGST 600  
GATGGCGGAT CGCGGAACCTA TCGTATCCCG GCCATTTTGA AAACGGCTAA TGGAACTCTC 660  
ATAGCGATGG CCGACAGACG AAAATATAAT CAGACGGATC TGCCGGAGGA TATAGATATA 720  
GTCATGCGGC GCASTACGGA CGGAGGGAAA TCGTGGAGCG ATCCAGGAT TATCGTACAG 780  
GGAGAGGGGC GCAATCATGG CTTTGGCGAT GTAGCCCTGG TGCAAAACCA AGCAGGAAAG 840  
CTCCTGATGA TCTTTGTGCG TGGAGTAGGC CTGTGGCAGT CTACCCCTCA TCGTCTCAG 900  
CGCACTTATA TATCGGAAAG TCGGGACGAA GGACTGACTT GGTGCGCTCC TCGGGATATA 960  
ACCCATTTCA TCTTCGGCAA GGATTGTGCC GATCCGGGAC GCAGTCGCTG GTTGGCCTCC 1020

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TTTTGTGCTT CGGGACAAGG GCTTGTGCTG CCATCCGGTC GTATCACGTT TGTGGCTGCC 1080  
ATCCGCGAAT CAGGGCAGGA GTACGTCCTG AACAACTATG TCCTCTATAG CGACGATGAG 1140  
GGCGATACAT GGCAGCTTTC CGACTGTGCA TACCGCCGTG GCGATGAGGC AAAGCTTTCA 1200  
TTGATGCCCG ATGGCAGGGT ACTGATGAGC ATACGCAATC AGGGACGGCA GGAGAGCCGA 1260  
5 CAGCGTTTCT TCGCTCTCTC CTCCGACGAT GGCCTTACTT GGGAGAGAGC CAAGCAGTTC 1320  
GAGGGCATCC ATGACCCCGG CTGTAATGGA GCTATGCTTC AAGTGAAAAG GAACGGGAAGG 1380  
GATCAAGTGC TGCACCTCCCT GCCTCTCGGC CCGGATGGGC GTCGCGATGG AGCTGTCTAT 1440  
CTCTTCGATC ATGTCTCCGG CCGCTGGTCC GCTCCCGTTG TTGTCAATTC AGGATCGAGT 1500  
10 GCCTACTCGG ATATGACTCT GCTGGCGGAT GGAACGATCG GTTATTTTCGT CGAAGAGGGC 1560  
GATGAGATCT CATTGGTTTT CATTGCGTTC GTCCTTGACG ATCTCTTCGA TGTCCGGCAA 1620

## (2) INFORMATION FOR SEQ ID NO:60

- 15 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 879 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: circular
- 20 (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- 25 (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:  
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- 30 (ix) FEATURE:  
(A) NAME/KEY: misc\_feature  
(B) LOCATION 1...879

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:60

35 AAGTCTCCGA GCGATTCGGC TTGCGGTCG GTATGGAGCG CGAATACAAT ATCTGGACTC 60  
GTCGGTGGGA AACGCATTAC TTTGCTTATC CTGTATTCTA TGGCGATAAG AAGTAGTAAT 120  
ATAGAATCAA TACAGTGCTT TGTGATGAAA AAAGAAAAAC TTTGGATTGC GATCGTCGCC 180  
GGTTTGGCTT TCGTATTGGG CCTTTATGCT CTTGGCCGCA GTGTCGCTCA GCTACGCCGC 240  
40 TCTCAGCCTT CCGTGACTGT GACCGGTATG GCCGAGCGTA ATTTCAAATC CGATCTGATC 300  
GTTTGGACTG CTTCTGACCA GCTCCAGATG ATGGATCTCG AATCGGCCTA CAAGGCTTTG 360  
AAGGAAAAAC AGATATTGGT AGCAGACTAT TTGAAAAACA AGCAGCTGCC CGATTCTGCT 420  
TATATCTTCT CAAGCGTAGC CATCTCTAAA GAATACAACT ACTATTACGA TCCTCGGCAG 480  
GAACAAAACG TCAGGACCTT TGCCGGGTAT CTGCTCAGCC AGACAGTTAC GGTGACCTCA 540  
45 CAGGACATCG AACATGTGGA GAAATATATCT CGCGATATAA CGGAGCTGAT CAATCAGGGG 600  
GTAGAGATTA CCTCCGACCG TCCGGCCTAT TACTACACCA AGCTCAATGA TCTGAAGGTG 660  
GAGATGCTGC GCAATGCCCT CGAAGACGCT TTCAATCGTG CTTCCGGTCAT TCGCGAGGGG 720  
AGCGGTCTCT CCGTGGGTAA GATGCTATCT TCTTCGATGG GCGTGTTCGA GATAGTGGGG 780  
CTCAACTCGA ACGAAGATTA TAGCTGGGGA GGTTCGTTCA ATACGTCTTC CAAGATGAAG 840  
50 ACGGCAAGCA TAACGGTTAA GGCTTCTTTC GCTTTGAAG 879

## (2) INFORMATION FOR SEQ ID NO:61

- 55 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 840 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: circular
- 60 (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- 65 (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:  
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- 70 (ix) FEATURE:  
(A) NAME/KEY: misc\_feature  
(B) LOCATION 1...840

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:61

75

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5 GGGAACTCC AAATGAAAA AACAAATTGCA ATTATCGCCT CAGCCCTCTT GGCTTTAGGA 60  
 GCCGTCCGGT GTAAGAAAA TGCTGACACT ACCGCTGTCA GTGAAAAGGA TAGCATAGCC 120  
 TTGTCCATGG GTATTTTGTA CGGACAGGAT TTTGCCAATC AGTTGGAAT GTCCCGCTTG 180  
 CAAGGCCAGC CGATTGATTC GGTAGCTTTC TTGGACGGTT TCAAATAIGG TATCGATACG 240  
 ACCGCTTCT CGTACAATCT GGGAGCCATC TATGCTTCCA ATATAGCTCG TCAGCTGGCT 300  
 CATGATTCCA TCGATATCGA CAAGTTCTAT GCAGCCATGC GTGCGGCTCT TCTTAAAGAC 360  
 ACCGTATCTA TCGCCATGAA GCCTGCAGAT GCACAGGCTT TCATGCAACG AATCCAAGCC 420  
 AAAAAGCAGC GAGAAAACAA TATGAAGCAG TTTGGCCAGA ACATCGAAAA GGGTAATGAA 480  
 10 TACATCGATA CCTTTAAAAA AGAAGATGGT GTAACGTGTA CGACAACCTGG TCTGGCATAC 540  
 AAGACTCTTC AGGAAGGTAC GGGAGCTACT CCCTCTTTGG CCGATACTGT ACGTGTCAAG 600  
 TATGTGGGTA CTCTGGTCTGA TGGTAAAGAG TTCGACAAAA ACGAAGAAGG AATCGAATTT 660  
 GCCGTTACCG GTGTGATTAA AGGCTGGACG GAGATGCTCC AACTCATGAA GGTGCGTCAG 720  
 AAAGTTCGCG TGGTAATCCC ACAGGAGCTG GCTTATGGGG AGACCGGCAA CTATACCATC 780  
 15 GAACCGTTCT CTACCCTGAC GTTCGAGATG GAACCTATCG GGATCAAGCC CGGGAAAAAG 840

(2) INFORMATION FOR SEQ ID NO:62

20 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 2409 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular  
 25 (ii) MOLECULE TYPE: DNA (genomic)  
 (iii) HYPOTHETICAL: NO  
 (iv) ANTI-SENSE: NO  
 30 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS  
 (ix) FEATURE:  
 35 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...2409  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:62

40 TGTCGAAAGC AGAAGCTCTC AAACCCGAAG AGGAGCCGGT ATCCGTGCAG ACGGATATCA 60  
 TTCCGACAAA GCGATAAGAA TCCGATGAAA GTATTACGGC AAGTATTCTT CCCCATCCTT 120  
 TTTGTCTAC TGACAGGTGC CTGCTCCACC ACAAGAATC TGCCGGAAGG CGAACAGCTG 180  
 TATATCGGAA TGGGCAAGAC ACAGATACTC CGGCAGGACA AGAGCCACGC CGGCCAACAG 240  
 45 GCTCTGACCG AAGTGGAGAG TACACTGAAA GTTACACCCA ATGGAGCTAT TTTCGGCAGT 300  
 GCAAGTGCTT CCTTACCCAA GATACCATTG GGGCTATGGC TATACAACAG CTTCGTGGGG 360  
 GATTCCACTG TCATTTGCAA ATGGATATTC GACAAGTTTG CAGCCAAGCC GGTTTTTCATC 420  
 AGTCAGGTCA AATCCGATAG CCGGGCTAAG GTGGCGACGA ACATCCTCCG CGAACACGGG 480  
 TACTTCGATG CTAAGATAAA AAGCAGTGTG ACCACTCTGA AAAAGGACTC GCTCAAAGCC 540  
 50 AAAATCTCCT ATACGGTGA TATGGCTCTT CCTTATCATT ACGACAGCAT CATTCCCTTA 600  
 CCGATCAGCA CTTTCCCGCA CAGCATTCTG GCTTACAGGC AGACTCCGTC TTGTATCAGG 660  
 AAAGGAGACC AGTTCAATTT GGCAAAGCTG CACGAAGAGC GTCAGACCAT CAGTGCCTG 720  
 CTGAGAGACA ATGGTTACTA CTACTTCCGC CCACAGGATA TTATCTACGA AGCCGATACC 780  
 CTCCTCGTAA GAGGTGCCGT ATGCCGTGCGA GCCAAGCTCT CGGAAGATAC TCCACCCCAA 840  
 55 GCCATGCGCC CGTGGAGGAT AGGGAACCGG ACAGCAGTCC TGCTCGGAAT GAACGGAGAA 900  
 AGCCCGACAG ACTCGCTCGA AGTGGAGGAT ATGAAAGTCC TTTACTATCG TAAATGCCG 960  
 GTTCGCCCCA AGATTTTGCG CAAACGCTTT CTTTTCTTCT CCGGCAATCT GTATCGGCAG 1020  
 AAAGACGATG AGACGACACG CAAATCCTTG GCTCGTTTGG GAGCCTTCTC CGTTATCGAT 1080  
 CTCATTTTTT TGCAACGCGA TTCCATTTCG GGCCTTTTGG ATGTGCGACT GCTAACCCAC 1140  
 60 CTCGACAAAC CTTGGGATGC ATCATTAGAG ACCTTGTTCA CGAGCAAAAG CAATGACTTC 1200  
 ATCGGTCCCG GACTGAATTT TGCTCTTGCT CGGCGCAATG TATTCGGCGG AGGAGAAAAT 1260  
 CTTTCTTGGA ATATCGGTGG ATCGTATGAG TGGGAGACCG GCAATCGTCC CGAAAAATAGC 1320  
 AGCAATCGGC TGATCGATAT AAATTCGTAC AACATGAATA CGGCCGTGAA CCTCTCGTTT 1380  
 CCCTCGATTG TATTTCCCGG TCTGCTGGAT AAATACATAT ACTACCCAC GACTACGACT 1440  
 65 TTTCAGGCTT CTGCCACCGC GCTGAACAGG GCACACTACT TTAGCATGTA CTCTTTCGGC 1500  
 TTTTCGACCA CTTACGAATT TCAGCCCTCC AAGGAACACC GGCATGCTAT TTTCCGCTC 1560  
 AAGCTCAACT ACAACCTCCT GGGGCATCAG ACAGAAACTT TCCAGGCCAT TACGGCGAAC 1620  
 AATCCGCCCC TGCTGCTCAG CCTTCAGAGT CAGTTCCTTG CTCAAATGGG GTATATCTAT 1680  
 ACGTTCAACA AATCGTTTC AGAGAAAAGT CCTCATCATC TTTGGATGCA ATTCGGAATA 1740  
 70 TCCGAGGCAG GCAATCTCCT GAATCTGATC TATCTGGCAG CCGGCAAGAA GTACAGCGAC 1800  
 ACCAAGAATT TCGTCGGCGT CCCCTTCTCT CAGTTCATCA AAGCCACGGG AGAAGTCCGC 1860  
 TATTCCTATA CCGATAGCCG CAATCAGTCA CTGGCAACCC GTTTCGGGAC AGGCGTGATA 1920  
 TATAGCTATG GCAATATGCG AGTGGCACCC TATAGCGAGC AGTTCATATG AGGCGGTGCC 1980  
 AATAGTATCA GAGCTTTCAC CBTCCGTAGC ATCGGCCCCG GACGGTTCAA TCCGGATTCC 2040  
 75 GACAATCAGT ATTCCTATTT GGATCAGGTG GCGCAATTCA AACTCGAAGC CAACGTGGAA 2100  
 TATAGAGGCA AGCTTTTCGG GGATCTCCAC GCAGCCGTTT TCCTCGATGC GGGCAACGTT 2160

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5 TGGCTCTTGA GGGAGGATTC TTCCCGTCCG GCGGGTGCTC TGTCCGAAGT GGGATCGGTG 2220  
 AGCAATTTCC TGAATAGCAT CGCTCTCGGC ACCGGTGTGC GCCTTCGCTA CGATCTGGCA 2280  
 TTTCTCGTGG TTCGTGTGCA TGTGGGCTTC GGTCTCCACC TTCCTTACAA TACGGGTAAG 2340  
 AAAGGTTACT ACAATATCCC ACGCTTTAAG GATGCCATCG GTTTCATTG GGTGTGCGG 2400  
 TATCCCTTC 2409

## (2) INFORMATION FOR SEQ ID NO:63

- 10 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 2349 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular
- 15 (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- 20 (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- 25 (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...2349
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:63

30 TCTCTCTCCG CGTATATCCG TTTCTCTATG TCCTCGCATT CCGTTCGGTA TCTAATCGGC 60  
 ATTGCCGGCT GCTTGCTCCT CATGCTTGCT TCCTCCTGCT CCGTCACCCG TTATGTGCCG 120  
 GACGGTAGCA GACTATTAGA CAGGGTAACG ATCGCAAGCG AAACGGGCAG TATCGCTCTG 180  
 35 CCGGAAGATA TTCGGGACTA TACCCTCCAG CAACCCAAAT ACAGACTGTI CGGGATGACT 240  
 CGCTGGCTAC TGCGCGTCTA TAGCAGCTCG AATCCGAACA GCAACAGCTG GTGGAACCGT 300  
 TCGCTCCGGA AAATGGGCGA ACCGCCGTGC CTCATCGATT CTGTCCTCAC CGATCGTACT 360  
 GCCAACCGTC TGGCAAAGGC GATGGCCGGC GATGGCTTTC TCGATGCTAC TGCTCGTGCC 420  
 GTGGTAGACA CCGGCTTGTA CAAGAAAGCT CGCATTAATT ATCTGATTCA GCCCGGAAGC 480  
 CGTTATTATA TACGCAATAT GGCTTTGGAT GTGAAGAATC CACTCCTTCC TCCCGTTGCG 540  
 40 CTTGGCAATT CGCTTCCTTC GGCATACAAG GTCCGGATCA GCGAGGGTTC TCCCTTGTCG 600  
 CCCATCGTAC TCGATGAAGA GAGAAAGGCG ATAGCTCGTC ATATGCGCAA CAACGGCTTC 660  
 TGGAAAGTTCT CCGCCGAGGA TGTATTATAT GAAGCAGATA CTACCGTTTC AGGAGGATCG 720  
 GGTACGAAAT CTGCCGATCT GAAATTAGTG GTCAATGGCA TCGGGCGTTA TCCATATCGG 780  
 45 ATCGGCAGGG TATTCTTTCA TGCCGATTAT GATCCTCTCG AATCGGACTT CAGAGTTTCA 840  
 GAGCTGCCAC GTATCGATTC GATTTGCGGT GCGGATTACA CTGTTTACTA TGGGAGTAGG 900  
 GGACGTTATA TCCGGGCATC GGCTCTCAGC CCGTCCGGTGT CCGTTACACC GGGAGCTTTT 960  
 TTCTGCCAGG ATGATGTGGA ACGCTCTTAT ATCAAGCTGA ATGCGCTCCC TATCGTTCCG 1020  
 AACGTGAATA TCCGATTGTG GGAGCACAAT GGTAAAGGATG AGATTGCTCT GCGGATAAGC 1080  
 50 TCTCGCCTTG TGGACTGCTA TATTCTTACC GTTCCGGCCA AGAGCAAATC GTTGAAGCC 1140  
 GAAGTCTTCG GCACCAATTG CGCTGGAGAC TTCGGGGCGG CTTTGTCTCT CGGTTTCACC 1200  
 GATCGCAATT TGTTCGTGGG GCGGAGATG TTCAATATCA AACTCAAGGG TGCTTACGAA 1260  
 GCCATTGCGA AGGGTTGCGA CAGCTTCATG GAATATGGGG TGGAAAGCTC GCTCCGTTTC 1320  
 CCTCGTCTCC TCTTCCCATT CATTTCTGAC GAAACGCGCC GGCGGCTACG GGCATCCACG 1380  
 55 GAATGGAAGA TCGGGTATAA TTACCAGACA CGTCCGGAGT TTGATCGGGT GATTCTCTCC 1440  
 GCTCAACTCA ATTATTATG GCAGACCTAC CTGCACAATC GTCTGCGTCA TACGATCCGC 1500  
 CTGCTGGATG TCGATTATCT CCATCTCCCG TACATCGATC CCGACTTCGC CCAATCCCTT 1560  
 CCGCCTACGA CTGCACTGTA TAACTACACG GAGCAGTTTA TCCTCGGCTC GGCATATATA 1620  
 CTGAATATTA CCACGGCTTC GTCCATGGAG CGTACCGTAT CCAATCCTTT TACGGCACGG 1680  
 60 TTCAGTATCC AGACAGCCGG CAACCTGCTG CAAGCCATT CTTATCTGAC CGATTCTCCG 1740  
 AAAGACGAAC ACGGTTGTA TAAAATGTTT GGTCTGCACT ATGCTCAGTT CGTCAAGCTC 1800  
 GATCTCGATC TGGCTAAAAC CGTTCTTCTC GAAAAGGACA ATACTTTGGC ACTGCATCTG 1860  
 GGTTCGAGAC TGGCTTTCCC TTATGGCAAT GCTCGCCATA TACCCTTTGA GTTACGTTAC 1920  
 TTTGCGGAG GATCGAACAG CGTTCGCGGC TGGAGTGTCC GTACCTTCGG CCGGGGAGT 1980  
 ATGAAGATGA CTCCGGACAA GACCTTCTTC GATCAGATGG GTGATATTCG TCTGGATCTG 2040  
 65 AATGTCGAAT ACAGGACAAA GCTGTCTGAG AAGTTTGGCG CAGCAGCTTT TGTCGATGCC 2100  
 GGCAATGTCT GGACGATAAA GSAGTATGAG AATCAGGAGG ACGGTCTCTT TCGTTTCGAT 2160  
 CGCTCTTACA AGGAATATGC TTTGGCCTAC GGTCTGGGSC TTCGTCTCGA CTTCGATTAT 2220  
 TTCTTCTGCG GGCTGGATGC CGSACTGAAA GCCTACGATC CTCAGCAGAC AGGGCGTTAC 2280  
 70 AAATGGGCTA TCACACGCCC AAACCTTTCT TCCAATTTCG CTTGGCACAT TGCAGTAGGC 2340  
 TATCCGTTT 2349

## (2) INFORMATION FOR SEQ ID NO:64

- 75 (i) SEQUENCE CHARACTERISTICS:

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(A) LENGTH: 2625 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: circular

5 (ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

10 (iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:  
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

15 (ix) FEATURE:  
(A) NAME/KEY: misc feature  
(B) LOCATION 1...2625

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:64

25	GTGGAATCTA AATTGTTATG TCTTATGAGA AAAAGAATTC TACAACTTTT CCTGACCGCA	60
	TTGCTGCTGG CATTAGGCTC CTCTCTCGCC ATAGCGCAAA CAGTGGTGAC CGGTAAGGTG	120
	ATCGATTGAG AAACGTCCGA ACCGCTCATC GGTGTATCCG TAAGCACCGG TCAGGGAGCA	180
	TCCCTCCGCG GTGTAAACAC CGATATGGAT GGTGGCTTCC GATTCGAAGT ACCGGCCAAA	240
25	TCTGTCTTGA CTTTCCGTTG CGTAGGTTAT GCTACCGTAA CTCGCTCTAT AGGCAGAGGT	300
	TCTCAAGAAG ACCTCGGTAC GATTCTCCTC GATCCCCAGG CCATCGGCTT GGATGAGATT	360
	CAGGTAATAG CCTCTGTGGT GCGCAAGAGC CGTATGACGC CGGTACCGGT TTCCAATATC	420
	CGTGTGGCTG ATATTGAGGC AGCATCGTTG AATGTCGAAT TTCCCGAAGT GGTAAATCC	480
30	ACTCCCTCTA CCTATACGAC AAAAGGAAGC GGAGGTTTCG GTGATGGTCG TACCAATGTG	540
	CGTGGATTG ACACCTACAA CTTCGGTGTA CTCATCAACG GAGTTCCGTG CAATGGTATG	600
	GAAGACGGGA AAGTATATTG GAGCAATTGG AGTGGTCTGA TGAATCAAGC CAGTACCAT	660
	CAGATTGAGC GCGGACTCGG AGCCTCCAAG CTCGGTATCA GCTCGGTAGG TGGTACGATG	720
	AACATTATCA CGAAGACTAC GGACGCCAAC ACCGGAGGTT CGGCTTATGT CGGTATGGGT	780
35	AATGATGGAT TGCACAAAGA ATCGTTCTCC ATTTCTACGG GTATGAACGA CGGTTGGGCT	840
	ATCACCATTG CAGGCTCCCA TATGACGGGT CTGGGTTATG TGAAGGGGCT GAAGGGACGT	900
	GCATTCTCTT ACTTCTTCAA CGTTTCGAAG AAGTTCAATG AACGTCATAC CCTCTCTCTT	960
	ACCGGATTCG GTGCACACA ATGGCACAAC CAACGTTCTT CCAAAATATC TGTAGCCGAC	1020
	TATGACAAAT ACGGCATCCG TCACAATCAA TCCTTCGGCT ATCTGCGAGG CGAACTGACT	1080
40	CCTACGGCTT ATGCTTACAA TACGTACCAC AAGCCCCAGT TCTCGCTGAA CCACTTCTGG	1140
	AAGATGGATG AAAATACCTC TCTTTATACG qCANICTACG CATCTTTGGC TACCGGTGGA	1200
	GGTCGTCGCG CTTATGGAAA GAACAGTAAG TGGGTATTGA TCAACTACAA CACCGGACAA	1260
	CCCTATGAAC AAACAAAGGT GACTCCCGAT GGACTTATCG ACTACGATGC CGTACTGGCT	1320
	GCCAAATGCG CGSCGAGCAA TGGCTCGGAA GCAATTTTTC CCCTTGGCTC CAACTCTCAC	1380
45	AAGTGGTTTC GTCTACTCTC TTCAATCAAG AAGAAACTTA ATAGTTCGCT GACTTTGACA	1440
	GCCGGATACG ATGGGCGTTA CTACCGTGGC GACCACATG ACAAGATCAC CGATCTGCTC	1500
	GGCGGTAGCT ACTACATAGA GGATCCCAAG ACAAGCTCG CATACCATGC GGAAGGTGAG	1560
	CAACTGAAAG TGGGTGACAT TGTAATTCGG GACTACACAG GCGAAATCAT GTGGCACGGC	1620
	CTCTTCGCAC AGATGGAGCA TTCGTCCGAA TGGATCGATG CATTCGTATC AGGATCTATC	1680
50	AACTACGAAC TATACCGCAA TCACAACAT TGGCGGTAGCA AGTCCACCGG CTACCTGCCC	1740
	GGCGTATCGC CGTGGAAAAG CTTCTTCCG TGGAGTGCCA AGGCAGGTCT GAGCTACAAG	1800
	TTGCGACAGG GACACAATGT ATTCGCCAAT GSGCGTTTCT TCACACGTGC ACCACTCTTT	1860
	GGCAATATCT ATGCTGCGGG GGCTATCATT CCCAATGACA AAGCCAATAT GGAAAAAGGTG	1920
	CTTACAGGAG AGGTGCGGCTA TGGATTACAG AATCACAAAA ACTTCGAGTT CAATATCAAC	1980
55	GGATACTATA CGAAGTGGAT GGATCGCGTG ACCTCGAAGA GAATCGGAAA CGAGTATGTT	2040
	TATCTCAATG GCGTTGATGC TGTTCACGTG GGGGTAGAGG CTGAGGTGAG CTATCGTCCT	2100
	ATTCTGTCAG TCGACCTTCG CGGTATGTTT TCTCTCGGTG ACTGGACTTG GCAAAACAAT	2160
	GTAAGTTACA CTTCTTACGA CGAAGCCGGC AATGAGACAG GGCAGGATAT AACCTATATC	2220
	AAGGGTCTTC ACGTCGGAGA TGCAGCACAG ATGACGGCTG CTGTATCGGC AGACATAGAG	2280
60	CTGTTCGAAG GTTTCCATGT CATAGGTAAG TACAACCTTC TTGGCAAGAA CTATGCAGGA	2340
	TTCAACCCCG CAACCGGTAA TGCACAGCAG TACGAAGCGG ATGGCAAAGA AATCGTGGAA	2400
	TCATGGAAAT TGCCGATGT AGGTCTGTTC GATCTGTCTG CATCTACAA TTTCAGCTT	2460
	GGTTCACTCA GCACCATAT CTATTTCAAC ATGGACAACG TAGCCGACAA GCGATATGTG	2520
	AGCGATGCCG ACGACAATAT CATCGGTAAG AAACACGATG AGGCTTCGGC TCTCGTATGG	2580
65	TACGGTTTCG GCCGCACTTG GTCTACCGGT ATTCGTGTAA ACTTC	2625

(2) INFORMATION FOR SEQ ID NO:65

70 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 1380 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: circular

75 (ii) MOLECULE TYPE: DNA (genomic)

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(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:  
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:  
(A) NAME/KEY: misc\_feature  
(B) LOCATION 1...1380

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:65

15	AACAGATGTA ATCCCTCGCG TCAATACTTC CACCTATCGC AGAATGACGT TGGAGATCT	60
	CTCCGAGCTT TTCTAATCCA TCTATCTATG AAGTTTTCAA TCCGCCTTTT CCTCTGCATC	120
	ATCTTTCTCC TCTCTGCATT TATCCTGCCT GCTCTCGGAC AAAAATCCAA GCAGGTACAG	180
	CGACTTGAGA AGCAACGTAA GGAGGCCCTC AAAGCCATCG AAAAACCAGA TCGCGAAGTA	240
20	CGAAATACCA AGAAAGACAA GCAAGACAAA CAAAAGCATC TCAACCTCCT GAACAAGCAG	300
	GTTGCTCAAC GCAAGCAGAT GGTACAACTC TTGGACAATG AGGTCAAAGA GTTGCAATCC	360
	GACATTGATT CCATGACGGG TGTATGTCAT CAGCTCTCTG TAGAAGAGAA AGCCCGATCC	420
	GATGAATATG CCCAAGCTCT ACAGTCTATG CAAAAGCGGA AACGCTCGTT GGATCGCATC	480
	CTTTTCATTT CATCGGCCAA GAGCTTTGAC GAAGGCATGC GACGGATGCG TTTCTTGGAA	540
25	CAATACGCTT CTGCATACAA GCTGGCATCT GTCCGGCTGC GCGATACAG TAGCAAGTTG	600
	GAGACTGAAC GTGCGACTGT AGAAGACGCC AAAAAGSAGA AAGGACATCT CTTAGTCATC	660
	AGAGAAGAGG AAAAAAAGAA ACTCGAAGGA CAGCAAGCCG AGCAACGTCG GCAGGTGCAG	720
	GCTTTGGGAG CCAACAAAAA AGACTTGGAA GCGCAGCTGC GAAAGCAGAA AAAGCAAGCC	780
	GAAGCTCTGA ACAGAAAGAT CGAGAAACAG ATTGCCAAGG AAATAGAAAC TGCCGAACGT	840
30	CGTGCTCGAG AASAACGTGA ACGGTTGGCA CCGGAAGCCA AAGCCAAGGG TAAGCCGGTT	900
	CCTGCCGAAC CGGAACGGAA GCGGAGAGCC AAAGGCGGCT ATGCTATGGA TGCCCTCTGAG	960
	CGTGCTCTCT CGGGCAGCTT TGCACAGAAC AAAGGTCGCC TGCCCGGCCG CGTTTCGGGC	1020
	AGATACCGAA TCGTAAGCGA CTTTGGCGTG CATCAGCACA GTGAGCTGAA AAAAGTACAA	1080
	GTTAATAATG GAGGTATCGA CATCGCTGTA GCAACAGGAT CCGATGCTAC CAGCGTATTC	1140
35	GATGGTGTAG TGTCCAGTGT ATTCTGTGATA CCGGGTTATA ATTGGCCCGT AATGGTTCGT	1200
	CACGGTAACT ATATCACGGT TTATGCGAAT CTGAGCAAAG TGTATGTAAA TTCCGGCACT	1260
	CGTGTTAAAA CGGGTCAGGC TCTTGTCGT GCCTATACGG ATCCTTCCAA CAACCAGACC	1320
	ATTATTCACT TCGAAATCTG GAAAGAACGC AGCAACAAA ACCCAAGACT ATGGTTACGA	1380

(2) INFORMATION FOR SEQ ID NO:66

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 1026 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:  
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:  
(A) NAME/KEY: misc\_feature  
(B) LOCATION 1...1026

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:66

65	AGTTTTTATC AAGAAATAGA CAGACTTATG AAAAAGTATT TGTTATATGC CTCGTTGCTA	60
	ACGAGTGTTC TGCTCTTTTC CTGTTCAAAG AACAACTCTA ACGAGCCGGT GGAAGACAGA	120
	TCCATCGAAA TTTCTATAAG GGTAGATGAT TTCACCAAAA CGGGTGAGGC AGTAGCCTAT	180
	GAAAGGAATC AAGGAAGTGC TGCCGAAAGG CTCATTACCA ATCTTTACCT CTTGTTGTTC	240
	GATCAGTCAG GGGCGAATCC GGGGAAATAC TATATTACCG GTAACACTTT CACCGGAGGG	300
	ACCTGGCTTC CTGACGATAT GAAGGTGAAG TTGGATATGA CACAATCCGA GGCCGGAGAG	360
70	CGCAAAGTAT ATGTCGTAGC CAATGTTGAT AATGCGGTTA AAACGGCTCT TGATGCTGTC	420
	GCTAACGAAA GCGATTTGCA GACTGTAAAG AGGACGACTG CAATGCCGTG GTCGACCGAT	480
	ATAGCCCTC CTTCCTGAT GTCCGGAAC AAGACACACG ACTTCTTGGC CAATCGTCTT	540
	TTGGACAATG TGCCCTTGT GCGTGCCATT GCCAAGGTGG AGCTGAATAT CTCGCTGAGT	600
	GAGAAATTC AGATTGTGCC GATAATTGTC AATGGTAGTT TGAGTGAGTT CAAGTTCAGA	660
75	TACGTAAACT TCGACAAGGA GACCTACGTA GTGAAGCCAA CGACCAAGCC GGACAATCTC	720
	ATTAGTTCCTG CTAATGGTGT TTGGCCTCAG ATTACAGATT GGACTGTATG GGGTGCTTCC	780



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TTAAATACTT CTCCTGCTCC GSATGCGGGC ACAGSTTATA CATTGGATGC AAATGGCAAG 840  
 GTACGGGCAC TACGGATTGT TACCTATCTG AATGAGCGCG ATAGCAAAGG GGCTACGGTA 900  
 GAGGTGCGAT TGCTCGTGT GSATGATGGC ACCCTTCCTC CTCGGAATT CGGTCCGGAG 960  
 CTTTATCGTT TGCTTTTGCC GGACAAGATC CTGCGCAATC ATTGGTACAA GTATGAAGTC 1020  
 5 GAGATT 1026

## (2) INFORMATION FOR SEQ ID NO:67

- 10 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 987 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular
- 15 (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- 20 (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- 25 (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...987
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:67

30 AACCTTAGGA CACAGCCTTT CTTTTGGTA GATTTGCAAT CTATGATCAG AACGATACTT 60  
 TCACGATATG TATCCTCGAA CTTTTGGAGT CCGGGAGCTA CCTTTTTTTT CACGATTTTC 120  
 CCGGCCTTCA TCCTCGCCGC TACTGCTTTG CCGGCTTGTG GAGGGGGTAC TGCTTCAGGC 180  
 TCCGATCGTA CGCTGGCTGT GACCATCGAG CCACAGAAAT ACTTCATCGA GTCCATTGCG 240  
 35 GATAAGTCGG TGCAGGTGGT GSCATTGGTA CCGGCCGGCA GCAATCCGGA GGAATACGAC 300  
 CCTTCGCCCTA CCGTGATGAA GCGTTTGTCC GAAGCAGATG CTTACTTCTA TATAGGAGGA 360  
 CTGGGGTTCC AGCAAAGAAA TCTCGCTGCC ATTGGGGACA ATAACCTAA GCTCCCTCTT 420  
 TTGGAATGG GCAAAGCCTT GGCGGATGCC GGAAGTGCGA ATCTCCACGG CTCTGCACA 480  
 GATCATTCTC ATACAGACCT GCATGCCCAT GATCCGCACT ATTGGAGCAG TGTGGTAGGG 540  
 40 GCAAAGGCAC TCAGTCGTGC TGCATACGAC GCGCTTGTGG AGCTTTATCC GAACGAGAAA 600  
 GACAAATGGG ACAAAGGGCA CGACCGTCTC AACGGACGTA TCGACAGCGT GAAGAGACTC 660  
 GTCGATACCA TGTTTGCCAA TGGCAAAGCA GACAAAGCCT TCGTCATATA TCACCCATCG 720  
 CTCAGCTTTT TCGCCCAAGA GTTCGGCCTG CGGCAGATCG TCATAGAGGA AGATGGGAAA 780  
 GAGCCTACGG CTGCCCACCT TCGTCGTGTG ATCGATCAGG CACGTGCCGA TGGTGTGAGA 840  
 45 ATCGTATTTA TCCAACCGGA ATTTGAAACG CGTCAGGCGG AGGACATCGC ACGCGAGATC 900  
 GGTGCTCGTC CGGTAAGGAT CAATCCTCTG CGCAGCTCGT GGGAGGAGGA AATTTTACAT 960  
 ATTGCTCGCG CTTTGGCTCA TGAACGG 987

## 50 (2) INFORMATION FOR SEQ ID NO:68

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 2634 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- 60 (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- 65 (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...2634
- 70 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:68

GCAGATTCTA TCGATATCC TCTTTACTTT TTTGGGCGGA ATCGGAAGAA ATGCTTTAGG 60  
 GAACCTATTC CCACCTTATA CAATAAAAC ATGATCGGAA AAAAAATCTT TTTTATCCTG 120  
 75 CTGGCGCTCA TTGCTTCAG TGGGCTGAAC GCAGCGACAG AACTGAGTT CAAGTACCCG 180

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5	ACCGATGCCA	ATATCATCGG	TCACGTCAAA	GACAGCAAGA	CGGGTGAACA	CCTTGTCGGT	240
	ATCACTATTG	CTATCAAAGG	CACTACCTTT	GGTACATCTA	CAGATGCAAC	CGGGCACTAC	300
	TATCTTCGTA	ACTTGGCTCC	GGGTGAGATC	ACTTTGATTA	TGCGTGGCAT	GGGCTATAAG	360
	AGCCAGGAGC	GCGTAGTCCG	CGTAGAAAAG	GACAAGACTA	TCCAGGTGAA	TTTCGAAGCA	420
	GAAGAGGATG	CCATCAATCT	GGACGAAGTC	GTGATTTCCG	CCAACCGCGA	ACTGACGCTT	480
	CGCCGCTTGG	CTCCTACTCT	GGTAAATGTA	TTGAACGAAA	AAGTCTTCTG	GCAAGTCAAT	540
	GCTTCTAACC	TGGCTCAAGG	CTTGTCATTG	CAGCCGGGAG	TTCTGTGTAGA	GAACAACTGT	600
	CAGAAGTGTG	GTTCATCA	AGTTCGTATC	AATGGACTGG	ATGGTCGTTA	TGCACAGATC	660
	CTCATCGACA	GCCGTCCCAT	CATGAGTGCC	CTTGCCGGTG	TTTACGGTCT	GGAGCAGATC	720
10	CCTGCCAATA	TGATCGAAGC	TGTGGAGGTA	GTACGTGGTG	GAGGATCGGC	CTTGACGGT	780
	TCTTCTGCTA	TTGCCGGAGT	GGTGAATATC	ATCACCAGG	AACCTTCTCA	CAATTCTTTC	840
	ACATTCAATG	AATCTCTGAG	CTTTACCGGT	TTGAGCAAGC	TGGATAACAA	CACGAACCTC	900
	AATGCCCTCA	TGCTCAGCGA	TGACAACCGT	GCCGGTGCCA	TGGTATTCCG	GCAGGCTCGT	960
	TACCGCAACC	ATTGGGATGC	TAACAATGAC	GGTTATTCCG	AATTGGGTAA	AATAGATGCC	1020
15	CGCTCGCTGG	GAGCGCATTC	TTATTTCGCG	TTGAGCGACT	ACAGCAAAT	GACGGGAGAG	1080
	TTTCACACGA	TCAGTGAATT	CCGCCGTGGT	GCCGATCGTA	TCCATTGGCC	TCCTCACGTA	1140
	GTGGGTGTAG	CTGAACAAAC	TGACCATAGC	GTATTTAGCG	GAAACTTGAA	ATACGATCTC	1200
	TTCTCTTCCA	ACTATAAACA	CCACTTCCAG	GCTTATACTT	CCGACAGAT	CGTAAATCGC	1260
	AAGAGCTATT	ACGGAGGTAT	CGGAGAGATT	GACGTCAATG	GCCACCCCGG	TGGTACGGAA	1320
20	GGCTACCCTA	TCCCTCAAGA	TCAATACGGC	AATAATTATG	GCGTGACCAA	AGGCAAGACA	1380
	TATATGGGCG	GTATCCAGTA	CAGCTACGAC	TTGGACAAAT	TCCTCCTCAT	GCCTTCGCAA	1440
	CTTTTGTTCG	GAGCCGAATA	TACGGGTGAT	GAACCTCAATG	AATGTGATGCC	CATCCTTTCA	1500
	TGGCAGACCG	GCGAGGATGC	CAATGGGAAT	ACCATTCCCC	TCTATCCCGA	ATTGGATCAG	1560
	AATATCAACA	CTACAGCCT	ATTCGGTCAG	AACGAATGGA	AAAATGACAG	ATGGAGCATC	1620
25	CTTGTTGGCG	CTCGCTTGGG	CAAGCATAGC	GAAGTCAAGG	ATATGATTCT	GAGTCTCTGT	1680
	ACCACACTGC	GTTCACACGT	GAATCCGGAC	ATCAACCTGC	GCGCTACATA	TGCAAAAGGG	1740
	TTCCGCGCAC	CGCAGGTATT	CGATGAAGAC	TTGCACGTAG	GGGTGTAGG	CGGTGAGGCA	1800
	CAGAAAGTAT	TCAACGATCC	GAACCTCAAG	CCTGAAATTT	CTCATGCATT	CAGTTTGAGT	1860
	GCCGATATGT	ATCATCGTTT	CGGTAACGTC	CAGACCAACT	TCCTTGTTGA	AGGCTTCTAT	1920
30	ACTCGTTTGC	TGGATGTATT	CACCAACGAG	GAGCAGCCTG	ATCAGCACGA	TGGCATCAAA	1980
	CGCTACACGC	GTATCAACGG	TAGCGGAGCC	AAAGTATTGG	GTCTCAATCT	GGAAGGTAAG	2040
	GTCGCATACA	AGTCCTTCCA	GCTCCAAGCC	GGTCTTACCC	TGGCCAGCAA	CAAATACGAC	2100
	GAAGCAGACG	AGTGGGGTCT	GAATACGGTG	AAAGACACCA	ACGGAGCTTT	TGTTACCGAG	2160
35	GCCAAATGCA	ATGGACAACA	GGAAATACA	AACGAATCCA	TGACGGATAC	GCAGATCACC	2220
	CGTACCCCCA	GCGTATACGG	TTATTTTACT	TTGGCCTACA	ATCCTGCTCA	CTCATGGAAC	2280
	ATAGCCCTTA	CGGGAGCATA	TACCGGTGAG	ATGTATGTAC	CCCACGCTAT	CGAATATGGT	2340
	GTGAAGCTCG	CCGAACCTGA	TATTATGCG	AACAATCCTG	AGATTACCGA	CGAAACCGGA	2400
	AAGGCTCCCC	GTATTGATGA	GCTGAAGAAG	ACACCTGCAT	TCTTCGATTT	GGGCTTGAAA	2460
	GTGGGTATG	ACTTCCACGT	ATTCCAGGCT	ACTGAGGTTT	AACCTCATGT	AGGTATGAAC	2520
40	AATATCTTCA	ACTCTTTCCA	GAAGACTTTC	GATCGTGGAG	CTGCACGTGA	CAGCGGATAT	2580
	ATCTATGGTC	CTACGCAGCC	GCGTACAGGC	TACATGGGCT	TGGTAGTGAA	GTTC	2634

## (2) INFORMATION FOR SEQ ID NO:69

- 45 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 618 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular
- 50 (ii) MOLECULE TYPE: DNA (genomic)
- 55 (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PORYPHYROMOHAS GIIIGIVALIS
- 60 (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION: 1...618
- 65 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:69

70	AAACAGATAG	TTATGACAGT	AAAGCGCGCA	GTGCGAATAG	CACCTTCTCAC	GCTGATAGGC	60
	ATTCTTTTTT	CCTCACCTTC	TCTTGTTCGG	GCGCAAAGTC	TTTTTCAGCAC	CGAACATGTC	120
	TTGCAACTAT	ACAACAAGAT	ACTCTATGGA	GAGTCGGCGG	CGGATACCGT	CGCAGAGAAA	180
	ACGGCAGGTG	AGTCGGCATT	TCCTTTTATA	GACAAACTCA	TCAATCTCGG	CCGCACTTTC	240
	CTCGGCAAAC	CATATCGCTA	TCGCGGTCCT	TCCCCATGGC	CGATGGACTG	CTCGGGCTAT	300
	GTGTCTTACC	TCTACTCCAA	ATTCGACATC	AACTCCAC	GTGGTGCGGC	AGCACAGAGC	360
	CAATATACGA	ATCCTATCGA	GCGCGAGGAT	GTTCTGTCGG	GCGACCTCCT	TTTTTTCAAA	420
	GSCCGCAATG	CACGAGCAA	CCGTATCGGG	CATGTAGCTT	TGTCGTATC	TGTCGATGAA	480
75	GATGATATTA	CCATGATGCA	CAGCCGCAAT	TCGCGAGGGA	TCGTGATCGA	AAAACCTCAAT	540

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CGCAGTGCAT ACTTCTCCCG TCGCTTGGTG AGCTATGGCA GGGTACCCGG AGCCAAGAGA 600  
GTGATCCAC GAAAAAGT 618

## 5 (2) INFORMATION FOR SEQ ID NO:70

## (i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 1401 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: circular

## (ii) MOLECULE TYPE: DNA (genomic)

## 15 (iii) HYPOTHETICAL: NO

## (iv) ANTI-SENSE: NO

## (vi) ORIGINAL SOURCE:

- 20 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

## (ix) FEATURE:

- 25 (A) NAME/KEY: misc\_feature  
(B) LOCATION 1...1401

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:70

30 AAAGGTACGT GGAATAGAAA AAACCGAAGA GAAGAAATGA AACGGACAAT CCTCCTGACG 60  
GCACTGACCG TCCTATCTTC GCTCTCCTTG CTTCGTGCAC AAAATGAATC CGAAGCATCA 120  
ACCAATCCGA TGTCAGGCCT CTCCCTGGAA GACTGTATCC GGATAGCCAA GGAGCGCAAC 180  
CTGAATCTGC GCAGACAGGA GATCGAACAA GAAAACCGAA TCATTAGTCT CGATGCAGCA 240  
CGACACAGTT TCCTGCCCTC GGTCAATGCA GGCATCGGAC ACAACTATAG CTCGGACGT 300  
TCGAAAGACA AAACGGGAGT AACCGTAGAT CGCTCCTCGA TGAATACCAA TCTCAGCATC 360  
GGAGCTTCGG TGGAGTATT CAGCGGCACA CGTCGTCTGC ACGACCTCAA GCAGCAAAAG 420  
35 TACAACGTGG AGGATGGTAT AGCCCGACTT CAAAAAGCGC GTGAAGACCT CAGCCTGCAA 480  
ATCGCGGCTC TCTATATCAA TTTGCTCTTC CGTCAGGAAA TGAATCGTAC GGCAGAAACA 540  
CAGTTGGCAC TGATTCGCGA GCAACGCAAT CGCACGGCCG AAATGGTTTC CGTAGSTAAA 600  
TGGGCAGAGG GTAAGCTCCT CGACATAAAT GCCCAGATGG CCAAGGACGA ACAACTTCTC 660  
GTACAATATC GTTCGGAGGA GGAGCTGGCT CGTCTGGACT TGGGGCAAGC CCTCGAACTG 720  
40 GAGCACCCCG AAAGCATTGC AGTCAAGGCT CCCGACACAG ACGTTCTCGT AGCAGAAAGG 780  
TTGGGATCTC TCCTTGCTCC CGAAGAGATC TATCGCACGG CTCTCGGCTT GAAACCGGCA 840  
CTGATTCGCA GCGAGCTGCA AATAGCTTCG GCACGCGAAG GTCTGGCCTC GGCTCGTGCG 900  
GCATACTTCC CGACGCTCAG CCTCTCTGCC GGATACAGCA ACGGTTACTT CCGCGACCTC 960  
GGCAAGGAGT ATGCGGCCAT CAACCCCTCC TTCTCCGAAC AGTGGAGAA CAACGGCAGC 1020  
45 TACAGTATCG GACTCTCTTT GAATATCCCC ATCTTCTCTG CCATGCAAAAC GCAAGATCGC 1080  
GTTTCGGAGCA GTCGCTTGCA AATACGCTCA AGCGAGCTTC GACTCGTCTG AGAGAAAAAA 1140  
GCCCTCTATA AAGAGATCAG GCAAGCATAA AGCAATGCCG TGGCAGCCGA TAAGGCCATC 1200  
GCAGCAGCCG AAAACAGCAA GGCCGCTACG CTCAAGGCAT ACGAATACGC TCGCGACAGC 1260  
TTCGAGGCAG GGCCTTGTG TGCTACGAA TATGCCGAGG CAAAAACAAA ATACGCCCTC 1320  
50 AGCCAAGTGG AAGAACTTCG TGCCAAGTAT GACTTCATAT ACAAAGCCAA AGTTTTGGAT 1380  
TTCTATCAGG GCAAAGACTT C 1401

## 55 (2) INFORMATION FOR SEQ ID NO:71

## (i) SEQUENCE CHARACTERISTICS:

- 60 (A) LENGTH: 1353 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: circular

## (ii) MOLECULE TYPE: DNA (genomic)

## 65 (iii) HYPOTHETICAL: NO

## (iv) ANTI-SENSE: NO

## (vi) ORIGINAL SOURCE:

- 70 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

## (ix) FEATURE:

- 75 (A) NAME/KEY: misc\_feature  
(B) LOCATION 1...1353

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:71

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	AAAACATCAT	ATCGGAATAA	TATGCGTTTC	CAACATTATC	TCATCTGTAC	GGCTGCCGTA	60
	GCGGCTTTGG	CTGCGAATCC	CCTTACGGGC	CAATCGAATA	TGACCCCTCGA	AGAGTGCATA	120
	GACTATGCAC	GCCGGCACAG	TTCGGCCGTG	GCGCTGTCCG	CTGCGGAACT	GGAGCAGTCC	180
5	AAGGCCGATT	ACCTTCAGGC	CGTCGGCAAT	TTTCTGCCCC	GTGTATCGGC	CGGAACCGGT	240
	GCTTCGTGGA	ATTTCGGACG	CGGATTGGAT	GCCGAGACGA	ATACCTACAC	CGACATCAAC	300
	AGCTTCAACA	ATTCGTACAG	CATACATGCC	ACGATGACCC	TTTTTCGACGG	TTTGCAGAGT	360
	GTCTATCGAC	TGCGGATGGC	GCATGCACGC	CGGGAGGCTT	CGCGCCTCTC	CGTTCGCGAG	420
	CAGCAGGAGC	TGGCAGCTCT	CGGCACCCAG	GAGGCCTACT	ACGACCTCGT	CTATGCGCGC	480
10	CAAAATGCAAG	AGCTGGCCAT	GCAGAAGTAC	GAGGAGAGCA	GCCGCTTCCA	CCGGCAGACG	540
	GCTCGAATGG	AAGAGCTGGG	GATGAAGAGT	CGTCCCGATG	TCCTCGAGAT	GCAGTCGCGA	600
	ATGGCCGGTG	ACCGTTTGGC	CCTGACTCAA	GCGGACAATC	AGTGCATCAT	CGCTCTGATC	660
	CGGCTCAAAG	AAAAAATGAA	CTTCCCCATC	GATGACGAAC	TCGTCTGAGA	CGATATGCCG	720
15	GCTGACAGTC	TCTCCGCCGA	CATGGCCGAA	TCGGACAGCT	CGGCCGGCGT	CTTCGCCCGT	780
	GCTGCCCATC	ATCATCCCGT	CCTCCTCCGT	GCCAAACTCG	ACGAGCAGGC	TGCCACCGAC	840
	CGTTTGGGAG	CCGCGCGAGG	TGCATTCCCTG	CCGAGTGTGT	CGGTATCCGG	AGGATGGAAC	900
	ACGGGATTCT	CACGCTTTTT	GAATGGATCG	GACTATACGC	CCTTCAGCGA	GCAGTTTCGG	960
	AACCGTCGGG	GGGAATACGT	CAGTCTGAAT	CTGAGTATCC	CCATCTTTTC	GGGATTTCAGC	1020
20	CTTGTGAGCC	ATCTGCGTCA	GGCGCGTGCC	GAACGACAGG	CGGCAATCGT	CCGACGGGGC	1080
	GAAGCGGAGC	GCAGGCTCTA	CAGCGAGATC	GCCCAAGCCA	TGGCCGACCG	GGATGCCGCT	1140
	CTGGCTTCCT	ACCGCCAGGC	GAAGGAGCAT	ACCGACGCCA	TGCAAAACGC	TTACGAAGCC	1200
	GTCTTGCAGC	GTTATGAGGA	GGGGCTGAAT	ACGGCCATCG	ACCTGACCAC	TCAGGCCAAT	1260
	CGGCTCCTGG	ATGCCCGTGT	GCAGCGACTG	AGAGCGGCCA	TGACCTACCG	GCTCAAAATGC	1320
25	AAACTCATAG	CCTATTACGG	CTGCCTTTCG	GAC			1353

## (2) INFORMATION FOR SEQ ID NO:72

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 2886 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...2886
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:72

50	GCCATTTTTG	TCGTATCATT	GCAAATTGAA	AAAATAACAG	AGAATAAGTA	TAATTCAGAC	60
	AAGAGCATGA	ACAAATTTTA	CAAATCACTT	TTGCAGTCAG	GACTGGCTGC	CTTCGTGTCC	120
	ATGGCAACTG	CACTGACCGC	TTCTGCACAG	ATTTTCGTTCG	GAGGGGAACC	CTTGAGTTTC	180
	TCTTCAAGAT	CCGCCGGAAC	GCATTCAATC	GACGATGCAA	TGACTATCCG	CCTTACTCCG	240
55	GATTTCAATC	CGGAAGACCT	GATCGCACAG	AGCCGTTGGC	AATCGCAAAG	AGATGGCCGG	300
	CCCGTCCGGA	TAGGACAAGT	AATACCGGTG	GATGTGGACT	TTGCATCCAA	GGCTTCGCAC	360
	ATCTCTTCCA	TCGGAGACGT	AGATGTATAT	CGCCTGCAAT	TCAAGTTGGA	AGGAGCCAAA	420
	GCCATTACGC	TTTATTACGA	TGCATTCAAT	ATTCCGGAGG	GCGGACGCCT	CTATATCTAT	480
	ACCCCCGACC	ATGAAATTTGT	GTTGGGAGCA	TATACGAACG	CCACTCATCG	CCGCAACGGA	540
60	GCTTTTGCCA	CAGAGCCGGT	ACCGGGGAGT	GAGCTTATTA	TGGATTATGA	AGTGTCTCGC	600
	GGAGGGACTT	TGCCTGACAT	CAAGATCTCC	GGTGCGGGTT	ATATATTGCA	CAAAGTCGGC	660
	GGACGCCCGG	TAACGATAAA	CCATTACGGG	ATCGGTGAGG	ACGATTCCGA	TTCGGATTGC	720
	GAGATCAACA	TCAATTGTCC	TGAAGGTGCA	GACTGGCAGS	CAGAGAAGAA	CGGTGTGGTG	780
	CAAATGATCA	TGGTAAAAGG	ACAGTATATC	TCAATGTGCT	CAGGCAACCT	GCTCAATAAT	840
	ACGAAAGGAG	ACTTTACTCC	GCTGATCATT	TCTGCCGGAC	ACTGTGCTTC	CATAACAACC	900
65	AATTTCGGTG	TAACGCAATC	CGAGTTGGAT	AAGTGGATCT	TCACTTTCCA	CTATGAAAAA	960
	AGAGGATGCA	GCAATGGTAC	ATTGGCCATC	TTCCGTGGCA	ACAGTATCAT	CGGAGCTTCC	1020
	ATGAAGGCTT	TCCTCCCGAT	CAAAGGTAAA	TCCGATGGTC	TCTTGCTGCA	ACTCAACGAT	1080
	GAAGTCCCTC	TGCGCTATCG	TGTCTATTAC	AATGGATGGG	ACAGTACGCC	CGATATTCCC	1140
70	TCGAGCGGTG	CCGGTATTCA	TCATCCGGCC	GGAGATGCCA	TGAAGATTTC	CATCCTAAAG	1200
	AAGACTCCGG	CTCTGAATAC	ATGGATCTCC	TCCAGTGGTT	CGGGAGGGAC	TGACGATCAC	1260
	TTCTATTTC	AATACGATCA	AGGTGGTACG	GAAGGAGGAT	CGTCCGGTTC	TTCTCTCTTC	1320
	AATCAGAATA	AGCACGTGGT	CGGCACACTG	ACCGGAGGTG	CCGGCAATTG	TGGCGGGACG	1380
	GAGTTCTACG	GCAGACTGAA	CAGTCATTGG	AACGAGTATG	CATCCGATGG	CAATACGAGC	1440
75	CGCATGGACA	TCTATCTGGA	TCCCCAAAAC	AATGGCCAGA	CGACCATCCT	CAACGGAAACG	1500
	TATCGTGACG	GTTATAAGCC	TTTGCCCTCT	GTGCCCGGCG	TATTGTTGCA	GTCTACAGGC	1560

	GATCAGGTCG	AATTGAATTG	GACGGCTGTT	CCTGCCGATC	AATATCCATC	ATCTTATCAG	1620
	GTCGAATACC	ACATATTCCG	AAATGGAAAG	GAAATAGCTA	CSACAAAGGA	GTTGTCTCTAT	1680
	TCGGATGCCA	TCGACGAAAG	TATTATCGGT	AGCGGTATCA	TTCGATACGA	AGTAAGCGCA	1740
5	CGCTTCATTT	ATCCCTCGCC	GTTGGATGGA	GTGGAATCTT	ATAAGGATAC	GGACAAGACT	1800
	TCTGCCGACC	TTGCCATAGG	AGACATTCAG	ACCAAGCTGA	AGCCGGACGT	AACACCTCTC	1860
	CCCGGAGGAG	GAGTATCATT	AAGCTGGAAA	GTTCCCTTCT	TAAGCCAGTT	GGTTTCCCGA	1920
	TTCCGAGAAA	GCCCCAATCC	TGTGTTCAAA	ACCTTTGAAG	TGCCCTATGT	TTCTGCCGCA	1980
	GCCGCACAAA	CCCCCAATCC	TCCCGTTGGC	GTAGTCATTG	CAGACAAGTT	TATGGCCGGT	2040
10	ACATATCCCG	AAAAGGCTGC	TATCGCTGCC	GTTTATGTAA	TGCCATCCGC	TCCGGACTCT	2100
	ACTTTCCACC	TCTTCTCTCA	GAGCAACACA	AACAGAAGAT	TGCAGAAGGT	GACAACTCCC	2160
	TCCGATTGGC	AGGCCGGAAC	ATGGTTGAGG	ATCAATTTGG	ATAAGCCGTT	CCCGGTGAAT	2220
	AATGACCATA	TGCTTTTTGC	CGGTATCAGA	ATGCCTAATA	AGTACAAGCT	CAATCGTGCT	2280
	ATCCGTTATG	TAAGAAATCC	GGATAACCTT	TTCTCCATTA	CCGGTAAGAA	GATTTCATAT	2340
	AACAACGGAG	TCTCTTTCGA	AGGCTACGGA	ATACCCCTCG	TCTTGGGCTA	TATGGCTATC	2400
15	AAATATCTGG	TGGTAAATAC	CGATGCTCCG	AAGATCGATA	TGTCGCTTGT	ACAGGAGCCT	2460
	TATGCTAAGG	GAACGAATGT	GGCTCCATTC	CCCGAATTGG	TCGGCATATA	TGTCTATAAG	2520
	AACGGAACAT	TTATCGGCAC	ACAGGATCCA	TCCGTCACAA	CTTATTCGGT	TTCAGACGGA	2580
	ACAGAGAGCG	ATGAATACGA	AATAAACTG	GTATATAAGG	GATCGGGCAT	TTCGAATGGC	2640
20	GTTGCTCAGA	TTGAGAATAA	CAATGCTGTC	GTTGCATATC	CGTCTGTTGT	AACAGATCGT	2700
	TTTCAGCATTA	AGAAGGCTCA	TATGGTTTCC	GCTGCCGCC	TCTACTCATT	GGATGGCAAG	2760
	CAGGTTTCGT	CTTGGAAACA	CCTCCGCAAT	GGCGTGACAT	TCAGTGTTCA	AGGACTTACG	2820
	GCCGGTACTT	ATATGCTCGT	TATGCAGACG	GCAAACGGCC	CTGTGAGCCA	AAAGATCGTG	2880
	AAGCAG						2886
25	(2) INFORMATION FOR SEQ ID NO:73						
	(i) SEQUENCE CHARACTERISTICS:						
30	(A) LENGTH: 2106 base pairs						
	(B) TYPE: nucleic acid						
	(C) STRANDEDNESS: double						
	(D) TOPOLOGY: circular						
35	(ii) MOLECULE TYPE: DNA (genomic)						
	(iii) HYPOTHETICAL: NO						
	(iv) ANTI-SENSE: NO						
40	(vi) ORIGINAL SOURCE:						
	(A) ORGANISM: PORYPHYROMONAS GINGIVALIS						
	(ix) FEATURE:						
45	(A) NAME/KEY: misc_feature						
	(B) LOCATION 1...2106						
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:73						
50	TGGAAAAAAA	GTAATCCTCA	ATACCGGGGC	AGGACAGCAA	ATTACCGAGA	TCATTATAAT	60
	ACAGAAAGCT	ATTTAAGCCT	AAGGAGGAAT	CAAACAATGA	AATATCTTAT	CAGACTCTTC	120
	TTATCATTTA	TGTTACTCTC	TCTCTGGACG	GGCTGTACAC	ACGAGGAGCT	CTCTATTTCG	180
	GATGGCGAGA	ATACGCTTGT	TTTACGCGTA	GAGACCGGTA	AAGCCCCAAA	TGCTCGTGCC	240
	ACAGAACCCG	GTCAGGGCAT	ATACAATGAG	AATAAAGTAG	GCTCCATTTC	TGTGCTCTTC	300
55	TATTTAGAGG	GACAACTTCG	TTGGCAGGTG	AAGTCTACAG	ACTATCAAAT	CCATGAAGGG	360
	GCCTATATCA	TTCCGGTCAA	AGAGCAAATG	CGACCACTAT	TCAATGGCAA	CAACAACCTC	420
	AGCATCTATG	TAGTGGCCAA	TCTCGATTTC	AATGCTCCGG	CCACAGAAGC	TGCGCTTTCT	480
	CAATTTGTGG	TAGAGAAATC	TATTGAAGTC	TCTTCTACGA	CAGCCCCCTG	CGATTTCTGT	540
	ATGCTTGCTC	ATGGCAATAA	GCAGATCAAT	ATGGCTACGA	CAGAAGGGAA	ACTGTTGGGG	600
60	GATTATAAAC	TCAAAAGAGT	GGCAGCAAAG	ATTTCGCATG	TAAAACCCAC	CATCAATGTG	660
	CAAGGATATG	AAGTGGTCGG	AAATATACAG	GCAAAGTTTC	GCAATTCGGT	AACGAAGGGG	720
	TTCCCTTACCA	CAGAAGCTCA	AGAGATCCCA	GCTGCTGCAT	CCTATAAGAC	ATCGGAATAT	780
	CTTGATATTG	CAGAGTCGGC	ACCTGCCAAT	TCTATCCATT	TCTATTCTTA	CTATAACAAA	840
	TGGACACTCT	CCACACCGGA	GAAGCGACCG	GAATTCCTTA	TCATGGTCAA	ATTCAAAAAG	900
65	ACAGGACASC	CGGACAACAC	AGCCAAACCG	TACTACTACA	GAGTGCCCTC	CGAATCTCAG	960
	GACAAATCAG	ATAAAGTGAA	TGTCCTCTAT	AATCTGAATG	TGAAAATCGA	AATCTTGGGT	1020
	TCTTTACAAG	AGCCGGAAGC	TGTTTCTGTA	AACGGCACAC	TCGCAATAGA	AGAATGGATT	1080
	CTCCATCAGG	ATGCAATCAA	TCTGCCTGCC	ACCAATTACT	TGATAGTGGA	ACAGCACGAA	1140
70	ATCTTCATGA	ATAAAGTGAA	CACATACTCG	GTGAAATATC	AAACTTCGCA	GAAACCAACT	1200
	AGCATTAGCA	TACAGTCAGT	TACCTTTAGC	TACGTCTCTT	CTGATGGCAC	TCAGCACAAAT	1260
	GATCTTGTAG	CAAGTAGTAG	CGACCAAGTAT	CCTACGATTA	CAAGCGATAA	TACAAGCATC	1320
	ATAATCACTT	CCAAGATACC	GTTTAATAAC	GTACCAAAGA	AGATCGTTTT	TGAGGTAAC	1380
	AATGGGGTAG	CCGGTTTGAA	AGAGACTGTC	ACAGTACTCC	AATATCTCTG	ACAATTTATT	1440
	GTCAATACAC	TTGGCAGAGC	ATCGGCATGG	AGACCAGACG	GATCTTTGGC	TCCGGGGCTT	1500
75	AACAATAAAG	CGATTTACCA	TGTCGTAGTA	CTGGTTCCAC	CCGAGAATTT	ATTTGAAGAT	1560
	GGGACACAGA	CAATCATCGG	TTATCCCCCC	ACTGAAACAA	TTTCTTTTCA	TAAGAAAGAG	1620

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5 AACAAATACCT ATCCGATAGT ATGGTCTGAC ACAAATACGA CAAAACAGGA CCTTGAGACA 1680  
 TCAAGAATGA TTTCACCTTC CTTTGAGTTA GCCTCCCAAC TTGGGGCTAC TCTCCCGATG 1740  
 CCTATCTCG AGTATTGGCC AGGGACATCA TATCTCCTTG ACTATTCCGGG AAACATAAAT 1800  
 AATAAGAGAT ACGCCTTGTT TAATTGCGCT TTTTACTGGG AGAAAAGAAA AGTTAATAAC 1860  
 GAAGAAATTA AATTCGATGA CTGGCGTTTG CCGACAGAAG CTGAGATCAA ATTGATAGAT 1920  
 AAGCTGCAAC ATAATGAGCA GAGTGTGTG CAAAGCTATCA TGACAGGGAA TTATTATTGG 1980  
 GATAGTTACT CTGCAAAATGG GTCTTATAAA ATGCAAGGAG GAGGGGGCCA AGGAAATTCC 2040  
 TCCAAAGCCT ATGTTCTGTT CGTGCGGGAT GTGAAAAAGC CGATTCTGTA CAAGAAGTCA 2100  
 10 GGTAAAG 2106

(2) INFORMATION FOR SEQ ID NO:74

15 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 3936 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular

20 (ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

25 (iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

30 (ix) FEATURE:  
 (A) NAME/KEY: misc feature  
 (B) LOCATION 1...3936

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:74

35 AAGAGGGTAG ATAGCTATGA ATGCAGACAA AAAGCTTGCA AATGTGCAAT TTGTGTGATA 60  
 CAAAAATTTA CTAATGTAAA ACTAAATGAT ATGCGAAAAA TTTTGAGCTT TTTGATGATG 120  
 TGCTCTCTGC ATTTAGGTCT ACAATCTCAG ACTTGGCATG GAGATCCGGA CTCAGTGGCA 180  
 GCCCTACCTT CTATCGGTAT TCAAGAGTCA AGTTGTACCC GAATCACGTT CGAGGTGTGT 240  
 40 TTCCCCGGAT TTTATAGTGT GGA AAAACGA GAAGGCAACC AAGTCTTTCA GCGCATTTCC 300  
 ATGCCGSGTT GTGGCTCGTT TGGGAATCTG GGGGAAGCTG AATTGCCTGT TTTGAAAAAG 360  
 ATGATAGCCG TTCCGGAATP TTCAACAGCT AACGTGTCTG TAAAAATCAA AGAGACGGAG 420  
 ACATTCGACA ATTAATAATAT CTATCCTAAT CCTACCTATG TCGTAGAGGA GTTGCCTGAG 480  
 GGGGGGACCT ATCTGGTAGA GGCTTTCCGG ATAAACAATG ACTATTATAG CCAAAATGTA 540  
 AGCCTCCCTT CTACTCACTA TGCTATTCT CAAGACGGGT ATTTTCGCTC ACAAAGATT 600  
 45 ATCGAATTTA CCCTGTATCC TTTTCGATAC AACCCTGTCC GACAAGAAAT TCTATTGCA 660  
 AAAAAAATCG AGGTTACAAT AACTTTCCGAT AATCCTCAGC CACCTTTACA AAAAAACACC 720  
 GGCATATTTA ACAAAGTAGC CTCTCTGCA TTTTATTAAT ATGAAGCTGA TGGCAATCG 780  
 GCGATAGAAA ATGATATGGT GTTCAGTCGT GSTACAACAA CGTACATAAG CGGAAATGTT 840  
 GCCAGCAACC TCCCTCAGAA CTGTGACTAC TTGGTTATTT ACGATGATAT GTTCAACGTA 900  
 50 AATCAACAAC CACACGACGA AATCAAAACGG CTGTGCGAAC ATAGAGCCTT CTACAACGGC 960  
 TTTGATGTAG CTGCTGTAAG TATAAAGGAC GTATTGAATA GCTTCCCATC AAATGCCACC 1020  
 TCATACATCA ACGAAACTAA ACTGAAAAAT TTCATTGCTT CAGTTTACAA CCAAGCAAT 1080  
 GCGAAGAGGA CTTTAGATGG CAAACTGGGA TACGTGCTAC TGATCGGAAA ACCATTGAGC 1140  
 AAATATTTGG CTGACACTGA TAATACAAAA GTCCCAACCT CTTTATTTC TAATGTCTCC 1200  
 55 TTAATTCCAA GTCATCCAAC TTTTGGTTCC ATATGCGCCT CCGACTATTT TTTTAGTTGT 1260  
 GTTTGCGCCC TTGATACTGT CGGCGATTG TTTATCGGTC GATTAGCGT CACCAATGCT 1320  
 CATGAATTGC ACAATCTGAT TGAAAAGACT ATCAACAAAG AAATCTCATA TAATCCTATT 1380  
 GCACACAAAA ATATTCTTTA CGCAGAAGGG AAAGGCTGCG ATGCTCCAAT CTTACGTTTA 1440  
 TTCTTAAAG AAATCGCCTC TGGTTACACA GTCAACTCTA TCTTAAATC TAATCAGGTC 1500  
 60 TCTGCAATAG ACTCGATATT TGACTGCTTG AATAATGGTT CCCATCATTT TTATTTTAAC 1560  
 ACTCATGGAA TGCCGACTGT TTGSGGGATA GGGCAGGGAC TCGACGTCAA TACTCTAACA 1620  
 GCCCGATTGA ACAATACATC TTGCGAGGGA TTATGTACGA GTCTATCATG TAGTTCGGCT 1680  
 GTAGCAGATT CAACTATTAG ATCGCTTGGA GAAGTCTTGA CCACATACGC ACCTAACAG 1740  
 GGATTTCTCG CTTTCTTAGG AGGAAGCAGA GCCACCCCAAT ATGCCGTTTA TTTAGAAGGC 1800  
 65 CCTGTCTCT CGTCAGAAAT TTATGAATAT TTACCTTATT CTTTATATCA CAATCTCTCG 1860  
 ACTGTTGTTG GCGAAATGTT GCTATCATCC ATTATCAATA CTAATTCTGT TGATACGTAT 1920  
 TCGAAATTCA ACTTCAATTT GCTTGGGAC CCTGCACTAA ACATTATGGC TCATGGCATG 1980  
 GAGGTTAGTA ATTGATTAC ACTACCAAC AACCCATTA TAAGCAGTCC GATAACAATA 2040  
 70 AAAATGTTG GCTGCCTAAA AATACCGGAA AAAGGAGTTT TGCATTTTAC TAATAATGGC 2100  
 TCCATACAGG TCATGTCCGG AGGAACCTCG GAATATAGGCA ATCAGGCTAA AATATCCGGA 2160  
 GAGACCGGTG CTAACCCAC CTTATTACC GTTACGGCG ATGGTCTTGC GATTAAACAAG 2220  
 CAGGTAGAGA TAGACAATAT AGACCGACTT AACTTGTTTT CTACGCATTC GGTACATGCC 2280  
 AAATTTTCAAT TTGACAGTGT GAAATTCAAC AGTGCCCGGC TGTATACAAC GAACTGTATT 2340  
 75 GTGGAGATAA GCAATTGCGA ATTTACCAAT CGAAGTGACA TTATTTCAA GAATTGTGAC 2400  
 CTAAGCGTTG AAAACAGTAT GTTAGCAGT TCGGGGATAA CGGTATTCAA GCCTATGGCT 2460

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	ACAAGCTCCA	TCACCGGATT	ATCTACAAAA	GCAAAGATTA	CCGACAATAC	TTTTTTTGCG	2520
	ACAGGAAACT	TCGCCTACCA	TATCACAAC	ACGCCAGGCT	TAACAGCAAC	CTCCAATGCT	2580
	GCCATCAAGT	TAGACAATAT	TCCTGAGTAT	TACATTTCCG	GTAATAAAAT	AGTCAATTGC	2640
5	GATGAGGCTC	TTGTACTAAA	TAATAGTGGC	AACAGAACGA	ACAGACTCCA	CAATATCACA	2700
	CGGAATGTGA	TAAAAAATG	TAGGATTGGG	AGCACGCTTT	ATAATTCCTA	TGGTATTTAC	2760
	AACCGAAATA	AGATCAGTAA	CAATCATATA	GGAGTACGTC	TCCTCAACAA	CAGTTGTTTT	2820
	TATTTGATA	ATGCTCCTGT	AATCAATGAA	GAAGATAAGC	AGACGTTTAT	TTCTAATAGG	2880
	ACTTGGCAGC	TCTATTTCATC	AAACGGTACA	TTCCCTCTCA	ACTTCCATTA	CAACAGCTTG	2940
10	CAGGGGGGAG	ATACAGATAC	ATGGATTTAC	AACGACACGT	ATACGAATCG	CTATATTGAC	3000
	GTTTCAATA	ATCACTGGGG	CAACAATGAT	TTGTTTGATC	CGAATCAGGT	TTTCAATACG	3060
	CCAGACTGT	TCATTTGGAT	ACCTTTTTTG	GATGGATTGC	CAATGGGGAG	ATCGGGCAAT	3120
	AGCTCTGCTG	AAGCAGTAGA	ATCCAAACA	GCATTGGACT	GTATTGGCAA	TAGCGATTAT	3180
	CTTTCGGCAA	AAGTGGCTCT	CAAGATGATG	GTTGAAACCT	ACCCGGAATC	CGACTTTGCA	3240
	ATAGCTGCTT	TGAAGGAAT	GTTCAGGATA	GAGAAAATGT	CAGGCAACGA	TTACGAAGGC	3300
15	TTGAAAGATT	ATTTAGATC	CAATCCAACC	ATCATCTCTT	CCCAGAACTT	GTTCCCGACA	3360
	GCTGATTTCC	TGCTCGCGCG	ATGCGATATT	GTGTGTGAAA	ACTATCAGTC	TGCCATCGAT	3420
	TGGTACGAAA	ATCGCTTGAA	TAGTGAAATC	TCCTATCAGG	ACAGTGTTTT	TGCAGTCATT	3480
	GACCTTGGTG	ACATTTATTG	GAATATGCAG	TTAGACTCAC	TCAGAGGGAC	TGGTATAGAT	3540
20	TTGAACATAC	TTTCCTGTGA	ACAAAGGAAA	TCGCTCGAAA	GCCATCAAAA	TGTAAAAAAT	3600
	TATTTGTGT	CAACTCTTCC	CGAATCAACA	GGTACTCTCC	TGCCCTCCAT	AGAATGCAAC	3660
	AAATCAAGCC	TTGATAAATC	CAAGATAATC	TCTATTTCGC	CCAATCCGGC	GAAAGCTGTT	3720
	GTAACAATAA	TCTACTATAC	CGATAACCCT	TCCTGTTCTG	TAATAAAAT	ATATGGAATA	3780
	AATGAGCCT	CGGCTGATAT	AACCGGGTTG	CCCAAACATC	TATCCGAAGG	TTATTACAGC	3840
25	ATACAGTTCA	ATACATCCAA	CTTTGATCCC	GGTTTCTACC	TGGTAACGCT	AAATGTTGAT	3900
	CAGAAAATTA	TAGATACGGA	AAAATTACGA	ATCAAA			3936

## (2) INFORMATION FOR SEQ ID NO:75

- 30 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 2814 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular
- 35 (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- 40 (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- 45 (ix) FEATURE:  
 (A) NAME/KEY: misc feature  
 (B) LOCATION 1...2814
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:75

50	TCAGAAAATT	ATAGATACGG	AAAAATTACG	AATCAAATAA	TGGCTATCAT	GATGAAAAGT	60
	ATTGTTTTTA	GAGCATTTCT	AACGATTTTG	CTCTCGTGGG	CAGCGATCAC	GAATCCGACT	120
	GCTCAAGAGA	TCTCAGGCAT	GAATGCATCC	TGTCTGGCTG	CTCCGGCTCA	ACCGGATACT	180
	ATCTTATATG	AAAGTTTTGA	GAATGGACCT	GTTCCCAATG	GCTGGCTTGA	GATAGATGCT	240
55	GATGCTGATG	GTGCCACTTG	GGGAAGCCCA	TCAGGCTCTT	TCTCTGTACC	TTACGGACAC	300
	AATGGCCTTT	GCACCTACTC	CCATATACGT	TCCGGTATCT	CAACAGCGGG	CAACTATCTG	360
	ATTACACCCA	ATATAGAAGG	AGCCAAACGG	GTCAGTACT	GGGTATGCAA	TCAGTATAGT	420
	ACCAATCCGG	AACATTACGC	AGTAATGGTA	TCGACAACGG	GGACTGCCAT	TGAAGACTTT	480
	GTTTTGTTGT	TTGATGATTG	CATAACAGGG	AAACCGACTC	CTCTTGATG	GCCTAGACGA	540
60	ATCGTGGACT	TACCGGAAGG	GACCAAATAT	ATTGCATGGC	GACATTACAA	AGTCACCGAC	600
	TCACACACAG	AATTTCTTGA	ATTGGATGAT	GTCACGTGTG	ATAGGTGATG	CGAAGGGCCC	660
	GAACCTGCTA	CCGACTTCAC	AGTAATCAAT	ATTGGTCAGA	ATGTGGGACG	ATTGACTTGG	720
	AACTATCCGG	AGGATTATCA	ACCGGAAGGA	AAGGGGAATG	AAGAGTTGCA	GCTTAGCGGC	780
	TACAACATCT	ATGCGAACGG	TACACTACTG	GCACAAATAA	AAGATGTCTC	CATACTGGAG	840
65	TATGTGGACA	GCACCTACTC	TTTGGGAGAG	AATCCCTTGC	AAGTGGAGTA	CTGCGTTACA	900
	GCCGTTTACG	ATGAAAGCAT	AGAATCTTCG	ACCGTATGTG	GCACGCTGCA	TTACGCCACG	960
	GATGCCATCC	TTTATGAAAA	TTTTGAGAAT	GGACCTGTTC	CCAATGGTTG	GCTTGTGATA	1020
	GACGCTGATG	GAGATGGATT	TAGCTGGGGA	CACATTTTGA	ATGCATACGA	CGCTTTTCCC	1080
70	GGCCATAATG	GAGGCCATTG	CTCCTGTGCG	GCTTCTTATG	TTCCGGGTAT	AGGCCCGGTG	1140
	ACTCCCGACA	ACTATCTGAT	TACCCCAAG	GTTGAAGGAG	CCAAACGTGT	CAAGTACTGG	1200
	GTAAGCACGC	AGGATGCCAA	TTGGSCAGCG	GAACATTACG	CGGTGATGGC	TTCCGACAACG	1260
	GGGACTGCTG	TCGGAGATTT	CGTCATATTG	TTCGAAGAAA	CCATGACAGC	GAAGCCGACC	1320
	GGCGCATGST	ATGAAAGAAC	CATCAACTTA	CGTGAAGGGA	CTAAATACAT	CGCATGCGCG	1380
75	CATTACAAC	GTACCGATAT	ATATTCTTGG	AAGTTGGACG	ATATCACTGT	ATTCGGGACT	1440
	CCTGCATCAG	AGCCCGAACC	TGTTACCGAT	TTCGTTGTCT	CGCTTATTGA	AAACAACAAG	1500

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GGACGATTAA	AGTGGGAATTA	TCCTAACGGC	TACGAACCCG	ATAAGACTGA	TGATAAAGAC	1560
CCATTGCAGC	TTGCCGGCTA	CAATATCTAT	GCAAACGGCT	CGCTCCTTGT	TCACATACAA	1620
GACCCGACTG	TTTTGGAGTA	TATCGATGAG	ACTTATTCTT	CACGAGACGA	TCAGGTGGAA	1680
GTGGAATATT	GTGTCACTGC	CGTTTATAAC	GACAATATCG	AGTCCCAATC	GGTTTGCGAT	1740
AAGCTGATTT	ATGATTCTCA	ATCGGACATT	ATCTTATATG	AAGGCTTTGA	GGCCGGAAGT	1800
ATTCTCTGAAG	GCTGGTTGTT	GATTGATGCT	GATGGCGACA	ATGTTAATTG	GGACTATTAT	1860
CCTTGGACTA	TGTATGGACA	TGACAGTGAG	AAGTGTATTG	CATCCCCTTC	GTAATTACCG	1920
ATGATTGGCG	TTTTAACTCC	GGATAACTAT	TTGTTTACAC	CCAGACTCGA	AGGAGCCCAAG	1980
CTTGTCGAAGT	ATTGGGTAAG	TGCGCAAGAT	GCTGTTTATT	CGGCTGAGCA	TTATGCTGTG	2040
ATGGTTTCTA	CTACGGGAAC	TGCTGTTGAA	GATTTTGTC	TCTTGTTCGA	AGAGACAATG	2100
ACCGCTAAGG	CTAACGGTGC	ATGSTATGAG	CGAACTATTA	CATTGCCTGC	AGGAACAAAA	2160
TATATTGCCT	GGCGGCATTA	TGATTGCACC	GATATGTTTT	TCTTGCTCTT	GGATGACATT	2220
ACGGTTTATC	GTTCTACTGA	GACTGTTCCC	GAGCCTGTTA	CTGATTTCGT	TGTCTCGCTT	2280
ATTGAGAATA	ACAAGGGTCG	CCTGAAATGG	AATTATCCTA	ACGGCTACGA	ACCCGATAAG	2340
ACTGATGATA	AAAAACCAT	GCAGCTTACC	GGCTACAACA	TCTATGCAAA	TGGCTCGCTC	2400
CTTGTTCCAG	TACAAGACCC	GACTGTTTTG	GAGTATATCG	ATGAGACTTA	TTCTTCACGA	2460
GACGGTCAGG	TGGAATGGA	ATATTGTGTC	ACTGCCGTTT	ATAACGACAA	TATCGAGTCC	2520
CAATCGSTTT	GCGATAAGCT	GAACATATACT	ATCACATCCT	TGGATAATAT	TCAATCTGAT	2580
ACAAGCTTGA	AAATATATCC	TAATCCGGCA	TGCTATGTGG	TAAGGATAGA	GGGATTGAGT	2640
CGGAGCAAGT	CGACAATCGA	GTTGTATAAT	GCGCTGGGAA	TTTGCATATT	AAGGGAAGAG	2700
ACTCATTCAG	AGAAAACGGA	AATCGATGTT	TCACGTCTCA	ATGACGGAGT	CTACTTGATT	2760
AAAGTAGTCG	GTGGAATATA	AACAACAACC	GAAAAGGTAG	AGATAAAGAG	GCCG	2814

25 (2) INFORMATION FOR SEQ ID NO:76

- 30 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1818 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular
- 35 (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- 40 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...1818
- 45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:76

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ATAATCTTCT	GTACGATTCA	TCACTCTGAG	TTGGAATATA	TGAACAGCAT	CATGAAATAT	60
CAATTATATA	CGGCCGTCAT	AATGGCTCTC	TCTGTATCAT	CCGTTTGCGG	TCAAACCCCA	120
CGAAATACAG	AAACCAACG	CCCGACACG	CTGCGCAGG	AGCTTACTAT	CGTTAATGAC	180
CAGACTGTGG	AGATGGAGCA	TGCGGATCCG	CTTCCGGCTG	CATACAAGGC	CATCGAACCT	240
CGATTAACAC	CTTTCGGTCC	GGAATATAAC	AAGCGTACAT	TGGGATTTGT	CCCTGAAGTT	300
TCCTCTTCAG	GCAGGAACAA	TCTTCCGAAT	ATCCTGCCGA	CGGAAGGTCA	TATGAAGCAC	360
CGGGGGTACC	TGAATATCGG	TATCGGCCAT	ACGCTAAACC	AGCGAATGGA	TGCCGGCTAT	420
CGTCTGATAG	ATGCAGAGCA	GGAGAGACTG	AATCTTTTCC	TCTCCTATCG	TGGGATGAAA	480
TGCGGCTTCA	ATACCGGTGA	CTTGCACGGC	GACAGAAAGG	ATAGACGAAT	GATGGCAGGA	540
GTGSACTACG	AGCAGCGCAG	GCCTTCTCTT	GTGCTTGCTA	CCGGCTTGTA	TTATTGGAAC	600
CATTATTTCA	ATAACTACGG	ACGGGGAGCT	ACCACCAATG	TGGGCAGCAT	CCCTCAGCTA	660
TCGACACCTG	TTACTCCTCA	GATGGACAA	GGGACCCACA	ACGTCCGTGT	ATACTTGGGT	720
GCAAAAAATG	ATGTGATCGA	TGCCAGGATC	GACTATCGTT	TCTTCCGTTC	TATTCCCTAT	780
CTGGGTACCG	ATCCGATGAA	GGCTCTCACA	GAACATACGC	CTGAACGTAA	CGTGACGATG	840
AGTAATGAGT	TGTCCGATGA	TATTAAGCTC	GGTGTGGAAG	TTGCTACGGG	AGGATTGTTT	900
TTTGCCAAAA	ACAGCGAAAT	GATTCAAACG	GGCGTTCTGT	CCGAAACCGA	CCGCAACCTG	960
TATTATGTGG	AGGGCGCGCC	CACAATCGGA	TTTGTGCGAG	ACTCGGACAA	TATGCAATGG	1020
AACATACAGG	CCGGAGTAGG	GATTTCTTCC	CATTTCCGAG	CCAAAGGGAG	GTTGTTTTTC	1080
TGGCCTAAAC	TGGATGCTTC	GCTTAGTATC	TTCCCTTCAT	GGCGTGTGTA	TGCGAAAGCC	1140
TTGGCGGGTG	TGATTCGAAA	TGGTCTCGCC	GATGTTATGC	AAGAGGAGAT	GCCCTACCTG	1200
ATGCCCAATA	CGATTGTACT	CCCTTCGCGC	AATGCTTTGA	CCGCCCAATT	AGGGGTGAAG	1260
GGGAATATAG	CCGATGTGGT	ACGTATGGAG	GTTTATGGCG	ACTTCTCCAA	GCTGACAGST	1320
GTGCCCTTCT	ATACTCCGAC	TCTACCTTCA	TATAATCCAT	CCGACTTGTA	TCAGTATAAT	1380
GTGAGTTTCT	TGCCGATATA	TGCCGACGGC	AGCCGCTGGC	GCGCAGGTGG	TAAGCTGGAA	1440
TACTCTTATC	GCGATATGCT	CCGCTTCTCG	GTAGACGCAT	CCTATGGCAA	GTGGAATTTG	1500
GATGGAGGAC	TTGTGCGCTC	CATGCAGCCC	GATCTTATAT	TGAAGGCAGA	AGTAGGTGTT	1560
CATCCCATTTG	CCCCATTGGA	TGTCAGACTC	CGGTATACAC	AGCTGAACGG	ACGSTATCGG	1620
TATTCTTTTCG	GCTCGGCTGG	CTCGGAAGCC	TTGGGTATCG	GTAATGTACA	TCTTCTTAGT	1680



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GCGGATGTTT CATAAAGCT GAAAAAGAAC TTGAGCCTTT ATCTCAAAAT CGATAATATG 1740  
CTGGCGGAAA CGACAGAGCT TATCGGTTAT TATCCTATGC AGCCGTTCCA TTGTTTCGCC 1800  
GGTTTATAGCT GGACTTTC 1818

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(2) INFORMATION FOR SEQ ID NO:77

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 1071 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:  
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:  
(A) NAME/KEY: misc feature  
(B) LOCATION 1...1071

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:77

AACTCCCATG CAACAGTCTC CGTTATATGT TCAATGATGG AAAAATGTAT CTTTGCTCAC 60  
TATCCACATA ACCTTGTGTT CATGATTCGC AAGCATTTTCG GTATCATTTC GGGATTTCCTT 120  
TCTCTTGTGT TTTCGGCAGG TGCTCAACAA GAGAAGCAGG TGTTTCATTT TCTGAACCTT 180  
CCGGCTACTG CACAGGCTTT GGCTGCCGGA GGCAAAGCTA TCACCATCGT AGACGACAAT 240  
CCCGGACTGG CTTTGTAGAA TCCGGCTCTG CTCGGATATG AATCCGGTGG CCGCGCCTTT 300  
CTTCCTATT TATATTATAT GAGTGGTTTCG CATATGGGCA ATGCCTGTTA TGCCTCGTCC 360  
GTCCGAGAGC GTGGCATGTG GGGTGTGGC ATGCGTTTCC TGAACACGG GTCTATGCAA 420  
GGATACGATC AGAATGCGAT TGCCACCGGC TCTTTTAGTG CTTCGGATAT AGCTGTACAA 480  
GGATTTTACA GCCATGAACT GAGCAACCAC TTCCGCGGTG GAGTCAGCCT AAAAGCATTG 540  
TATTCTTCTA TCGAGACGTA TAGTTCCTTT GGCTTGGTG TGGATGTCGG TATCAGTTAT 600  
TACGACGATG ACAAAGGATA TTCCGCTTCC GCTCTGTTCA AGAACGTAGG GCGCGCAACTG 660  
AAAGGCTATA ATGAAGAACG GGAACCGCTC GATTGGGATT TCCAGCTCGG CTTTTCCTCG 720  
AGTTTTATCA ATGCTCCGTT TCGCTTGCAC ATCAGCTTGT TCAATCTGAA TCCGCACTAT 780  
TTCAAGCGTC TTGTACCACG CGATCTGTCC AAGATGCAAA AGTTCCTCCG ACACCTCTCG 840  
ATAGGAGCAG AATTTACTCC TTCCGAGAGG TTTTGGGTCC GGCTGGGATA TACGCCACAG 900  
ATTGCACAGG ATTTGAGGT GGAAGGCGGC AACAAATGGG GAGGTCTTTC GGCCGGCGTC 960  
GGTTTCACTT CAGGTGTAGT ACGTGTAGGC GTATCTGCTG CCACCTATCA TCCTGCAGCT 1020  
CTTTCGTTCA TGTGTTCCGT AGGTATCCGT TTGGACGATA AGAGCATCTT C 1071

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(2) INFORMATION FOR SEQ ID NO:78

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 1011 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:  
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:  
(A) NAME/KEY: misc feature  
(B) LOCATION 1...1011

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:78

CCTCAGCCCG TCGGCCTTAA AGAAATAACC ATTAAACCCA TGTGCCTCGA ACCCATAATT 60  
GCTCCGATTT CATCCGAGTT GCTCGAGCAG GAGCTGACTG CCGATCGTTT TCTGCGGATG 120  
ACAAACAAAG CCGGCAATGA GATCTATGTT TTTACGGCCG AAGAAGCTCC GCATTGCATG 180  
AAAGAAGTAG GCCGACTGCG AGAAGAAGCC TTTCGGCATT ATGGCGGAGG TACTGGCAAG 240

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5 GCGATCGATA TAGACGAGTT CGACACCATG CCCGGGAGCT ACAAACAGCT GATCGTATGG 300  
GATCCGCAAA ACAAGGCTAT ACTCGGAGGC TACCGCTTTA TCTATGGGCG GGACGTTGCT 360  
TTCGATACCG ATGGCAAGCC TTTGCTGGCA ACGGCAGAGA TGTTCGCTT CAGTGATGCT 420  
TTTTTGCACG ATTATCTCCC CTACACAGTC GAATTGGGAC GTTCGTTTCTG GTCGCTCCAG 480  
15 TACCAATCGA CACGGATGGG CACAAAGGCC ATTTTGTGTC TGGACAATCT TTGGGACGGT 540  
ATCGGAGCAC TCACTGTAGT CAATCCAGAG GCACTCTATT TCTATGGCAA GGTGACCATG 600  
TACAAAGACT ATGATCGGCG AGCTCGCAAT CTGATCCTGT ATTTTCTTCG CAAGCACTTC 660  
TCCGATCCGG AAGGCTTGST CAAGCCTATT CATCCCCTAC CGATAGAGAT CAGTGCGGAG 720  
GACGAAGCCT TGTTCCTCTC ATCCGACTTT GACACCAATT ACAAGACTCT CAATATAGAA 780  
10 GTGCGCAAGC TGGGTATCAA TATCCCTCCT CTCGTGAGTG CATATATAGC TTTGTCTCCG 840  
GAGATGCGTG TTTTCGGCAC TGCAGTGAAT GAGTCTTTCG GAGAGGTGGA GGAACCGGC 900  
ATATTCATTG CTGTGGGTAA GATCCTGGAA GAGAAAAAAC AACGGCACAT AGAGAGCTTC 960  
ATCCTCAGCC GGAACGAAAA AAAAGGTCTC GACAGTAGCA ATGGCCGATC A 1011

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(2) INFORMATION FOR SEQ ID NO:79

(i) SEQUENCE CHARACTERISTICS:  
20 (A) LENGTH: 1698 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: circular  
  
25 (ii) MOLECULE TYPE: DNA (genomic)  
  
(iii) HYPOTHETICAL: NO  
  
(iv) ANTI-SENSE: NO  
  
30 (vi) ORIGINAL SOURCE:  
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS  
  
(ix) FEATURE:  
35 (A) NAME/KEY: misc feature  
(B) LOCATION 1...1698  
  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:79

40 TACGACGGAG CGAGACTGGT CTATACCCTA TTTCCGAATA GAAACGACAT TCACCCTATG 60  
AAAACCATTT TAAGATACAG CCGCCTTCCG GTCGCTCTCT TCTTTTGCTT TTTGGGAGCT 120  
GTGCACCTGT CTGTGAGGCG GCAGATGCTC AATACTCCTT TCGAGCTGTC GGATCAGATC 180  
GTCCGTGCTC CCACCGAAAG GCAATACAGG GAGATTGTG TGCAAACGAA AGAAAAAGG 240  
GGGGCCGATC TTTTCCCGTT GAGCGATAAG CTGCGCGATT CGGCCTATGT TCGTTTCGGC 300  
TCGGCCTATG GCGATATTGC GGGCGACTAT CTTCCGTACA ACGGCAATAA CTACTCCTCG 360  
45 CTCTCGCTCG AATCGGGTGG TCGCATCAGT GTCCGTAAT ATGGCACATT GCAGGGCAGT 420  
GCTTCCTACT CACGTGGCAT GCACAAACGC ATCGGCTGGA ATGCTCTGCG CAACGCCGAA 480  
GCCTACTATC CCTATTGGT GTCCGATTGG ACCGGCGGAG ACTATCATTT CGAAGACTAT 540  
CGGCTTGCCG GCTACTATTC TTTTCGCGCC GGCCGCTTGC CCCTCGGTAT AGGCTTCTCA 600  
50 TACAGGGGCG AAGTTGCTTA TCGGCTGACC GATCCGCGTA CGACCAATAC GACCGGTGCA 660  
TTGGAGCTTT CTGTGCTAC CTCTTTGACG CTGCTCGAG AGAACAGGCT ATCGCTTTTCG 720  
GCTGCGTATC TCTATCATAG ACAACACCTC ACACAGTACA ACTGGCGTCC CGGGCAGCAG 780  
GACAAATTCT TCGTCAGCTA CGGTTTCGGT CAGGTGGATG TCAGCAACAG CCCTATCTGG 840  
TTCGGTATCT CCAGAAATGAA CTACGTCAAC GGATGGAAGC TTAGCTCCCG TCTGGATACC 900  
CGTAGGGGCG ATGCCATCGG TCTCGACTAC AGCGGCTACT TCCTCGATAC CGAAGAGAGG 960  
55 TCGTCCATCA ATCTCTTTGC TTTGCTTTAC AATCGCCTGC GACTCTATGG TAGCTGGCAT 1020  
CTGTGCGACT TCGATTTTTC ATTTTCAGCC GACTATGCTC TGGCCCAAGG GATAGAGCGG 1080  
ATATACGAAG ACTACAAGCC GGATGATAAT TATCATATCT ACGACCTCCG TATCTTGGCC 1140  
ATTCCGCCGT GGTATATGCT CAATGAGTTT TCTGCCCAAG CCCAAGCCTC CTACCGTATT 1200  
CGCACGGATA GAGGTGTGTC CCTGAGAGTG AGTGCCGGTA GTGATTCTTA CGGCTATGAT 1260  
60 GAGACGATAC GCAAGCATGG ACATCATACC ATGAGCGGAA TGCTACGTCC TTTTGCCGGT 1320  
ATAGCCTATG ACCATGCCGG ATCCAAATTG GATTTGGAC TTTGCTTTC GGCTGCTTAT 1380  
CGAATGGTGC TGACGCATTG GTATAAGATT CGTACCATCC AGAAAGAGCA GCTCGACTAT 1440  
CAGCTGGCCT ATTTGCCCTA TGCCTATCGT AATAGAGAAG GCGTGGAGGT GCGTTCTCT 1500  
CTGTACGTCT CGATTCCGAT GCAGAATACC CACCGCCTGA TGACAGAGCT GCGGTTGTAT 1560  
65 GGCGACCTGA TGAAAAGAAA GGACGGTATA GCCTATGGCA AAACGCCCGG TGTATCTCA 1620  
CATATCTGT CCGATCCGCA AGCCGAACGA ACGTCCGSCC ATACCATCGG GGCTATCTGC 1680  
AATATCTCCT ACCTCTTC 1698

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(2) INFORMATION FOR SEQ ID NO:80

(i) SEQUENCE CHARACTERISTICS:  
75 (A) LENGTH: 2457 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double

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(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

5 (iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

10 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc feature

15 (B) LOCATION 1...2457

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:80

AGGACGAACG	TTTTCTTATC	TTTGTCCCAT	AAAATTGGGA	GAAGGGGTGC	TTCTGTAGC	60
AATCGGAATG	CGTGGATGGC	TGAGAACAAA	CCCTCATCAC	CTGAACCGGA	TAATACCGGC	120
GTAGGAAACT	CTCCGTCTGA	CTATCTTCAC	GGCGAAGCAA	TCATTCCCCC	TCTCTCTTCT	180
TTGTCCAAC	TCAATGATAA	GAGATTTATG	AAAAAACTTC	ACATGATTGC	CGCCTTAGCC	240
GTCCGTGCCT	TCTGCCTGAC	GGCACAAAGCA	CCCGTCTCCA	ACAGCGAGAT	AGATAGTCTT	300
AGCAATGTGC	AGCTCCAGAC	CGTACAGGTC	GTAGCTACTC	GCGCCACGGC	GAAAACCCCT	360
GTGCTTACA	CCAACGTTCC	CAAGGCGGAA	CTTTCCAAGT	CCAATTATGG	TCGTGACATC	420
CCCTATCTGC	TGATGCTGAC	TCCCTCCGTG	GATGCCACCA	GCGATGCCGG	TACGGGTATC	480
GGATATTCGG	GCTTTCGGGT	GCGTGGCACC	GATGCCAATC	GCATCAACAT	AACTACCAAT	540
GGAGTACCCC	TCAACGACTC	CGAATCTCAG	TCCGTCTTTT	GGGTGAATAT	GCCCGACTTC	600
GCCTCTTCCA	TCGAAGACCT	TCAGGTGCAG	CGAGGTGTGG	GTACTTCCAC	CAATGCTGCC	660
GGAGCTTTTG	GGGCAAGTGT	CAATATGCGT	ACGGATAATT	TGGGACTGGC	TCCTTATGGC	720
CGTGTGATTT	TGAGCGGAGG	TTCGTTGGGC	ACATTCCGCC	GATCGGTCAA	ACTCGGTAGC	780
GGACGCATCG	GTCCGCCATT	GGCAGTGGAT	GCCC GCCTGT	CCAAAATCGG	TTCGGACGGC	840
TACGTGGATA	GAGGAAGCGT	GGATCTGAAA	TCCTATTTTC	CACAGGTGGG	CTATTTCTGG	900
AGCAACACGG	CTCTCAGGTT	CATCACTTTC	GGAGGAAAAG	AAGTTACGGG	TATCGCATGG	960
AACGGTCTTT	CCAAGGAGGA	TGAAGCCAAA	TATGGCCGCC	GATACAACAG	TGCCGCTCTT	1020
ATGTACGTGG	ACGCGCAAGG	AGTACCGCAC	TACTACCACA	ATACCGACAA	TTACGAGCAG	1080
CGTCACTACC	ATGCCATCAT	GACGCACAGC	TTCTCTCCTT	CCGTTATCCT	CAACCTCACG	1140
GCACACTACA	CGGCCGGATA	TGGCTATACG	GACGAATATC	GTACCGGACG	TAAACTAAAG	1200
GAATATGCAC	TGCAGCCCTA	TGTGGAAAAC	AGTGTGACCG	TGAAGAAAAC	GGATCTCATC	1260
CGTCAGAAAT	ATCTGGACAA	TGACTTCGGA	GGACTCATCG	GTTTCGCTTA	CTGGCACACC	1320
GGTGCATGGG	ATTTGCAGTT	CGGGGCCTCG	GGCAATATCT	ATAAAGGAGA	CCACTTCGGC	1380
CGTATCACTT	ACATCAAAAA	GTACAATCAG	CCCTTAGCTC	CCGACTTCGA	ATATTATCGG	1440
AACAGGGCAG	ACAAAAGAGA	AGGTGCAGCC	TTTGCCAAAG	CCAACCTGGC	GATCACTCCG	1500
GAACTGAACA	TGTATGCCGA	CCTCCAGTAT	CGTACCATCG	GCTACACGAT	AAACGGCATC	1560
ACGGACGAAT	ATGATGAGGT	ACAGGGAAGT	ATGCAGCACA	TCGATTTGGA	CAAGACCTTC	1620
CGCTTCTCTA	ATCCGAAGGC	CGGTCTTACC	TATAGTTTCG	ACGATGCTCA	TACTGCCTAT	1680
GCTTCTGTTG	CGGTAGCACA	CCGCGAGCCT	AACAGAACCA	ATTACACCGA	AGCCGGAATA	1740
GGACAGTATC	CTACGCCTGA	GCGACTGATC	GACTATGAGC	TGGGCTACCG	CTATGCTTCG	1800
CCCTCTTCTT	CGGCCGGAGT	AGGTCTCTAT	TATATGCAAT	ACAAGGACCA	ACTCGTGCTG	1860
GATGGCCGTT	TGAGCGATGT	GGGACAGATG	CTCACAAGCA	ACGTCCCCGA	CAGCTACCGT	1920
ATGGGACTGG	AGCTGACTCT	CGGTTGGCAG	ATCCTTCCTC	GTTTGCTGCG	TTGGGATGCT	1980
TCTTTCACTA	TGAGTGCCAA	CAAAATCGAC	CGCTACGTAC	AATATACATC	CGTATATGAT	2040
GCGGACTACA	ACTGGCTCGA	ACTCAAGGAG	GAGACCCTCG	AAAGCACGGA	TATAGCCTAC	2100
TCGCCCAATG	TCATTGCCGG	CAGCATGCTT	ACCCTCTCTC	ATGCCGGTTT	CGAAATGGCT	2160
TGGACGAGCC	GCTTCGTGAG	CAAGCAATAT	CTGGACAATA	CACAGCGCAG	CGATCGCATG	2220
CTTTCCTCCT	ATTGGGTGAA	CGACCTCCGC	CTCGGCTATG	TGCTGCCGGT	TCACTTCGTT	2280
AAGAGAGTGG	CACTGGGCGT	ACAGCTCAAT	AATCTCTTCA	ACCTCATGTA	TGCGTCCAAT	2340
GCCTACATCT	ACGATGCCGG	TTACGTACAG	GCATCCGAG	AACTAAGTGC	ATATGCCGAT	2400
CTCGGTTATT	ATCTCAGGC	CGGATTTAAT	GCATGGGTA	GTCTGACAA	CGATTTTC	2457

(2) INFORMATION FOR SEQ ID NO:81

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1596 base pairs

65 (B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

70 (iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

75 (vi) ORIGINAL SOURCE:

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(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc\_feature  
(B) LOCATION 1...1596

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:81

10 TACAGGCGAT CGGGAAGGGT TTGTCTCGT ATCCTCCGGA ACAAACGTTT CTACGCAGAT 60  
ACTCGGTTAC AGCCGAGAAG AGCGGTTCTGA CTACGAGCCG GCACCAGAAC AAAGATGAAA 120  
AGAAGGTTTC TATCGCTGTT ACTGCTGTAC ATACTCTCTT CCATCAGCCT TTCTGCTCAG 180  
CGGTTTCCGA TGGTGCAGGG AATCGAGTTG GATACCGATT CGCTTTTCTC TCTGCCCAAG 240  
CGTCCTTGGC GCGCCATCGG TAAAACGATA GGCGTCAATC TGGCCGTATG GGGCTTCGAT 300  
15 CATTTTCATCA TGAACGAGGA CTTTGCAGAC ATCAGTTGGC AGACTATCAA GAGCAATTTT 360  
CAAAACAGGT TTGGCTGGGA CAATGACAAG TTTGTACCA ACCTCTTCGC ACATCCTTAT 420  
CACGGATCGC TCTATTTCAA TGCAGCGAGG TCGAACGGTT TGAGCTTCAG GCACTCTGCT 480  
CCGTTTGCCT TCTTTGGCAG TCTCATGTGG GAGCTGCTTA TGGAAAACGA GCCACCGAGT 540  
ATCAACGACC TCTGTGCCAC CACCATAGGC GGTATAGCTT TGGGGGAGAT GGGGCACAGG 600  
CTGTCCGACC TGTCTATCGA CAATCGTACC ACAGGGTGGG AACGTATGGG GCGCGAGGTG 660  
20 GCTATCGCTC TGATCAATCC GATGCGCTTT CTCAACCGTC TGACAGCAGG AGAGGTGACT 720  
TCTGTCCGGA GTCCGACGGG ACAGATATTT CAGTCTGTCC CCATAAACAT AGTCGTCCGAT 780  
GCCGCTTTC GCTTTTGGC AGACAAGCGG CATGCCCGAA CCGGTGCCAC GGCTCTGACC 840  
CTGAATCTGA GATTCCGACTA CGGCGATCCA TTCCGAAGCG AGACTTTCTC TCCATACGAT 900  
TTCTTCCAAT TCAAAGCCGG ATTGAGTTTC TCCGAATCGC AACCTCTGCT GAGCCAGATC 960  
25 AATCTGATCG GAATCCTAAG CGGATGCCAA CTGCTCGCAC ACGAACGAAC GGTTTTGGTG 1020  
GGAGTCTCT TTCAGCACTT CGACTACTAC AATTCCGAAA AACGAATAAG CAAAAATTCTG 1080  
GAGGAGGTAC TCGTCACCCC ATACCGTATC TCGCAAGTGG CAGCTCTGGG AGGCGGTCTT 1140  
ATCTTCCAGC ACCACGGAAA ATTTGACGA CGTCTCTGG AGCTATATGC CGAGACCTAC 1200  
30 CTGAATGTGC TCCCGATGGG AGCCAGTCTG TCGGATCACT ACAACGTGGA CAATCGGGAC 1260  
TATAACCTCG GCAGCGGATT GAGCGGCAAG CTATACCTTG GTGCTACGTA CAATGATCTG 1320  
TGGAGCTGGC TCTTGGGAGT CGAAAGCTAT CGGCTCTACA CATGGATCGG GTATGAAGAG 1380  
CCGCACCAGA AAAATACCGA TGTCAGCTCT TTTATGGTGC AGGGGGACGA AAGCAAGGCG 1440  
CGCCTACTGG TGACGAGTTC CGAGTTCGCA TTTTCATCTG GCCCCTGGCA TGTAGCCATC 1500  
35 GTCGCTCGCC GTTTCATCCG CAAAACAGCC TATCAATTCT ACCCTAACGT ATCATTTCGAT 1560  
ACCGGCGACA TACAGTCTCG TGTCGGATTT CACTTC 1596

(2) INFORMATION FOR SEQ ID NO:82

40 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 900 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: circular  
45 (ii) MOLECULE TYPE: DNA (genomic)  
(iii) HYPOTHETICAL: NO  
50 (iv) ANTI-SENSE: NO  
(vi) ORIGINAL SOURCE:  
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS  
55 (ix) FEATURE:  
(A) NAME/KEY: misc\_feature  
(B) LOCATION 1...900

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:82

60 AAAAGAAGAA AAAACAGAT GAAACGACTG ATTGTTTTTC TGGCAATGGG TGGCTTGCTG 60  
TTCACCCCTT CGAACGCACA AGAAGCAAAC ACTGCATCTG ACACCTCCAA AAAGGACTGG 120  
ACTATAAAG GTGTGACCGG ACTAAATGCC TCTCAGACTT CTCTGACCAA CTGGGCTGCC 180  
65 GGTGGAGAAA ACACGGTGGC AGGTAACCTC TATTGAAACA TAGATGCCAA CTACCTGAAA 240  
GATAAATGGA GTTGGGACAA CGGTTTGGCT ACAGACTTCG GTCTGACCTA CACAACAGCC 300  
AACAAGTGGG ACAAAGTGT AGACAAGATC GAACTCTTCA CGAAGGCCGG CTATGAGATC 360  
GGCAAACATT GGTACGGAAG TGCCTTTTCT ACTTTCCTCT CACAGTATGC CAAAGGATAT 420  
GAGAAGCCCT CGGATCACTT GACAGGAGTC AAGCATATCT CTAATTTCTT CGCTCCTGCA 480  
70 TATCTCACTC TCGGTATTGG TCGGACTAT AAGCCCAATG AGAAGTTCTC TCTCTACCTC 540  
TCTCTACAA CGGGCAAGCT GACTGTAGTA GCAGACGACT ACCTCTCAAG TTTGGGAGCC 600  
TTCCGGGTGA AAGTTGGTGA AAAGACAATG TTCGAACTTG GTGCTTTGGT AGTGGGTTCC 660  
GCCAATATAA ATCTGATGGA GAATGTCAAT TTGATAACCA AGGCTTCATT CTTCTCGGCT 720  
TATACGCAGC ACTTTGGCAA CATGACATC AATTGGGAGG CTATGCTGGC CATGAAGATC 780  
AACAAAGTTC TCACGGCTAC GATAGCCACC AATCTTATCT ACGACGATGA TGTGAAGATC 840  
75 AACGATGGCC CGAAAATCCA GTTCAAAGAA GTTGTGGGCG TGGGTGTTGC GTACACTTTC 900

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## (2) INFORMATION FOR SEQ ID NO:83

- 5 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 663 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: circular
- 10 (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- 15 (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:  
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- 20 (ix) FEATURE:  
(A) NAME/KEY: misc\_feature  
(B) LOCATION 1...663

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:83

25 ACGAGAGAGA GTGTGTTACA TTGTAGAACA AAACCTCAAAA AAGAACGAAA AATGAAGAAA 60  
ATGATTTTGG CAGCTACTAT GCTGCTCGCA ACAATCGGTT TTGCAAATGC TCAGAGTCGT 120  
CCTGCTCTTA GACTGGATGC TAACTTTGTC GGTAGTAACT TAATGCAAAA AGTCGCAAAC 180  
30 ACGAGCGTGA ACAATAAGAT GATCGTAGGC TTACGTGTTG GTGCTGCTGC TGAGTTCGCT 240  
CTTAGCAATG ATGGATTCTA TCTCGCCCCC GGATTGGCCT ATACGATGAG AGGTGCTAAG 300  
ATGGAATCAC TAAAGTGAAAC GACAACTCGC TTGCATTATC TGCAAATACC GGTGAATGCC 360  
GGTATGAGAT TTAGCTTTGC TGACAACATG GCTATTTTCAT TGGGAAGCAGG TCCCTATTTC 420  
GCATATGGTG TCGCCGGAAC GATTAAAGACT AAAGTTGCAG GCGTTACGGC TTCTGTAGAT 480  
GCCTTTGGTG ATAACGGATA TAACCGTTTC GACTTGGGCT TGGGCTTGTC TGCTGCCTTG 540  
35 AGCTACGACC GTTATTACGT ACAAATTGGA TATGAGCATG GATTGCTTAA TATGTTGAAG 600  
GATGCTCCGG ATAAGACTTC TTTGCGTAAT CATGACTTCT TTGTGGGTCT CGGTGTTGCG 660  
TTC 663

## (2) INFORMATION FOR SEQ ID NO:84

- 40 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 744 base pairs  
(B) TYPE: nucleic acid  
45 (C) STRANDEDNESS: double  
(D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- 50 (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:  
55 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:  
(A) NAME/KEY: misc\_feature  
60 (B) LOCATION 1...744

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:84

65 ATCAAACGAA TAGAAATGAA AAGGATTTTT ACTGTAGCCC TTGTGCTACT TGCTTCGGTC 60  
ACTATGGCCA TCGGACAAAG CCGCCCGGCA CTTCGCGTAG ATGCCAACTT CGTAGGCAGC 120  
AATCAGAGCA TGAAAGAGAGA CCGATATGTG TGGGACACCA AAATGAATGT CGGCCTGCGG 180  
GTCCGTGCCG CTGCCGAATT CATGATCGGA TCAAGAGGAT TCTACTTGGC TCCGGGTCTG 240  
AACTATACGA TGAAGGGCTC CAAAACCGAA TGGGATATAC CCGAAATGGT TCCTGGTACC 300  
TATATTACGA TGGTTTCCAC TCGTTTGCAC TATCTGCAAC TGCCGATCAA TGCCGGCATG 360  
70 CGGTTGCGACC TGATGAATGA CATGGCGGTT TCGATCGAAG CGGGTCCTTT CCTTGCTATC 420  
GGTATATATG GTACATATCG GCAGAAGTTG GAAGGATGGA AGCCGAACAA CTACAGCACA 480  
GAGTTTTTTG GCCCAACGCT TGGTGGCCCA ACAAATATCC GCTGGGACAT CGGGGCAAAAC 540  
ATAATAGCCG CATTCACCTA TAAGCGTTAT TATATACAGA TAGGCTATGA ACATGGATTT 600  
GTGGATATTG TGTCAGGTGG AGGTTCTGAT ATTCCCGGAC TGAACGACAA TAGGCAATCC 660  
75 TCTTCGACGA CCGCTCTAAG AGAAAAGGGA AATAACGAAT ACGCTTATAA TCGTGACTTC 720  
TTCGTGGGCA TAGGTTACCG CTTT 744

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## (2) INFORMATION FOR SEQ ID NO:85

- 5 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 633 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular
- 10 (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- 15 (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- 20 (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...633

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:85

25 AAAAGAAAGA GTATGAAAAG AATGCTGCTG CTTCTCGTTG TATTATTATA TGGAATTGCA 60  
 GSCCGATTGG CTGCACAAGA CGTTATCAGA CCATGGTCAT TGCAGGTCGG AGCGGGATAC 120  
 TCCGATACGG AGAACATCCC GGGAGGATTG ACCTATGGTT TCTATTGGG AAAGCGTATG 180  
 30 GGGAGCTTTC TGGAAGTGGG GCTGTCCATG TACAACTCCA CACGTCAAAC AGCCAACAAT 240  
 GCAGACTCCT TTGCATCGAA CGAAGGAGAC GGATCTTTTC AGGTAAATAT GTCTTCTCCG 300  
 AATGAGAAAGT GGTCAATTCT CGATGCAGGC ASTGCCAACT GCTATATGAT CGTCGTCGGA 360  
 GTCAATCCTC TCCATCTGTT TTGGCAGAAT AGCCGGCACA ATTTGTTTCT GGCAGTACAA 420  
 GCCGGCCTGT CCAATAAGCA CAATATTCAT TTCATCTATG GAGACAAGGG AGCCAAAGTC 480  
 AGTATCTACA CCAATTCGAA TACCTACATC GGTACGGAG CACGTGTAGC CTACGAATAT 540  
 35 CAAATTCATA AAAACGTGGG GCGGGGTGCC GCTGTAATGT ACGACCACGG CAATAAGATG 600  
 CTTACGGCCA TGGCCACGCT CTCCACTCAT TTT 633

## (2) INFORMATION FOR SEQ ID NO:86

- 40 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 2859 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular
- 45 (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- 50 (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- 55 (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...2859

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:86

60 ATCCGAATGA GAGTATCCGA TCTCTGTTCC AGACTTTTCAT GGTATTATACC CGTAATCCTT 60  
 GTCGGATTGC TCTGTGCTAC TTTGGTCGCT GCGGAACGTC CTATGGCCGG AGCAGTCGGA 120  
 65 TTGCACCACC GTCGGCATGC TGCCTGTCTT GATTCTACAG CGAAAGACAC GGTGCCTCTC 180  
 GCAAAACCTA TTCCTGACAG TGCTTTTTCGA GATTCCCTTC CTGCGGATTC CACGGGATCG 240  
 ATGCGGCAAG ATAGCGTGTA TGACGATGAA TTCGAATTGG AAGATATAGT GGAGTACGAA 300  
 GCTGCCGATT CCATCGTTTT GCTCGGACAG AATCGTGCCT ATCTTTTCGG CAAGAGCTAT 360  
 GTGAGCTATC AAAAGAGTCG CTTGGAGGCA AACTTCATGT ATCTCAATAC CGACAGCAGT 420  
 70 ACGGTTTATA CTCGCTATGT CCTCGATACG GCGGTTTATC CGATGGCCTT TCCTGTTTTT 480  
 AAGGATGGAG AGCAGTCGTT CGAAGCCCAAG AACTTTACCT ACAACTTCCG CACGGAGAAG 540  
 GGGATTATCA GCGGAGTGAT CACGCAGCAG GCGGAAGGCT ATCTGACTGC CGGTAAGACC 600  
 AAGAAGATGC CCGACAATAT CATGTTTATG CAAGGAGGGC GTTATACGAC CTGCGACAA 660  
 CACGATCATC CTCATTCTA TATCAATCTT TCCAAGGCAA AGGTGCATCC GGAGAAAGAC 720  
 75 ATCGTCACAG GTCCGTCGTA TCTGGTTATC GCGGATATGC CGCTGCCGAT AGGTCTTCCT 780  
 TTCCGGCTATT TTCCCTTTTC CAACAAATAC TCTCCGGTA TATTGATGCC CACGTACGGA 840

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	GAGGACAATC	GCTATGGATT	TTATTGAGG	AATGGTGGAT	ATTATTTTGC	CTTCAGCGAC	900
	TATATCGATT	TGGCATTGCG	TGGGGAGATC	TTTTCCAAAG	GGTCATGGGG	CATTTACGCC	960
	CAATCGAAAT	ATAAGAAGAG	GTATAAGTAC	AACGGCTCGT	TGGAAGCCAA	TTATCTGGTA	1020
	TCGAAGTCCG	GCGACAAATA	CGTGCCCGGA	GACTACAGCA	AGACCACCAG	TCTGAATATC	1080
5	CGATGGACAC	ACAGTCAGGA	TCCGAAGGCC	AATCCTTTGC	AAACGTTGTC	GGCCAATGTC	1140
	AATTTTGCCA	CCGGGAGCTA	TTTCCAGAAT	TCGCTGAATA	CCACCTATGA	TGTCAATGCC	1200
	CGTACTGCTA	CGACACGAAG	TTCGGCCGTG	AGCTATTCCG	GCAAGTTTCC	GGGTACTCCT	1260
	TTTTTCGATTA	CGGGTAGCAT	GGATATCAGC	CAGAACATGC	GCGATACGAC	GGTGAGCCTT	1320
	ACCTTGCCGA	ATCTTTCGAT	TAATATGTCC	ACGCGTTATC	CTTTCAAGCG	GAAGACCCGT	1380
10	GTAGGACCCG	AGCGATGGTA	CGAGAAGTTG	AGTGTGGGCT	ATTCCGGTCA	GCTTCGCAAT	1440
	AGTATCTTGA	CAAAAGAGAA	AGATTTCCTC	CAGAGCAATC	TCGTGCGCGA	TTGGAAGAAT	1500
	GGTATGCGTC	ATTCCGTACC	GATCAGTTTG	ACTGTCCCTT	TGTTGGATTA	TATCAATCTG	1560
	ACTATGGGGG	TAACTACAA	TGAGTGGTGG	TACACGAAAG	GCATACGGAA	GTCGTGGAAT	1620
	GAGGATAAGA	AAACATTCCCT	GCCTTCGGAC	ACGACCTATA	AATCCGCGAG	ACTGTACGAT	1680
15	TACAGTCTGT	CGGCAGGCTT	ATCTACCACA	TTGTACGGTA	TGTTCAAGCC	TTGGAACCTT	1740
	TTTTCTTCTG	GAGGCAATCT	CATTATGATC	CGTCATCGCT	TCACGCCGAC	TGTCACTTTC	1800
	TCCTATATGC	CGGACTTCAC	GAAACGCCGA	TATGGCTTTT	GGGAGCTTCT	TGAGCATACG	1860
	GATCAGAAGC	GCAAGCTGCA	TACGCTGCTC	TACTCTCCTT	ATTTGAGCA	GATATTCGCT	1920
20	GCTCCCTCCA	TGGGCAATGC	AGGATCTGTC	AATTTCTCTT	TTGACAACAA	CTTAGAGGCC	1980
	AAGATCAAAT	CCAAATCGGA	TTCGACAGGG	ATCAAGAAGA	TCAGCCTGAT	AGATCAGTTC	2040
	ACATGGTCTA	CATCCTATAA	TATGTTTGCC	GATTCGATCC	GATGGAGCAA	TATCTCGGCT	2100
	TCGCTGGCAC	TTCCGCTCTC	CAAGAGCTTT	ACCTTGCGCT	TGTCCGGTCT	GTTCGATCCC	2160
	TATTTGACGA	AGTATTATGA	GGGAGAAGAT	GGGAAGATCA	TTCCCTATAA	GAGCAACGAC	2220
25	CTGCGCATTT	TAAACGGCAA	GGGATTGGCA	CGCCTGATCA	GTACGGGTAC	TTCTTTCAGC	2280
	TATACGCTTA	ACAAAGAGTC	GCTCAGCGGA	TTGATAGCTC	TTTTCAGTGG	CAAAAAGGAG	2340
	CGGAGAGATG	AAAAGAAAAA	CACAGGGGCT	ACTCCTCATG	AAGGAGACGA	TGCTGCCGAT	2400
	ATACTTGAGG	GAGGAAGACC	GCAAAATGAA	AGTGGGGGGT	CGCTCCTCGA	GCGCAACCGT	2460
	CAGGGCGGAG	CAGTGGATCA	GGATGGTTAC	TTCCGATATT	CGATCCCATG	GAGCCTGTCC	2520
30	TTCCGACTATA	GTTGGAATAT	TGCTACCGAC	TACAATAGGT	ACAATGTCAA	TAAATGGAG	2580
	CACTACTACC	GGGTAACGCA	GAATCTGAGC	TTTCGCGGCA	ATATCCAGCC	TACACCGAAC	2640
	TGGAGCTTCG	GATTCAATGC	GAACCTACAA	TTCCGACTTA	AGAAAAATAA	ATCGCTTACC	2700
	TGCAACGTCA	CTCGCGACAT	GCACCTGCTG	GCTATCTCGG	CCAGTTTTCAT	CCCTATAGGA	2760
	GCATACAAGT	CCTATAAATT	CGTCATATCG	GTGAAGAGTT	CACCTTTGCA	GGATCTGAAG	2820
35	TATCAGCAGA	GCAATCGTCC	CATCACGAAT	ACTTGGTAT			2859

## (2) INFORMATION FOR SEQ ID NO:87

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 3753 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
- (A) NAME/KEY: miscfeature
- (B) LOCATION 1...3753
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:87

60	AAATGGAAAT	TGGCATGCGC	TTTGTATTGC	GCGTGTGTGT	TCGATCCATT	TGTAGTAACT	60
	AACGAGGTAA	TAATAATGAT	GAAACGATAT	ACAATAATTC	TTGCAGTTT	TCTTTTATTC	120
	TGCACGGTAT	TTACCTTTCA	AATAAAAGCT	CGCCCTTATG	AAAGATTGTC	AGATGTAGAG	180
	AAGCCTTGGA	TTTCAGAAACA	TTCAATGGAT	TCTAAATTGG	TGCCTGCAAA	TAAGGGTAAC	240
	TTAATTCAAG	CTGAAATTGT	ATACCAATCT	GTTTCTGAAC	ATAGTGACTT	AGTTATTTC	300
65	CCTGTGAACG	AAATAAGGCC	TGCAAAATCGT	TTCCCTTCGC	ATAGGAAGTC	TTTTTTTGCA	360
	GAAATCTAC	GGGCATCTCC	CCCGTAGT	CCCGTTGCCG	TCGACAAGTA	TGCGGTACCG	420
	GTTCGCAATC	CAATGGATCC	TGAAATCC	AATGCCTGGG	ATGTGACGCT	AAAAATCACT	480
	ACTAAAGCGG	TAACAGTACC	TGTCGATGTG	GTGATGGTTA	TCGACCAATG	TTCTGCAATG	540
	GGAGGGCAAA	ACATTGCCAG	ATTAAGTCT	GCCATTGCAT	CGGACAGCG	TTTGTGAAA	600
70	AAAAATGTTG	CTAAGGGGAC	GGCTACAGAA	GGGTGCGTA	TCGCTCTTGT	GAGTTATGAC	660
	CATGAGCCTC	ATCGCTTATC	TGATTTTACC	AAAGACACTG	CTTTTCTCTG	TCAAAAATC	720
	CGGGCTTTGA	CTCTTATTTG	GGGAACACAT	ACCCAGGGGG	GGCTTAAAT	GGCGAGAAAC	780
	ATTATGGCCA	CTTCTACTGC	TGTGGATAAG	CATATCATAT	TGATGTCTGA	CGGTTAGCG	840
	ACGGAGCAGT	ATCTGTATAA	AAATGTAAT	ACTGCAGACT	TCATTGGCAA	AACTGGAAAT	900
75	GCGAATGATC	CCATTGATTT	GGTTATACAA	GGAGCAATTA	ATTTCCCTAC	AAATTATGTT	960

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TCCAACAATC CATCTACACC TCTTACCCCA AATTATCCAA CTCATTCTTC TAAAGTTGGA 1020  
CGGAGAAATC TGCCGGAATC CAAATTTCGAT TATAGTAATC TGAGTGCAAG GATTACTTTT 1080  
GATGGTGTGG CTGGGCGCATT GGTCTATGAA CCGAGGTTTC CTCATCCCTA TTATTATTAT 1140  
TTCCCTTGTG ACGGTGCTAT CAATGAGGCT CAGTTTGCGA AAAACTCTGG TTATACAATC 1200  
CATACTATTG GCTATGACCT GGGAGATTTT GCCTTGGCCA ACAATTCGTT GAAACTAACC 1260  
GCTACAGACG AGAATCACTT CTTTACGGCG ACACCGGCCA ATTTAGCTGC AGCGTTTGAT 1320  
AATATTGCCC AAACATTATA TATAGGTATA CAGAGGGGGG AGGTGACGGA CTTTGTAGCT 1380  
CCTGGTTTCA TCGTTAAAAA TCTGACGCAA TCGGGAGATG TTACTCATTT GCTAAATGTT 1440  
TCAAAATGSAA CCGTGCACCT TGATGTCTCT ACTAAAAAAC TGACATGGAC TACTGGTACT 1500  
ATCCTGAGCT CATCAGAAGC TACCATAACT TATCGTATTT ATGCCGATTT GGATTATATA 1560  
CAGAACAATG ATATTCCGGT AAATACTACT TCTGCTATCG GCCCGGATCT TGGTGGATTC 1620  
GATACCAATA CCGAGGCAAA ATTGACCTAT ACCAATTCCA ATGGCGAACC GAATCAGCAG 1680  
TTCAATTTTCC CACGTCGAC GGTAAAGTTA GGTATGGTG TTATTAAGCG GCACATATGA 1740  
TTGGTAAATA AAGACGGTCA ACCCATACAG GCAAATGGAA CAGTTGTGAG TTCCCTAAGC 1800  
GAGGCTCATG TTCTACAGTC ACAAGATTTC TTTTGGCCCT CAGGTGGAGG TCATATTGTT 1860  
CCCAAAATTA TCGGTAACCT CAAAACGACC CAGGACATTAC AGTACTATTG CGTACCGCCG 1920  
ACTAACACGG TCATCACTAC TGCCGATGGT AAACGTTATC GTTTTGTGCA AGTCCCAGGC 1980  
TCCACGCGCA ATCCGGGCGA AATCGGTATC AGTTGGAAAA AACCGGCAGG AAACGCTTAC 2040  
TTCCGCTTACA AGCTCCTCAA TTATTGGATG GGAGGAACAA CAGACCAACA GAGTGAATGG 2100  
GATGTGAGCT CCATTTGGAC AGGAGCCCAA GTACCGCTCA CAGGAGAAGA TGTAAGATT 2160  
GCAACGACAG AAAATTTCCG TTCTCCGGCG GTAGCCGATT TGCGATGTCC GACAACCAAC 2220  
CCCAAAATTA TCGGTAACCT TATCAATAAT TCCGACAAGG ATTTAGTTGT TACCACAAGC 2280  
AGTCAATTGA CGATCAACGG CGTGGTTGAG GATAACAATC CGAATGTGCG TACGATCGTC 2340  
GTGAAGTGGT CGAAAGACAA TCCTACGGGG ACATTGCTTT TTGCCAATCC GGGCTATAAT 2400  
CAAAATGTAG GGGGGACCGT CGAGTTTTC CAGCAGGGAT ATGATTGTGC CGATTGTGGT 2460  
ATGTATCGCA GGAGCTGGCA GTATTTCCGGT ATCCCTGTCA ATGAATCAGG TTTTCCAATT 2520  
AATGATGTGG GCGGAAACGA GACCGTCAAC CAATGGGTTG AGCCTTTCAA TGCGGATAAG 2580  
TGGCGGCCAG CACCTTATGC ACCTGATACA GAGCTTCAAA AATTCAAGGG CTACCAGATC 2640  
ACGAATGACG TGCAGGCACA GCCTACGGGA GTTTACAGCT TCAAGGGTAT GATTTGTGTG 2700  
TGCGATGGCT TCCTGAATCT GACACGCGAG TCCGGTGTC ACTACTCGGG CGCCAACCTG 2760  
ATCGGCAACT CATACACTGG AGCCATCGAC ATCAAGCAGG GTATTGTCTT CCCGCCGGA 2820  
GTGAGCAGCA CCGTGTATCT GTTCAACACG GGAACACGCG ACCAGTGGCG TAAGCTTAAT 2880  
GGAAGCAGCG TTTCAGGCTA TCGAGCCGGT CAGTACCTCT CTGTACCTAA GAATACAGCG 2940  
GGTCAGGACA ATCTTCCGGA TCGTATTCCA TCGATGCATT CCTTCTTGGT GAAGATGCAG 3000  
AACGGAGCGT CTGTACGTT GCANATCTTG TACGATAAGC TGCTCAAGAA CACGACTGTA 3060  
AACAACGGTA ATGGTACGCA GATCAGATGG CGATCCGGCA ACTCCGGATC GGCGAATATG 3120  
CCGTCACTTG TGATGGATGT TCTTGGTAAC GAGTCGGCGC ACCGTTTGTG GATCTTTACC 3180  
GATGGGGGTC TTTCTTTCCG ATTCGACAAC GGCTGGGATG GTCGCAAGCT GACTGAAAAA 3240  
GGTTTGTGAC AACTTTATGC GATGTCTGAC ATCGGTAAATG ATAAATTCCA GGTGTCAGGG 3300  
GTTCCGGAGT TGAATAACCT GCTGATCGGC TTCGATGCGG ATAAGGATGG TCAATACAG 3360  
TTGGAGTTTG CTCTTTCCGA TCATTTTGGC AAAGGGGCTG TTTACCTGCA CGATCTTCAG 3420  
TCAGGAGCCA AACACCGTAT TACGAATTCT ACGTCGTATT CATTCGATGC CAAGCGGGGA 3480  
GATTCCGGGG CTCGTTTCCG CTGTCTATAT GGATGTGATG AGAACGTAGA TGATTCCGAT 3540  
GTCGTGAGTA CAAATGGCCG TGAAATTATA ATTCTGAATC AAGATGCTCT TGACTGCACT 3600  
GTAACCTTAT TCACAATAGA AGGTAAGCTT CTTCGCCGCT TGAAAGTATT AGCTGGTCAT 3660  
AGAGAAGTCA TGAAAGTGCA GACCGGAGGG GCCTATATTG TGCATCTTCA AAATGCTTTC 3720  
ACTAATGATG TGCATAAGGT GCTTGTGAG TAT 3753

- 50 (2) INFORMATION FOR SEQ ID NO:88
- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 1278 base pairs  
(B) TYPE: nucleic acid  
55 (C) STRANDEDNESS: double  
(D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- 60 (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:  
65 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:  
(A) NAME/KEY: misc feature  
(B) LOCATION 1...1278  
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- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:88

75 ACTATGGAAG TGAAGAAAAA CACAGTGGTG CTACGCCTTC TGATTGTTGTT CGTGGCCATT 60  
CTTCTCTTCC ACTCCTCACG GCTGTGGGGA CAGGAAGGGG AGGGGAGTGC CCGATACAGA 120  
TTCAAAGGAT TCGTGGATAC CTACCATGCC GTACGCAGCT CTTCTCCTTT TGATTTCATG 180



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AGCTCGCGTA CGAGAGTGAG AGGTGAGCTG GAGAGGTCGT TCGGTAATTC GAAAGTAGCC 240  
 GTATCGGTCA ATGCCACCTA CAATGCTCTA CTGAAAGACG AGACCGGCTT ACCTTTACGT 300  
 GAAGCCTTCT TCGAGCATCA GGAAGAGCAT TGGGGGTTGC GCCTCGGACG ACAGATTGTC 360  
 5 ATTTGGGGGG CTGCCGACGG TGTGCGCATC ACGGATCTGA TCTCCCCGAT GGATATGACC 420  
 GAGTTTCTGG CACAGGATTA CGATGATATT CGTATGCCGG TCAATGCATT GCGTTTCTCT 480  
 GTCTTCAACG AATCGATGAA AGTGGAAAGTC GTGGTACTGC CTGTATTGCA GGGGTACCGT 540  
 CTGCCTGTGG ATCCTCGCAA TCCTTGGAAT ATCTTCTCCC TTTCGCCCCAT TGCTCAGGGG 600  
 ATGAATATCG TCTGGAAAGA AGAAGCCGGC AAACCGGCTT TCAAGGTTGC CAATATCGAG 660  
 TACGGTGGCG GATGGAGCAC TACGCTCTCC GGTATCGACT TCGCTTTGGC TGCATTGCAT 720  
 10 ACATGGAACA AGATGCCCGT CATCGAAGTA CAGGGCATTG TGCCGACGGA AATCATCGTT 780  
 AGCCCTCGCT ATTATCGTAT GGGATTTGTC GCGGCGGACC TCTCCGTACC CGTCGGACAG 840  
 TTTGTTTTCA GGGGAGAGGC TGCCTTCAAT ATCGACAAAC ACTTCACCTA TAAGAGTCAT 900  
 GCCGAGCAAG AGGGTTTCCA AACAATCAAT TGGTTGGCCG GAGCCGATTG GTATGCTCCC 960  
 GGTGAATGGA TGATCTCAGG ACAATTCTCA ATGGAAGCA TATTCAAGTA TAGGGATTTC 1020  
 15 ATCTCCCAA GACACATTC TACCCTGATT ACTCTCAATG TTTCACAGAA ATTCTTCGGC 1080  
 ASTACACTCC AACTTTTCGA CTTCACCTAC TACGACCTTA CCGGCAAGG ATGTTTCAGT 1140  
 CGCTTTGCAG CTGACTATGC CTGGAACGAT CAGATACATC TGATGGCCGG ATATGACTGG 1200  
 TTCAGTAGTA AGGGCAGCGG TATATTCGAT CGCTACAAAG ACAATTCCGA ACTCTGGTTC 1260  
 20 AAAGCCCGCT ACAGCTTC 1278

(2) INFORMATION FOR SEQ ID NO:89

- 25 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1392 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular  
 30 (ii) MOLECULE TYPE: DNA (genomic)  
 (iii) HYPOTHETICAL: NO  
 (iv) ANTI-SENSE: NO  
 35 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS  
 (ix) FEATURE:  
 40 (A) NAME/KEY: misc feature  
 (B) LOCATION 1...1392

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:89

45 TACGGCAAAA GAAGAAAGCT CGGAACCTCC GTCCGACCTT CCGTTCTAAC CCAAATCAGA 60  
 TTTATTTTGG ACTTACACCT TATTACTGAT TTTTGTGAAG GGCTTCGGGT CAATCCTATC 120  
 GGTGCAGCAG CCATAGTGGC TTTCATTATC GACCTGCTTC TTCTTTGCTG TTCGGCTTTT 180  
 ATGTCTCTCT GTGAGGTGGC TTATTTTTC ACAAAGCCGA TCGATCTGCA GAACATCCGC 240  
 50 GAACGGAATC ACTCTTCCGA CATCGCGCTT TCCAATTTAT TAGACAATTC GAATCAGCTA 300  
 TTAGCTACTA TTCTGATCGG GAATAATGTG ATTAATGTAG CCATCGTTAT CCTTTCCAAT 360  
 TATGCCATCG AGCAGACATT CGTTTCTCT TCTCCGATCA TTGGATTCT GATCCAGACG 420  
 ATACTCTGA CCACGTGTTCT TTTGCTGTTT GGAGAGATTG TGCCGAAAGT GTATGCGCGG 480  
 AAGAATCCGC TGCAATACTC GCGCTTTTCT GCTGCAGCTA TGTCCGTTAT CTATAAGATA 540  
 TTGTCAACCG TTTCAAAATT GCTGGTCAAA AGTACCGGCA TCGTTACCAG AGGTATCAGC 600  
 55 AAGAAGAAAT ACGATATGTC CGTGGATGAG CTCTCGAAAG CGGTAGCCCT CACCACTACG 660  
 GAGGGAGAGC CGGAGGAGAA AGAAATGATT AACGAAATCA TCAAATTCTA TAATAAGACA 720  
 GCCTGCGAAA TCATGGTTCC GCGTATCGAT ATTGTGGATG TGGATCTGAG CTGGCCATTT 780  
 CGTAAGATGC TTGACTTCGT TGTTCGTCG GGTATTCCA GACTTCCCGT TTCAGAGGGG 840  
 TCAGAAGACA ATATCAAAGG GGTATTTCAT ATCAAAGATC TAATCCACA CATGGATAAA 900  
 60 GCGCATGAAT TCGACTGGCA TCCTCTGATT CGTAAAGCAT ATTTTGTCCC CGAAAACAAG 960  
 CGCATAGATG ATTTGCTCGA GGAGTTCAGA GCCAATAAGG TGCATGTCTC CATCGTTGTG 1020  
 GATGAGTTTC GTGGCACTTG CGGACTGATC ACAATGAGG ACATATTGGA AGAGATCGTC 1080  
 GGCGAGATTA CGGACGAGTA CGATGAGGAA GAACTCCCTT TTAAGGTTTT GGGGGATGGC 1140  
 65 AGTTATCTTT TCGAAGGAAA AACGTCTCTC TCCGATGTTT GACACTATCT TGACCTTCCG 1200  
 GAAAATGCTT TCGGTGAATT GGGGGACGAG GTAGATACGC TAAGTGGGCT CTTCTTGGAA 1260  
 ATCAAGCAGG AACTCCCCCA TGTGGCGCAT ACAGCASTGT ACGAGCCATT CCGCTTTCAA 1320  
 GTGACCCAAA TGGACAAGCG CCGAATCATC GAAATCAAGA TTTTCCCTTT CGAGCGCACT 1380  
 TGGGAGGTGC AA 1392

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(2) INFORMATION FOR SEQ ID NO:90

- 75 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 798 base pairs  
 (B) TYPE: nucleic acid

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(C) STRANDEDNESS: double  
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:  
(A) ORGANISM: PORIPHYROMONAS GINGIVALIS

(ix) FEATURE:  
(A) NAME/KEY: misc\_feature  
(B) LOCATION 1...798

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:90

ATAATTTATA	GATCAACAAT	GAAACTATTA	CTTTATCTCC	TATTGGTCTT	GTCGACTCTA	60
TCCCCGATGT	ATTGCGCAAAT	GCTGTTCTCA	GAGAATCTCA	CAATGAATAT	AGACAGCACC	120
AAAACCATAC	AAGGAACGAT	ATTGCCCCGA	CTGGATTTC	AAACCGAAAA	GGAAAAATGTG	180
TTACCTTCA	AAAATACTGC	CAATCTCAAT	CTGCTGATAA	AGCACGGTCA	AGTAATCAAC	240
TTAATTAATA	AGCTTGAGTT	TTCTACCTAT	GGCAATAAAG	TAACCGTAAG	TGGAGGATAT	300
GTACACACCG	AATACCGCTA	TTTGTTGCAT	CATGTTTTTG	AGGTTTATCC	TTATGTCGAG	360
TCGCAATGGG	CAGAAAGTAG	AGGAATGAAA	TATAAGGTTT	CTACGGGATT	ACAGTCGCGT	420
TATCGGCTGG	TAAATAGTGA	TAACTGTCTC	ATGTTTGCAA	CATTGGGGGT	ATTTTTCGAA	480
TTGGAAGAGT	GGGAACAGCC	AGCCACTAGC	CTCTTGCGAG	GAACGTATGC	ATACAGCCGA	540
AGTATCAAAA	GCCACCTGTC	TATCAGTTTC	AGACATCGGT	TGGGTGAACA	TTGGGAATTT	600
ACAACCTACG	CTATTACCA	GGGAAAGCCT	GACAGTTATT	TTAAGAAGGC	ACGTTTGGA	660
GGAGCTATCG	ACCTCAAATA	CCATATCACA	CCTACGATAG	GAATACGCGG	GGCCTATCGG	720
ATCATCTACG	ATACTGCCCC	TATTGTACCT	GTGCGGAAAG	ATTACAACAC	CGTTGATGTT	780
GGTATCGATA	TTTCGTTT					798

(2) INFORMATION FOR SEQ ID NO:91

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 2721 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:  
(A) ORGANISM: PORIPHYROMONAS GINGIVALIS

(ix) FEATURE:  
(A) NAME/KEY: misc\_feature  
(B) LOCATION 1...2721

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:91

ACTATATGCG	TTGCCTTCTT	ATCCGCTCCC	GTTGCGGCAT	TGCGCGAGTC	GCCGCCAATG	60
GGGGCGGAGC	GGAAGACTCC	CTCTCTCCTA	CCCCCTTCTT	TCGAGCATTG	TGATAAAGGA	120
AAGGGGTTCG	ACTACAGACT	ATTACACAAGC	AATAAACTTA	AAGTGTTTGC	CACAGGTAAC	180
AGCCGATACA	TACACAATAA	ACCAACAATC	ATCCAAGCAA	TGAACGAAT	CGTTTTATCA	240
TCTTCTCTGT	TCGTTCTGTC	CATACTTTCT	TTGATGGCAC	AGAACAATAC	CCTCGATGTA	300
CACATATCCG	GTACGATCAA	GGATGCCTCC	TCCGGCGAAC	CAGTGCCCTA	TGCCACTGTA	360
AGCATCCGGC	TGACAGGAGC	AGATACCACA	CAGGTGTTCC	GACAAGTGAC	TGACGGCAAC	420
GGCTACTTCG	TCATAGGCCCT	GCCGGCAGCT	CCCTCCTATC	ACCTGACAGC	TTCGTTTCGTA	480
GGTATGAAAA	CCCATACCAT	GCAGATTAGT	CGGGGAAATG	GACAGCACGA	CATCAATCC	540
ATCGACATTT	CTCTCGAATC	CGAGGACAAA	CAACTCTCCA	CCGTACCCGT	ATCGGCAGCA	600
CGACCACTGG	TGAAGATGGA	GATAGACCGC	CTGTCTCTATA	ATATGAAAGA	TGACCCCGCA	660
GCCAAGACGA	ACAACCTGCT	CGAAATGCTG	CGCAACGTTT	CTTTGGTAAC	GGTGGATGGT	720
CAGGGCAATA	TCCAGGTGAA	AGGATCTTCC	AACCTCAAAA	TCCACCTCAA	TGGCAGGCCC	780
TCGACCATGG	TGAGCAGCAA	CCCGAAGGAG	GTCTTTCGCT	CCATTCTCTG	CCATACGATC	840
AAACGGGTGG	AGGTCATCAC	CGATCCGGGT	GTAAAGTACG	ATGCGGAAGG	CACAAGTGCC	900
ATCCTGGACA	TCGTACCGGA	AGAAGGTAAG	AAGCTGGAAG	GATATTCAGG	TTCCATCACG	960
GCCAGTGTCA	GCAACAATCC	CACAGCCAAC	GGTAGTATCT	TTCTGACGGC	AAAGTCCGGC	1020
AAAGTCGGGC	TGACTACCAA	CTATAACTAC	TACGGTGGCA	AAAACAAGGG	CTCTCGCTAC	1080

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	TTTACCGAAC	GTACTACATC	CATGCTCCAA	ACGATAGAAG	AAGGCCAAAGG	GCAAGAAACC	1140
	TTTGGCGGAC	ACTTCGGCAA	TGCCCTCCTC	TCATTTCGAGA	TAGATTTCGCT	CAATCTCTTT	1200
	ACGGTGGGCG	GCAATGTACG	CCTTTGGGAG	ATGACCACCG	ACCGGAAACAG	CGTAGAAAAA	1260
5	AGCTTTGCCG	GCAGCAACCT	CATGTCTTAC	ATAGACAGAA	AACTCAAAAC	ACAGATGGAT	1320
	GCCGGATCAT	ACGAGCTCAA	TGCCGACTAT	CAGCACAGCA	CTCGCCTGCC	GGGCGAATTG	1380
	CTCACCGTTT	CCTACCGCTT	CACTCACAAT	CCTAATAATA	GCGAGACCTT	CATTGACCAA	1440
	TGGAAGCGCG	ATCCGCTCAA	CACAGCTAAT	ACGATCCAGT	ACGCCGGCCA	GCACTCCAAA	1500
	TCCGATGCGG	GCATGGACGA	ACATACGGCA	CAAGTGGACT	ATACACGTCC	CTTAGGACAA	1560
10	GCACATTCTT	TGGAAGCAGG	GCTGAAGTAC	ATCTATCGTC	ATGCCACGAG	CGATCCTCTC	1620
	TATGAGATAC	GACCATCCGA	AGATGCTCCG	TGGCAGCCCG	GCTCTCTATA	TGCACAGAAT	1680
	CCGTGGAACG	GAAAGTTCCG	CCACGATCAA	TACATCGGAG	CAGCCTATGC	CGGCTACAAC	1740
	TATCGTAAGG	ATCAGTATTC	TTTGCAAACC	GGCCTCCGAG	TGGAAAGCAG	CAGGCTGAAA	1800
	GCACTCTTTC	CCGAAAACGC	AGCAGCAGAT	TTCTCCCAAC	ACTCGTTCGA	CTGGGTGCCA	1860
	CAGCTCACGC	TCCGGTATAC	CCCCTCGCCC	ATGAAGCAGC	TTAAGCTGGC	CTATAACTTC	1920
15	CGAATCCAAC	GTCCCTGCAAT	CGGCCAATG	AATCCCTACC	GGCTACAGAC	CAACGATTAT	1980
	CAAGTACAGT	ATGGTAATCC	CGACCTAAAG	TCGGAGAAGC	GTCACCACGT	CGGTCTCTCC	2040
	TATAATCAAT	ACGGAGCCAA	GGTCATGCTT	ACAGCATCGC	TGCACATCGA	CTTCTGCAAC	2100
	AACGCCATCT	AGAATTACAC	CTTCTCCGAC	CCGGCCAATC	CCAATCTGTT	CCACCAGACC	2160
20	TATGGCAATA	TCGGACGAGA	GCATTCTTTC	AGCTTGAATA	CCTATGCCAT	GTACACGCCG	2220
	GCCGTATGGG	TCAGGATTAT	GCTCAACGGA	AATATCGATC	GCACATTCOA	AAAGAGCGAA	2280
	GCACTCGGCA	TTGATGTCAA	TTCATGGTCC	GGCATGGTAT	ACTCAGGCCT	GATGTTTACC	2340
	CTGCCGAAGG	ATTGGACTGT	GAATCTCTTC	GGAGGTATAT	ATCATGGGGG	AAGAAGCTAC	2400
	CAGACGAAGT	ATGATGGCAA	TGTATTCAAC	AATATCGGTA	TAGCCAAACA	GCTTTTCGAC	2460
25	AAAAAATTGA	GAGTCTCGCT	GAGCGCAAA	AACATTCATG	CGAAGTATTC	GACATGGAAG	2520
	AGCCGACCCA	TCGGCAATGG	ATTTACTATT	TATTCGGAAA	ATGCCGGTAT	ACAACGGAGT	2580
	GTTTCCCTCA	GCCTCACCTA	CAGCTTCGGT	AAGATGAATA	CACAAGTGCG	CAAGGTAGAG	2640
	CGTACGATCG	TCAACGACGA	CCTCAAGCAA	ACCTCATCCC	AAGGACAGCA	GGGTGGCGGA	2700
	CAAGGAAATC	CTACCGGCAA	T				2721

## (2) INFORMATION FOR SEQ ID NO:92

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1350 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...1350
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:92

	TGGTGCCAAT	CCGACCCAAT	ACCTCATTGC	CATGCAAGTAT	ATCGAAACGC	TCAAGGACAT	60
55	CAACAAGGGC	GATCAGACCA	AGACCGTTTA	CCTCCCGTTC	GAGGCTACCG	GTATGCTCGG	120
	TGCCCTTGGG	GGTATGAAGG	ATTTGGTGAA	AGGATGAGAC	TCTCTGCCAT	TCTTATCGCT	180
	TTGATTGTGA	TGCTGCCTGC	TGTGCTTAGC	GGGCAGCATT	ATTATCCCAT	GGCGGGAGAG	240
	CGACTGGAGA	CGGACAGCAT	TCGTCCGAAC	GAATCTCTGG	CATCGATCCG	AAGTGGCGCT	300
	TTCTTTTCGA	ACAATGAATA	CAATGCACGT	TCGGTCAAAG	GTTATACGTT	GCCGGGTGCA	360
60	CGGGTTTCCG	CTTTTGCTTC	TTACTCGCTG	CCGGCAGCAC	ATGGTGTGAA	GCTTTCTGCTC	420
	GGAGTATCTA	CCCTGAACTA	CTGGGGGGCA	AGTCGCTATC	CGGCCGGTAT	CGCTTATTC	480
	GATTTACCTT	ATTGGACGGA	CTATAACGAC	TATGTACGCT	TGCGTATCCT	GCCTTATGTA	540
	CAGGCCATGC	TGAAGCCGAC	GGCCACGACT	GCTCTCATGC	TGGGCAATAT	AGCCGGTGST	600
	ACGGCTCACG	GACTGATCGA	ACCGATCTAC	AATCCTGAGT	TGGATTGTAG	GGCTGATCCT	660
65	GAAGCCGGTG	TGCAATTTTC	GGGTGATTGG	ACACGTTTCC	GAATGGATGT	TTGGGTCAAT	720
	TGGATGAGCA	TGATTTTCAA	AAATGACAAT	CATCAGGAGT	CGTTTGTCTT	TGGCTTGTCC	780
	ACTACTTCGA	AATTTGTTATC	GGGTGAAGGC	AAATGGCGAC	TGCAACTGCC	CTTGACGGCT	840
	ATTGCCACGC	ATCGCGGGCG	GGAAATACAAC	TGGGCGCAGC	AGGATACCGT	GCATACATGG	900
	GTCAATGGAG	CTGTCGGACT	TAAGCTTTTC	TATCGCCCTC	GTACCGACAA	ACCCATGCAG	960
70	ATTTGGGGAT	CTGCTTATGG	TGTGGCAGCC	TTGTCAAGCG	GAGGATACTT	CCCTTACGAA	1020
	AGAGGGTGGG	CGGGTTATCT	TTCTCTCGGA	ATGGACTTGG	AGCACTTCGC	TTTTCTGTACC	1080
	GACTATTGGT	ACGGCAGGCA	TTACGTTTCT	CCCTTTGCTG	CACCTTTCGC	CAATTCCCTG	1140
	ACGTATGACA	AACAGCCTCT	TACGAACGGT	TGGGGCGATT	ATATTCTGCT	CTATGCCGAC	1200
	TATTCGTGGC	GGATGGCAGG	AAGTGTTCCT	TTGGCGGCTG	TTGCTCGGGT	ATGGTCCAG	1260
75	CCTTCGGATC	GTTTTGCGAT	GAGCCACGCC	TTGGAAGTGA	CGATGCGTAT	CGATCCCAAA	1320

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TTCCCAATAG CTTTCTGAA AGGCAATCAT

1350

## (2) INFORMATION FOR SEQ ID NO:93

5

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 1341 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: circular

10

(ii) MOLECULE TYPE: DNA (genomic)

15

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

20

(ix) FEATURE:

- (A) NAME/KEY: misc\_feature  
(B) LOCATION 1...1341

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:93

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```
CCGTTTTCAC CGCCATGGGT ATGTGCTGGA GCGGCTTCCT CAGTACGCAC ACGGCCATGC      60
TCGACAGTCT CAAGTACCGC CGCCTCATCA CACAGGCGAT CGGAGCACAT GCGATCGGCG      120
GACTCGTCGC CGGCATATTC GCCCATTGGC TCTTTGTCCT CATCTCACTC ATTTGATTTC      180
ATACCCGACC AACGTATGAA CAAATCGCTA TTATCATTGG CATGCCTCAT CCTGTGCGGT      240
ATGCCGGCCA TCGCCCAACA GACAGGACCG GCCGAACGCA GCGGCGAGCC TTCTCTGGCC      300
GAACGTGTAT TCGGTCTGGA GCAGAAGCAG AAAAAGCTGA AGGTGTACTT AGGCATACAG      360
TCGTTCTACG ACCAGCCGCT TGTGATGAC GAATCCCATC TCGGACACTT CAAGGTACAG      420
GAGCTGCGGA TGTCTGCTCA TGGCGAACTG AACCGCCACC TCAGCTTCGA CTGGCGACAA      480
CGTCTCAACC GTGCCGCCGA CGGCACTTCG TTTGCCGACA ATCTCTCCAA TGCCATCGAC      540
ATCGCAGGTG TGGACTGGCA CCCGAACGAC AAGGTGTCTT TCTTCTTCGG ACGTCAGTAC      600
GCGCGTTTCG GAGGGATAGA ATACGACATG AACCCCGTAG AGATCTACCA GTACAGCGAC      660
CTTGTGGATT ACATGACCTG CTATACTTCG GCGGTGAAC TCGCATGGAA CTTCCACCCC      720
GAACAGCAGC TGCAGCTACA GGTACTCAAT GCTTACAACA ACCGCTTCGC CGACCGCTAC      780
CACGTGACAC ACCGATGTCG TACCGCCACG AGCTACCCGC TCCTCTACTC GGCACAGTGG      840
AACGGTACCC TCCTCGGAGG AGCACTGCAT ATGCGTTACG CCGTGTTCGAT GGCTCATCAG      900
GCCCAAGAGC GTAATATGTG GTACTTCCTT GCGGGCAACC TGTTCATCC GGGCAAACGG      960
ATCAACGGAT ACCTCGACCT CACCTACTCG ATCGAGGGAT TGGACGACAA AGGCATTATG     1020
ACTGCTCGCT ACGGCAAGGG CAAGACCCCTC ACGGACGTCA AGTACTATGC TCTGGTATCG     1080
AAGTGGAAGT TCCGCATTTT CGATCAGGTC AATCTCTTCC TCAAAGGCAT GTACGAGAAC     1140
GGCTATGCGC CTGGCCAATA CGGCGAGAGC AGCCACACGC GCCACTCCTA CGGCTATATG     1200
GGAGGGGTGG AATATTACCC TACGGAGACC AACTTCCGTC TGTTTCGTCAC CTACATAGGA     1260
CGGCATTACC GGTACAGTGC GACCGAGACG GAAAGCACCA ATGCTCTTCG CGCCGGTCTG     1320
ATCTATCAGA TACCTTTCTT A                                     1341
```

50

## (2) INFORMATION FOR SEQ ID NO:94

55

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 681 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: circular

60

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

65

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc\_feature  
(B) LOCATION 1...681

70

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:94

75

TATAAGCAAG CTATAATGAA ACATTTGTTT AAGTCGACAT TAGTACTTCT TTGTGCTCTT

60

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5 TCTTTTCCG GTACCTATAC CTTTGCACAA GAAAATAATA CAGAAAAGTC ACGATTTGAT 120  
 TTTTCTGTTA GGCTGGGACA GGGATATATT GCAGGTTCAA CTACCAACCT GATGTATGGG 180  
 TATACATCTG CTAACGATAG ACTTTGTCT GGTGCAATT ATCTGGGCTT GACACCAAGT 240  
 AAGAAAGAAA ATGCAACCGG CGTAGCATTT CGTTTCTTAT CCCCCCTCC GGGTTATTAT 300  
 GTCGATATAT CCGGCAAGA AAATACCTTG AATTATGCGT TTTACGTTGT CGGAGCATAT 360  
 AATAGAATAG CCATTCCTAT ACGCCCTATC AAAAATTTTA ATTCATCTT CTCTACAGAA 420  
 GTCGGAATGG CTTGGATGAG TCGTCATGAG CAAATTTACA ATTCTACTTC GCAGACTTGG 480  
 GATAAGCAGC GCAAGTCGAG GTCGGGACTG GATTTTGGTC TCGGGATGCA TCTGCAATHC 540  
 CACATTAATA AGACCGTTTA CTTTATGGCA GGAACCGATC TTACGTCCTG CATGTTCGGA 600  
 10 AAAAGGATCA ATGACTACCA GCAAAAGGAT CGAACCTTCA TTGCACCTAT CGACAACAGT 660  
 ATTGGCATAG GATTAAACCT C 681

## (2) INFORMATION FOR SEQ ID NO:95

15

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1218 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular

20

(ii) MOLECULE TYPE: DNA (genomic)

25

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

30

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...1218

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:95

40 ATATTCATAG ACCCCGATAA GAATACAAAA CAAAACGAAC GAAATATGAT TATCAAGAAA 60  
 ATGCTGAAAA ATAAATTGGC CCCCTTGGCC ATACTGTTCC TTTTGTCTCC AAAGGCTATG 120  
 AAGGCTCAGG AGCAACTGAA TGTGGTACAC ACCTCTGTGC CATCGCTGAA TATCAGTCCG 180  
 GATGCACGTG CGGCCGTAT GGGGGATATA GGTGTGGCAA CGACGCCGGA TCGGTATTCA 240  
 CAGTATTGGA ATCCGAGTAA ATATGCTTTC ATGGATACGA AAGCCGGTAT TAGCTTCTCA 300  
 TATACACCCCT GGCTGTCCAA GCTGGTCAAT GATATTGCCC TGATGCAGAT GACCGGTTTC 360  
 TACAAATTGG GAACAGACGA GAATCAGGCT ATTAGTGCTT CTCTGCGTTA TTTCACATTA 420  
 45 GGAAAGTTGG AGACTTTCGA CGAATTGGGC GAATCCATGG GAGAGGCCCA TCCCAATGAA 480  
 TTTGCTGTGG ATTTGGGCTA TAGCCGCCAG TTGTCCGAGA ACTTCTCCAT GGCTGTTGCA 540  
 CTGCGTTACA TCCGCTCAGA CCAAAGCACT CACAACCCG GAGAGAATCA GGCCGGAAT 600  
 GCCTTTGCGG CGGATATAGC CGGTTATTTC CAGAAGTATG TGCTACTGGG TAATGCGGAG 660  
 AGCTTGTGGT CTTTGGGTTT CAACGTAAAG AATATCGGAA CGAAGATCTC CTATGACGGA 720  
 50 GGTGTACGA GTTTTTCAT CCCTACTTCG TTGAATCTCG GGACGGGGCT GTTGTATCCG 780  
 ATCGATGACT ATAACAGCAT CAATTTC AACCTTGAACCTTGA GCAAGCTGCT TGTACCCACT 840  
 CCTCCTATCA TGGATCAAAA CGATCAGGCC GGGTATGAGG CTGCACTCAA GAAATATCAG 900  
 GAAACTTCTT CGTACAGCGG TATATTCTCT TCTTTCGGTG ATGCGCCGGG AGGACTCAAG 960  
 GAAGAATTCC GTAGATTAC ATGGGGACTT GGGGCTGAAT ATAGCTATGA CGATAAATTT 1020  
 55 TTTGTTCTGT CCGGATATTC ATACCTGCAC CCCACCAAG GCAATTGCA GACTTTCACG 1080  
 GCCGGTGCCG GCTTCAAAAT GAACATATTC CGTATCGATG CTTCTACCT GTTGTCTACG 1140  
 ATCCAGAGTA ATCCGTTGGA TCAGACTCTG CGGTTTACGC TTGCTTTCGA TATGGATGGA 1200  
 TTGCGCAATT TGTTCAC 1218

60

## (2) INFORMATION FOR SEQ ID NO:96

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1356 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular

65

(ii) MOLECULE TYPE: DNA (genomic)

70

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

75

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

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## (ix) FEATURE:

(A) NAME/KEY: misc\_feature  
(B) LOCATION 1...1356

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:96

CTAATAATCG AAAAGGAAAT GAAAACAACA GTTCAACAAA TTATTCTGTG CCTGGCTTTA 60  
ATGATGTCAG GTGTATTGGG CGGAAACGCA CAGAGCTTTT GGGAAAGAAAT AGCTCCTCCT 120  
TTTATCAGTA ATGAGCCTAA CGTCAAGTAT ATAATTCCCA ATATGGGGAT TGATTCAAAG 180  
GGAACAATCT ATGTAACCGT GACAAAAAGG ATTCAGCAGG GAGCAAATTA TACTTCTGAG 240  
CAATTGGGTA TGTACTATCG ACCATTAGGT GATAATGAAC AGTGGTGGAA ACATGATCCG 300  
TATTTTGTAT ACAAGATAGT TGGGATATT CAGACAGATG CATATGGCAG AGTTTATGTA 360  
TGTACGACTT CTTCTCGAGA TCAAGAGTAT CAACTTTATA TAAACGAGCA GAACGAATGG 420  
AGGTGTATAT TCAAAACTTC TGTGTCTACA TATGAGCATG GTATGGCTGT TTTTCGCTCT 480  
TCGACAGGGG TGACTTATAT AGGTACCAGG CATCACATCT TCGCATCAGG TGTAAATGAT 540  
TTGAGTTTCA ACACATCTTA TGAAGACTCT ACACCTATGA GCTGTCGCTT TGCAGAGGCT 600  
ACGAATAGTG GCACCATCTA TCTGGCATTG ATGCATGAAA CCACAATGTC TACGACTATC 660  
CTTACTTATC AAAACGGTGA GTTCGTCGAT ATCTCGGAAA GTGAATTGAG TAACTCGATT 720  
ATTGCATCCA TGTGCTCTAA TAAAGAAGGT GATATAATAG CTCTTGTTAC TTCATATACA 780  
GGATTATGA TGGGAACCTT TCGCATCAGA AAAGCAGATG AAGGCAAATG GCAACTTGTT 840  
GGCGGAGATA TACAGAATGC GATCGTTCAA AATATATGCA TGATGGACGA CAACAAGATT 900  
GCTTGTGAAG TCTTCGGGAC TCCTAACGGA GTAGATGGTC GGACAAGGGT TTGTGTTTCT 960  
GACGCATCTG TCTTTGATTT TGAGTGGTAT GAAGATGAAA TATACGGAGG CCTGATATTT 1020  
GACACTTTCT TCTATAGCCC TTGGGACAAA CTTCCTTTATG CGAAATTTGG TGGGATTATG 1080  
CTCAGGAGTA AAGAGTCTT TATAACCTCT TTCATTTCTC CGACAGTTGT ACAAGGAGTG 1140  
GATGTCTATA CTTTGGCCGG GAAGATAAGG ATCGAAAGTG AAACCTCCGGT GTCTGAGGTG 1200  
TTGCTTTTCG ACCTGGCTGG CAGGATGGTA CTTCGGCAAA CCATTGATAA TAAATCTAT 1260  
TCGGACATAG ATACTAACGG ACTAAAGCGA AGCGGTATTT ACGTAGTCTC GGTGCGGCTC 1320  
TCTTCCGGAC AGGTATTTCAG TCATAAGGTG CAGGTA 1356

## (2) INFORMATION FOR SEQ ID NO:97

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 993 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: circular  
(ii) MOLECULE TYPE: DNA (genomic)  
(iii) HYPOTHETICAL: NO  
(iv) ANTI-SENSE: NO  
(vi) ORIGINAL SOURCE:  
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

## (ix) FEATURE:

(A) NAME/KEY: misc\_feature  
(B) LOCATION 1...993

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:97

GGCCTGTACG GTATGTCTGT TGTACCTATA ATAATTTATC TTTGCGGTAT ATCAAATTAT 60  
GCAAGACTCA TGATAATCCG GTGTCTTATC CGTCGTCGGA GAACCGTCCT GTTCGGGTTG 120  
ATATTCGTGG TAGGTCTTTT CTCTGCGATG GCGCAAGAGA AAAAGGATAG TCTCTCTACG 180  
GTTTCAGCCAG TGCCGAATAG CAGCATGGTG GAGCAGACCC CTCTTCTCTC CATTGATCAC 240  
CCCGTCCTGC CCGCTTCTTT TCAGAATACC CGTACACTGA AAAGGTTTAG AGACAAACAT 300  
CTTTCGGAAG CTTTGCTCAA TGGATTGAAG CCTCATCGCT CATCTTTGCA ATTGAATGAG 360  
GAACTCAACT TCGCGGCAGA GCGTCGGGAT TTCGTTTCTC CCCTCTTGCA AACTCGCCAC 420  
GCTGCCGGTG TCCTTTCATG GCGACCGACC GATAGGATGC ATTTTATATC ATCGGGCAAT 480  
ATCGGCTCTG GCCATGATTT ATTGACCGGT GTGCGCAAGG ACTTCGGATG GAATGCTGGT 540  
GCCGACTTCT TGCTGAGTCA AAATCTTACG GCACATGTCC AAGGCGGTTG GCAGCAGAAT 600  
TTGCGGCTTTA TACCTATGAC GGCTGTCAAT GGCCAACTGC GTTGGCAAGC CACCGAGAGA 660  
TTGAGTTTFA CCACCGGTAT CGATTATCGA CAGGTACAGT GGAATGCTTT CGATAATAGA 720  
ACGTTCTCGC TTAAAGGAAG TGCTCGATAC GAAGTGATGG ACAATGTCTT TGTCAATGGA 780  
TTTGGCAGCT ATCCTCTCTA CAGCAGTACG CGCTCAGGAC TCAATATGGC TGTTCGGATG 840  
CATGGATTCC GCCCTCAGTA CCGTGGATCG CTTGAGCTGA AAGTCTCCGA GCGATTCCGC 900  
TTTGGCGTGG GTATGGAGCG CGAATACAAT ATCTGGACTC GTCGGTGGGA AACGCATTAC 960  
TTTGCTTATC CTGTATTCTA TGGCGATAAG AAG 993

## (2) INFORMATION FOR SEQ ID NO:98

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(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 987 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...987

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:98

GAGACGAACT	CTTGGGATATC	CAGCGATTGC	AATTGCGACGA	CGATGAAAAC	GAATAGACGA	60
TACGCATTTG	TTTTGCCGCT	TCTGCTACTC	ACCGGATTGT	TGGCATGGGG	GCAGGATTCT	120
TCCACGSGTA	GCAATACAGC	GTTTGCAACT	GATTCTTCGA	GTAGAGAGTT	GCCCACGGAG	180
CAGTCCGCTT	ACCGCATTCA	TTCTGCCTAT	ATGGTCGGTG	GTGGCGGAAG	CATAACGCGC	240
GACACCTATT	TGTCACCCCT	TCGTTATGGA	GGATGGACAC	TGAATTTGTT	GGGAGAGAAG	300
ACGTTCCCTC	TCAAAGCCTC	CGATTCCCGT	TGGATGATCC	GTACCGGGCA	TGAGCTGGAT	360
TTTGGCCCTGA	TGGACAATCC	GGCCAATAAT	GCTCATTCT	ATTCCCTGCT	GTATAACGGT	420
TCCGCTGCGG	CTCTTTACCG	CCTTGGCGCT	AAGCATCTGC	GAGCCGCGTG	GATGGACAAT	480
CTGCGCTTGG	CATTGCGCCC	GGGCTTGGAA	ATCGGSGCTG	GAGGAATTTA	TAGTACACGC	540
AACGGAATA	ATCCTGCGAC	ATTGAAGCTC	TACACCAATG	CCATCGCCCA	AGCCTCGATA	600
GGATACTACG	TCCCTCCGA	AACTTTTCCC	CTGTATTTTC	GGTGCTCTC	CCAGATCAAT	660
CTCTTCGGTA	TAGCCTATGG	AAATGGTTTT	GGTGAGAGCT	ATTACGAGAA	TTTTTTGCTC	720
AATAACGGCA	TTGCAGGCTC	CCTGCATTTC	ACTTATCCGG	GCAAGTTTAC	TCGGTTCACG	780
ACACTCATAA	CGGCGGATAT	TCCCATTCCG	AACTTCTGTA	CGCTTCGTGT	CGGTTATCGC	840
TATTCCCAT	TGGGCTCTTC	GCTTAACGCA	TTGGATACTC	GAATCCACAG	TCATACGGCT	900
TTTATCGGTT	TCGTCACGGA	GTTTTACCGA	TTCCGTGGGC	GCAAAGCCAT	GAATACCGGT	960
CGGAGAACCA	GTCTTTACTA	TCATGAT				987

(2) INFORMATION FOR SEQ ID NO:99

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 957 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...957

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:99

TTTACGTCGG	GTACGATATT	CGTCCGTATA	GCCATATCCG	GCCGTGTAGT	GTGCCGTGAG	60
GTTGAGGATA	ACGGAAGGAG	AGAAGCTGTG	CGTCATGATG	GCATGGTAGT	GACGCTGCTC	120
GTAATTTGTC	GTATTGTGGT	AGTAGTSCGG	TACTCCTTGC	GCGTCCACGT	ACATAAGACC	180
GGCACTGTTG	TATCGGCGGC	CATATTGGGC	TTTCATCTCC	TTGGAAAGAC	CGTTCCATGC	240
GATACCGSTA	ACTTCTTTTC	CTCCGAAAGT	GATGAACCTG	AGAGCCGTGT	TGCTACCGAA	300
ATAGCCCAAC	TGTGCGAAAT	AGGATTTCAG	ATCCACGCTT	CCTCTATCCA	CGTAGCCGTC	360
CGAACCAGAT	TTGGACAGGC	GGGCATCCAC	TGCCCAATGG	CGACCGATGC	GTCCGCTACC	420
GAGTTTGACC	GATCGGCGGA	ATGTGCCGAA	CGAACCTCCG	CTCAAATCGA	CACGGCCATA	480
AGGAGCCAGT	CCCAAATTAT	CCGTACGCAT	ATTGACACTT	GCCCCAAAAG	CTCCGGCACC	540
ATTGGTGSAA	GTACCCACAC	CTCGCTGCAC	CTGAAGGTCT	TCGATGGAAG	AGGCGAAGTC	600
GGGCATATTC	ACCCAAAAGA	CGSACTGAGA	TTCGGAGTCG	TTGAGGGGTA	CTCCATTGGT	660

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AGTTATGTTG ATGCGATTGG CATCGGTGCC ACGCACGCGA AAGCCGGAAT ATCCGATACC 720  
 CGTACCGGCA TCGCTGGTGG CTACCACGGA GGGAGTCAGC ATCAGCAGAT AGGGGATGTC 780  
 ACGACCATAA TTGGACTTGG AAAGTTGCGC CTTGCGAAGC TTGGTGTAAAG CGACAGGGGT 840  
 TTTGCGCGTG GCGCGAGTAG CTACGACCTG TACGGTCTGG AGCTGCACAT TGCTAAGACT 900  
 ATCTATCTCG CTGTGGGAGA CGGGTGCTTG TGCCGTCAGG CAGAAAGGCA GGACGGC 957

## (2) INFORMATION FOR SEQ ID NO:100

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1842 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular

## (ii) MOLECULE TYPE: DNA (genomic)

## (iii) HYPOTHETICAL: NO

## (iv) ANTI-SENSE: NO

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature  
 (B) LOCATION: 1...1842

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:100

CCATATAATG TCCAATCTAT TAGCAACAAG ACGATTAAAA AACAAATGGA AAACCTTAAAG 60  
 AACATTACAG CCAGAGAGGA TTTCAACTGG GAAGAGTTTG AGGCCGGTGG CGTCCATGCT 120  
 GCCGTGAGTC GTCAGGAGCA GGAAGCTGCT TATGACAAAA CGCTCAATAC CATCAAGGAA 180  
 AAGGAAAGTG TAATGGGTAG GGTAACTGCT ATCAACAAGC GTGAAGTGGT TATCAATGTA 240  
 GGGTACAAAT CGGAAGGTGT GGTACCTGCA ACAGAATTCC GCTACAATCC CGAACTCAAA 300  
 GTGGGAGACG AAGTGGAAAT TTATATCGAG AATCAGGAAG ATAAGAAGGG CCAGCTCGTC 360  
 TTGTCTCACC GCAAGGGTCG TGCCGCTCGC TCTGGGAGC GCGTGAACGA GGCTCTCGAA 420  
 AAAGACGAAA TCGTAAAGGG CTATGTGAAG TGTCGTACCA AGGGTGGTAT GATCGTCGAT 480  
 GTATTCTGTA TCGAGGCTTT CCTCCCGGGA TCACAGATCG ACGTGCGCC CATTCGCGAC 540  
 TACGATGCAT TCGTTGAGAA GACGATGGAG TTCAAGATTG TGAAAATCAA TCAAGAATAT 600  
 AAGAATGTAG TTGTTTCCCA CAAGGTGCTC ATCGAAGCAG AGCTCGAACA ACAGAAGAAA 660  
 GAAATCATCG GCAAGCTCGA AAAAGGGCAG GTCATCGAAG GTATCGTCAA GAATATTACT 720  
 TCTTACGGAG TATTTATCGA CCTCGGTGGA GTGGATGGTC TTATCCATAT CACTGACCTT 780  
 TCATGGGCTC GTGTGGCTCA TCCGGAAGAA ATCGTACAGC TGGATCAGAA GATCAATGTC 840  
 GTTATCTCGG ACTTTGATGA AGATCGCAAG CGTATCGCTC TCGGACTCAA ACAGCTGATG 900  
 CCTCATCCTT GGGATGCTCT CGACACGAG CTTAAGGTAG GCGATAAGGT GAAGGSTAAA 960  
 GTTGTGGTGA TGGCAGATTA CGGTGCTTTC GTTGAGATTG CACAGGGCGT TGAGGCTCTT 1020  
 ATCCACGTAA GCGAAATGTC ATGGACACAG CACTTGCCTT CTGCTCAGGA CTTCCTGCAT 1080  
 GTAGGCGACG AAGTGAAGC CGTGATCTTG ACGCTCGACC GCGAAGAAGC CAAAATGTCT 1140  
 CTCGGTCTGA AGCAACTCAA GCCGGATCCT TGGGCTGATA TCGAAACTCG TTTCCCTGTA 1200  
 GGCTCTCGTC ACCATGCTCG TGTTCGCAAC TTCACCAATT TCGGTGTATT CGTTGAGATC 1260  
 GAAGAGGGCG TAGATGGCCT TATCCATATT TCCGACCTTT CTTGGACGAA GAAGATCAA 1320  
 CACCCACAGC AGTTTACGGA AGTAGGTGCT GATATCGAAG TTCAGGTAAT CGAGATCGAC 1380  
 AAGGAAAACC GTCGTCTCAG CTTGGGTGAC AAACAGTTGG AAGAGAATCC TTGGGATGTA 1440  
 TTCGAGACGS TATTTACTGT AGGATCTATC CACGAAGGAA CGGTAATCGA AGTGATGGAC 1500  
 AAGGGTGTCT TCGTTTCTCT GCCTTACGGT GTGGAAGGTT TTGCCACTCC GAAGCACATG 1560  
 GTGAAGGAAG ATGGCTCACA GGCTGTACTC GAAGAGAAGT TACCTTTCAA GGTATTGAG 1620  
 TTCAATAAGG ATGCCAAGCG AATCATTTGA TCTCATAGCC GTGTATTCTG AGATGAGCAG 1680  
 AAAATGGCTC ACGGTGAAGC CAATGCAGAG CGTAAGGCTG AAGCCAAAGC GGCTCAGAAA 1740  
 GAAGCTGCTG CCGAAGCTGC CAATCCTGCA CAGGCTGTAG AGAAAGCCAC TCTCGGAGAC 1800  
 CTCGSCGAGC TGGCCGCTTT GAAAGAAAAG CTTTCAGAAA AC 1842

## (2) INFORMATION FOR SEQ ID NO:101

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 729 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular

## (ii) MOLECULE TYPE: DNA (genomic)

## (iii) HYPOTHETICAL: NO



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(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:  
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:  
(A) NAME/KEY: misc\_feature  
(B) LOCATION 1...729

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:101

TCGACAATAA	TGAAAAAAGC	TATTCTTTCC	GGAGCGGCCT	TGCTCCTCGG	CCTATGTGCC	60
AACGCACAAA	ACGTGCAGTT	GCACTACGAT	TTCCGGTCATT	CCATCTACGA	CGAACTAGAT	120
GGACGTCCCA	AACTGACTAC	CACAGTGGAA	AACTTCACAC	CCGACAAATG	GGGAAGCACC	180
TTCTTCTTCA	TCGACATGGA	TTACACGGGC	AAGGGTATCC	AGTCGGCCTA	TTGGGAGATT	240
TCGCGCGAAC	TGAAGTTTTC	GCAAGCTCCC	GTTTCCATTC	ATTGGAGTA	CAACGGAGGC	300
CTCTCCACAA	GCTTTACTTT	CGGACACGAT	GCTCTAATCG	GTGCCACCTA	CACCTACAAC	360
AACCCCTCCT	TTACACGTGG	ATTTACGATC	ACGCCCATGT	ACAAGCATCT	GGGTGCGCAC	420
GACTTCCACA	CCTATCAGAT	CACCGGCACT	TGGTACATGC	ACTTTCTGGA	CGGTCTGCTT	480
ACCTTCAACG	GCTTCCTCGA	TCTTTGGGGT	TTCCCCCAAG	AGAACCCAAT	CGGGGGCCCT	540
GTGCTCAAAG	AAGGGGATAA	GTTCTATTTC	CTGTCCGAAC	CSCAGTTCTG	GATCAACCTC	600
AATGCGATCA	AAGGCATCGA	CAAGGATTTC	AATCTCAGCA	TAGGGACAGA	GATGGAAATC	660
AGCAGGAACT	TCGCTCGCAT	GGACAAATTC	TCCTGCATCC	CTACTCTTGC	GGTCAAATGG	720
ACTTTCAAC						729

(2) INFORMATION FOR SEQ ID NO:102

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 705 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:  
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:  
(A) NAME/KEY: misc\_feature  
(B) LOCATION 1...705

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:102

ATGAAAACAA	TTAGTAAGAA	CCATGCGGCA	CGGATCTGTG	CCGCCATTGC	TTTGTTTGCA	60
GTGTGTACG	GCCGGATAGC	TGCTCAGGAT	TTTCTCTATG	AAATAGGAGG	AGGTTTGGT	120
GCTGCTCAGT	ATTTTGGCGA	TGCAAAACAGA	GGCTTGTTTC	GTTCATCCGG	AGTAGGTTTG	180
GAGTTGGTCG	GACGTTACAA	TTATAATTTT	CGCTGGGCTT	TCAGTACCAT	GTGGATTGG	240
CGTACATTGA	GAGGCGATAC	CGATAAGTCC	GGGAATGTCT	TCCCCGATT	TGCTCAAGCG	300
GATTTTAAGG	TCGGCTTGAC	TCAGCTCCAC	GTTAGAAGCG	AATTAACTT	TCTCCCTTAT	360
AGCGATGGCT	ATAAGTATCT	TGGTACAGCT	CGGCTGTCTC	CTTATGTAGC	GGCCGGGTTG	420
TCTTTGGGTT	TTGCTTCGGG	TGCTAAAGGT	TCGGCTTTTG	CTCCCGGGAT	TACTGCGGGA	480
ATGGGAGTGA	AGTATAAGCT	TAAACCGCGG	ATCAATGTCT	GTATCGAGTA	TTCTTTCACG	540
GGGTTACTTA	CCGATGCTTT	GGATGCGCTG	ACGGATAAAA	GTGTTTGGCT	CGAGGATCCA	600
TATAAGATCA	ATGACTCCTG	GGTCAAAAAC	AAGGATGCTA	CAGGGGCCTT	AGTGCTTAGG	660
ATTACGTATG	ACTTCGGCCT	GCGTAAGACT	TTTTGTAATA	AACAA		705

(2) INFORMATION FOR SEQ ID NO:103

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 1308 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

70 / 490

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:  
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:  
(A) NAME/KEY: misc feature  
(B) LOCATION 1...1308

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:103

AATATAATGT	ATAAAGACTA	TAAGGGTTTG	TATGCGTCGC	TTCGGTGGTA	TGCCCTGATC	60
ATTGGGTTGC	TATTTGCAGC	AGACGGTATA	CAGGCTCAGA	ACAACAACTT	TACCGAGTCG	120
CCTTACACTC	GCTTCGGCCT	TGGCCGTCTC	GGAGAACGGA	CGACTATTAG	TGGGCATTCC	180
ATGGGAGGAC	TCGGCGTCCG	TCTGCGTCAG	GGCACATACG	TCAATGCCGT	CAATCCTGCT	240
TCATACTCGG	CTGTGGATTG	GATGACGTTT	ATCTTCGATT	TGGGTGCATC	TACCGGAATT	300
ACGTGGTATG	CCGAGAACGG	GAAAAAGGAC	AATAGGAAAA	TGGGAAACAT	TGAGTATTTT	360
GCCATGCTTT	TTCTATTTC	CAAATCCATT	GCTATGAGTG	CGGGAGTGCT	TCCTTACTCC	420
GCATCCGGGT	ACCAATTCCG	ATCCGTTGAT	CAAGTGGAA	GAGGCAGCGT	CCAGTACACC	480
CGTAAATACT	TGGGGACAGG	CAATCTGAAC	GATCTCTATG	TGGGTATAGG	TGCAACCCCG	540
TTCAAAAACT	TCTCAATAGG	AGCCAATGCT	TCATCCCTTT	TTGGGCGATT	CACACACAGC	600
AGGCAGGTAA	TCTTCTCCAC	GGAGGCTCCT	TACAATCCCG	TACATCTCTC	GACGCTGTAC	660
TTGAAGGCTG	CCAAGTTCGA	CTTCGGTATG	CAGTATCACC	TTCTTCTCAA	ATCAGATCGT	720
TCGCTCGTTA	TCGGTGCCGT	CTATTCTCCG	CGGGTGAAGA	TGCATAGCGA	GCTGACTCAG	780
ATAAAGAATC	AGGTTTCAGAA	CGGTGTAGTA	GTGGAGAGCG	AAACCCCAAG	ATATATCAAG	840
GGAATGGACT	ATTATACCCT	GCCTCATACA	TGGGGATAG	GTTTTTCTTA	TGAAAAGAAA	900
GATAAACTTC	TCTTAGGAGC	AGACGTCCAA	TATAGTAAAT	GGAAAGGCGA	GAAATTTTAT	960
AAATCCGATT	GCAAAATCCA	GGACAGAATA	CGGGTATCTC	TGGGCGGAGA	GATCATACCG	1020
GATATAAATG	CCGTTGGGAT	GTGGCCTAAA	GTTCGCTATC	GCTTCGGTTT	ACATGGTGAA	1080
AA'TTCTTACC	TGAAAGTGCC	GACTAAAGGC	GGTGTATATC	AAGGATACCA	TATCGTAGGT	1140
GCTGTATTTC	GTATAGGAAT	CCCGCTCAAT	SACAGACGTT	CGTTCGTAAA	TGTCTCTCTT	1200
GAATATGACC	GATTGATCCC	GAAGGAGGGT	ATGATCAAAG	AAAATGCTCT	GAAATTGACC	1260
TTCGGCCTCA	CGTTCAACGA	GTCTGCGTTT	AAAAAGCTGA	AACTGAAC		1308

(2) INFORMATION FOR SEQ ID NO:104

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 2835 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:  
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:  
(A) NAME/KEY: misc feature  
(B) LOCATION 1...2835

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:104

AATACCATTT	CGGAGAATGG	GAACGATAGC	ACCTATTTTT	CTTTTCAAAC	TTTTCTTATG	60
CGATCGATTT	ATCAATTACT	GTTGTCAATA	CTCCTTGCTT	CTCTTGGTTT	CGTCGGGCTG	120
GAAGCCCAAC	AAGCCGGAGT	AGCAGGTAGA	GTATTGGACG	AAGAAGGCAA	CCCCATGATT	180
CAAGCCCAAC	TACAGCTTGT	ACAGAGTACC	GGCCAAGTAG	CCGTGCCCG	AGGTGCCACT	240
AATGAAAAAG	GGTTGTTCAG	CCTGAAAACG	TCACAGGAGG	GTGACTACAT	TCTGCGCGTT	300
TCATATGTAG	GTTACTACTAC	CCACGACGAA	AAAATATCTC	TTAGAAACGG	GCAAACCAT	360
ACGCTCAAAG	ATATATCCAT	GAACGAAGAT	GCCGCTCTTC	TACAGAGTGT	GACGGTGCAG	420
GCTAAAGCGG	CAGAGGTCGT	GGTACGCAAC	GATACGCTCG	AATTCAATGC	CGGATCCTAT	480
ACCGTAGCAC	AGGGAGCTTC	TATCGAGGAA	CTGATCAAGA	AGCTACCCCG	AGCAGAGATC	540
GGATCCGATG	GGAAGATCAC	CATCAACGGC	AAGGACATTA	GCAAGATCCT	TGTCGATGGC	600
AAAGAGTTTT	TCTCCAAAGA	TCCACAGGTG	GCAATAAAGA	ATCTTCCGGC	CGATATGGTC	660
AATAAAGTAC	AGGTACTGAA	CAAACTGAGC	GAGCTGTGCG	GGATGAGCGG	TTTCGATGAT	720
GGAGAAGAGG	AGACCGTAAT	CAACCTGACG	GTGAAGCCCG	AAAAAAGAA	AGGCCTCTTC	780
GGAACGCTTC	AGGCCGGCTA	CGGTACCGAC	CAACGCTATA	TGGCCGGAGG	GAACGTCAAT	840
CGGTTTCGATG	GAAATAAGCA	ATGGACATTG	ATCGGTAGTG	CGAACAATAC	GAACAATATG	900
GGCTTTAGCG	AGATGGACAG	CGAGATGGGA	TCCATGACCT	TCTTCTCTCC	CCAAGGCGGT	960
GGTCGACGCG	GCTTCGGCAA	TAGTGGAGGT	GTTACGTCIT	CGTCGATGCT	GGGCGGCAAC	1020

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TTTCAGTGTCTG AATTCTCCTC TGCCCTTAAT ACAGGAGGCG ATGCACGCTA CGGATACAAC 1080  
GACAAAGGCCA TAGAGACGAC CAAACGCGTG GAAAATATCC TCGCCGAAGG GAATACTTAT 1140  
ATGGACGAAA ATATATTGGA ACGCTCTTTC TCTCACAATG GTCAGGCGCG ATTTAGGATG 1200  
CAATGGAAAC CGTCCGAACG TACCGAAGTG GTATTGAGC CGGATCTTTC GATATCCAAG 1260  
ATCGATGGGT TCTTTAACGA CACATACGAG ACGAAAGATG CCACCGGAAT CTCTATCAAC 1320  
AAAGGTTCTA TCCACCAAAC TACACAAGGA AACAACTTCA GACTGAACGG AGAATTGGAT 1380  
ATCAGTCACA AGCTCAACGA CGAAGGCCGT ACGATCAGTG CCTCCGTCAG TGGCGGTCTG 1440  
ACCGACGAAG ACGGAGATGG CATATATCAG GCTGTGCTCC AAAGCGTGGA GACGAATCAA 1500  
AAGCAATTCA ACGACAATC CAACCTGCAA TATCGGCTTC GCCTCTCGTA TGTGGAACCG 1560  
TTGGGTAAAA ACTACTTCGC ACAAGCGATT CTGAACAGAC GTTCTCTCCG TCGCAATTCC 1620  
GATCGTGAGG TGTACCGACT GGGCGATGAC GGGCAATACT CCATATTAGA CAGTCAGTAC 1680  
GGACTCTCCT ACAGTAACGA GTTCAACCCAG TATCGCATCG GACTCAACCT CAAGAAGATT 1740  
GCCAAAACGT GGGACTACAC CGTAGGATTC AATGTGGATC CCAACAGAAC TGTCAGCTAT 1800  
CGGAGCGTAG CCGGAGTAGA GCAGGACAAA CTGGCTTTCA ATCGTGTCAA TCTCTCCCG 1860  
ATGCTCCGAA TCAACTACAA ACCGAGCAGG ACTACCAACC TCCGAGTGGA CTACCGAGGA 1920  
CGCAGCACAC AACCATCCAT CAATCAGATC GCTCCCGTTC AGGACATCAC GAATCCGCTA 1980  
TTCTGTGACG AAGGCAATCC CGGTCTGAAG CCGAGCTATT CCAACAATGT GATGGCCATG 2040  
TTCTCGGACT TCGATGCCAA AAGTCAGCGA GCTTTCAACA TTGTTTTCTT CGGCAACTAT 2100  
ACATTCGACG ACATCGTCCC CAATACGCCAC TAGATCCGT CTACAGGGAT CCGTACCACT 2160  
CGTTACGAAA ACGCCTCCGG TACGTGGCAA GCGAATCTTC ATGGGACACT ATCGCTTCCA 2220  
CTCAAGAACA GGGCATTTC TTTCCAGGATG TCCTTGTTCA ACAGGTTGGC CGAAGGACAA 2280  
AGCTTCATCA ATGACGATAA GAACAAAGCT CTCTCTTTCC GAACGAGGGA ACGCTGACG 2340  
CTGACCTATC GCAACAATTG GATCGATACG AGTATCGGTG GCAATATCGG ATTCTATATG 2400  
GCGAATAATA GTCTGAGCGG ACAGAAAGAT TCTCGCACAT ACGATTTTGG CGGCAATTAT 2460  
TAAGCTTGCC CTATGGATTG CGTATCGACA GCGATGTTGA ATACAATAAG 2520  
AACTCCGGTT ACAGCGGAGG ATTCACTCTG GACGAATGSC TTTGGAATGC TTCGCTTTCA 2580  
TACAGCTTCC TCCGTGACAA GGCCTGTACA CTGCGTGTCA ATGGCTATGA CATCTCGGT 2640  
CAGCGGTCAA GTATACGCG TTCTGCTTCG GCCATCAATA TAGAAGAGAG CATGTCCAAT 2700  
ACGATCGGAC GCTACGTGAT GGTGGACTTT ATCTACCGAT TCAACGCCTT CAGTGGTGGT 2760  
GGATCTCGCA GCGATCATCA GCGTGGCAAT ATGAATCGTC CGGGCCCAAC TTTCGSCGGT 2820  
GGCAGACGAC CGTCC 2835

35 (2) INFORMATION FOR SEQ ID NO:105  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 1236 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: circular  
(ii) MOLECULE TYPE: DNA (genomic)  
(iii) HYPOTHETICAL: NO  
(iv) ANTI-SENSE: NO  
(vi) ORIGINAL SOURCE:  
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS  
(ix) FEATURE:  
(A) NAME/KEY: misc\_feature  
(B) LOCATION 1...1236  
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55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:105

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GGAGAGTATC CTGCAACAG TAACGACAAA AAAGAGATGG TTATGAAGCT GATTAAAAGA 60  
AGTTTGCTCC TGCTTGAGC GGTACTGCTG ATTACGCTTC CTGCGTACTC GCAGAATGAT 120  
GACATCTTCG AAGATGACAT CTATACATCG CGAAAAGAAA TACGTAAACA AAACCAAGTT 180  
AAAGACTGGC AAAACCAAGA GGACGGATAC GGCAGCGATA CGGAATATAC AGTGGCTTCC 240  
GATCGGGACA TTGACGCCTA CAATCGTAGA GATGGCCAGT CCTACGATGG GAAAAAGTTG 300  
TCCAAAGACA AGAAAAGAGA CTCCACTCGT TCTTCTGTTT CCGGTGCTA TAGTCGCGC 360  
TTGGCTCGAT TCTATAAGCC GAATACGATC GTCAATTCAG GTGCCGACAA TGTATATGTA 420  
ACTGATGATG GTGAGTATTT CGTCTATGGA GACGAATACT ATGATGACGC GTCGTCTGTA 480  
AACATTTACA TCAACAGTCC TTGGTGGCAT CCGTCCCTT ATACGTCATG GTATCCATCT 540  
TTCTCCGGCT GGTACAATA TACGTGGAAC TATCCATGGT TCTACTACGG TAGCCATATC 600  
GGATGGGGCG GTTATTACCC CGGATATAAT TGGTATTGGA GCTACTACTA TGATCCTTTC 660  
TACATCCCT ATGGAATCGG TATGGGTTGG GATATCCTT ATGGCTGGGG CAGCTATTAC 720  
GGTTGGGGTG GCTATCCGGG AGTGATACAT CACTACCACC ACTACCCCAA GAAGCCTAT 780  
TCCAATGGTC AGCATTCGG AGCTTACTAT TCTTATGGCC GACCGAATCG TATCAAAGGT 840  
GGAACTCCG GTGCCAAACT TGGGACAGGA GCCTACGATA GAATCAAAA TTCGTCTTCG 900  
CAAAAAATA AGTTCCGATT GCAGTCGAAC AAACCAATA ATAATCTGCA AAATGTCAAG 960  
TCGGGACGTA CCGGCGGAGC CAATAGAGAC CGAAATATAG AAACGGTAAC TCCAAACAAC 1020  
GGGCAAAAGC AGAATCGTCC CGTATTCCAG CAGAATCAST CCGGCAATGA CCGACCGACC 1080  
GGACGGAATA TCCGACGCGA GAGACAGGGG GAAAATAACG ATAGGACATT TTCGACTCCT 1140

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TCTCGTAGCA ATAGTAACGG TGGCTTCTCC ACGCCTTCTC GCTCTTCTTC CGGCTCTATG 1200  
AGCGGAGGTG GCGGACGTAG TGGCCGGGGA CGCAAT 1236

## 5 (2) INFORMATION FOR SEQ ID NO:106

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 1803 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: circular

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(ii) MOLECULE TYPE: DNA (genomic)

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(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

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(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc\_feature  
(B) LOCATION 1...1803

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:106

AGTAATAGCA GCTCCACAAA GTGGTTAATT TATTATCATA TAGAAAAGAC TAAAAGTATT 60  
ATGATCCGCA AGTTGATCTT ACTGCTTGCT CTGATGCCGG TAGCCTCTGT GGCTTTTGCG 120  
GTACCAACGG ACAGCACGGA ATCGAAAGAC AATCGTATCC TTACAAGCAT GCAATCCTCC 180  
TCTTTGAATA GGGATGATGC TCCGGATAAA TGGCAACCTA TGCATGCCAA TTTCAGTATT 240  
CAGAGCGATA TGCTGCTTTC TACTGCCCAA AAGTCCAAGA ACACCTGGTT CGGCAACTCC 300  
TATATCATGG GTATAATCAA GAACAATTAT CTGGAGTTTG GTGCCCGTTT CGAGGATCTC 360  
TATAAGCCCC TGCCCGGACA TGAACCCGAG ATGGGGCGTG GCGTTCCTCA CATGTATGTG 420  
AAGGGAAGCT ATCATTGGGC GGAGCTGACT ATGGGAGACT TCTACGATCA GTTCGGTAGC 480  
GGTATGGTAT TCCGCACCTA TGAAGAGCGC AACCTCGGTA TAGACAACGC GGTTCGCGGC 540  
GGACGTATAG TACTCACTCC TTTTGATGGA GTGCGTGTCA AGGTATTGC AGGACAGCAG 600  
CGTAACTACT TCGACCGCAC GGGCAAGGTA TTCAATTCCG GCCGAGGCTA CCTACTGGGT 660  
TCTGATCTGG AGCTGAATGT AGAGCGTTGG AGCAGTGCCA TCGCGGACAA TGAATATCAT 720  
TTGGCTATCG GGGGATCGTT CGTTTCCAAA CACGAAGCAG ACGAAGATAT ATTTGTGGGT 780  
GTAGGCGAAG ATCGCAAGCG ACTCAACCTG CCGCTCAATG TCCCGATTAT GGGCCTGCGC 840  
ACCAACTTTC AAAAAGGAGG TCTCGCCCTC TACGCAGAGT ATGGATACAA ATACAACGAT 900  
CCCTCGGCAG ACAATGACTA TATCTACCAC GACGGACAGG CTGCACTCCT CTCTGCCTCA 960  
TACTCCAAAA AAGGGATGAG TATCCTGTTG CAGGCCAAAC GTTGTGAGAA CTTTGCTTTC 1020  
CGCAGCAAGC GAAGTGCCCA GCTCACACCG CTTATGATCA ACTATATGCC GGCTTTTACC 1080  
CAAGCTCACA CTTATACGCT GGCGGCCATC TACCCCTATG CTACTCAGCC TCAGGGAGAA 1140  
TGGGCTTTCC AAGGTGAAC TCGTTACAAC TTTGCTCGCC GGACAGCTCT CGGTGGACGC 1200  
TACGGTACCG GCTTGCGTAT CAACGTTTCG CATGTGCGTG GTCTGGACAA AAAGATGCTC 1260  
AAAGAGAATC CCGACGAACT GATCGGAACG GATGGCTACA CCGTTTCTTT CTTCGGCATG 1320  
GGCGACCTCT ATTATTGCGA TATAGATGTG GAGATTACTA AAAAGGTAAG CCCAGGATTC 1380  
AACTTTACGC TCACCTACTT GAATCAGATC TACAATAACA AGGTACTGCA CGGTGCAGCC 1440  
GGAGAGAAGC CTGAGAAGAT CTATGCCAAT ATCTTCGTCT ATGATGGTAA GTATAAGCTG 1500  
AGTAATAAGG TAGCCCTCCG TACCGAACTG CAATATTTGC ACACGAAGCA GGATCAGGGT 1560  
GACTGGATCT ACGGCATGGC CGAGCTCTCT ATCCTGCCTT CTCTGATGCT TTCCTCTCG 1620  
GAGCAGTATA ATATCGGAGA GACCAAGAAA CATATGTCA TGGGGTCTGT CACCTATACT 1680  
CACGGAGCAC ATCGAGTAGC TTTCTCTGCA GGCAAAACCC GTGCAGGGAT GAACTGCTCG 1740  
GGAGGTGTAT GTCGTGTGGT CCCTGAGACT CAGGGATTCT ACCTTTCTTA TAGCACCAT 1800  
CTG 1803

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## (2) INFORMATION FOR SEQ ID NO:107

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 756 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: circular

65

(ii) MOLECULE TYPE: DNA (genomic)

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(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

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(vi) ORIGINAL SOURCE:

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(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc\_feature  
(B) LOCATION 1...756

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:107

10 AGGGGGTTCGA GTTCGGGCAT TTCAGCCCGT GGACGCGACA TCGGTCTCTT ATTTTGTGAGC 60  
GCGTTGCGCA GCTCCTCTCT CCATGGTTCA GAGCGACGCA GTCGGATAAG TTCTTCTGTA 120  
GTCATGTCAA TAAGGCAGAA AATAAGGTTA TTCCATCTCT CGGTATGCGC CCAAACGCAT 180  
GATCATCTCA TCGAAATCCA CTTGGTGTGC ATCGAATTCG GGGCCATCGA CACAGACGAA 240  
TTTCGTCTGT CCTCCACGCG TTATACGACA AGCCCCACAC ATACCGGTGC CATCCACCAT 300  
AATTGTATTG AGAGAAGCTA TGGTCGGTAT CTCGTAACGT TTGGTCAGGA GAGAAACGAA 360  
15 CTTTCATCATC ACAGCCGGCC CGATCGTAAC GCAGAGGTCT ACCGTTTCCC GTTTGATAAC 420  
GCTTTCCACT CCATCCGTTA CGAGGCCTTT CGTCCCATAA GACCCATCGT CTGTCATGAT 480  
GATCACTTCA TCGCTATTGG CTCGCATTTG TTCTTCAAGG ATAACCAGAT CTTTAGTTCT 540  
GGCAGCCAAT ACGACAATTA CACGTTGGCC TGCTTTGTGG AAAGCCTCCA CGATCGGGAG 600  
CAAAGGAGCC ACACCCACAC CGCCTCCGGC ACAACCACT GTGCCGACCT TTTCGATATG 660  
20 CGTACTCTGT CCCAGCGGAC CTACACATC CGTGATATAG TCGCCGACTT CGAGTTCGGC 720  
CAATTTCTTG GAAGATTGTC CCACGGCCTG AACCAC 756

(2) INFORMATION FOR SEQ ID NO:108

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2370 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc\_feature  
(B) LOCATION 1...2370

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:108

CTCTTGTTTT CTCTCCTTT ACCCCGAATG GATCGTCCTA AGCCTTCATA TATTGTTTGA 60  
ATAGCAGCCA TTCTCTGCTT GTTTGTGCGC AGGCCTTTGT TTGCGCAGAG CTATGTGGAC 120  
TACGTGATC CGCTGATCGG GACGCTAAGT TCTTTTGAGC TGAGTGCGGG CAATACCTAT 180  
50 CCGGTGATCG GTTTACCGTG GGGAAATGAAT AGCTGGACAC CGATGACCGG TGTACCCGGT 240  
GACGGCTGGC AATATACCTA CTCGGCACAC AAGATTGCGG GATTCAAACA GACCCACCAA 300  
CCCAGTCTTT GGATCAACGA CTACGGCCAA TTCTCCCTTC TTCCCTTAC GGCACCGCAG 360  
AAGCCATCAT CGAACGACTC CATAGCTCTG ACTAAATGGT GCAAGCAACT CTTTTCGGAC 420  
55 GAACAGACCT CGTGGTTCTC GCACAAAGCG GAGACGGCGA CGCCATACTA TTATAGTGTC 480  
TATTTGGCCG ATTACGACAC ACGCGTGGAG ATGGCTCCGA CCGAGCGTGC AGCTATCTTT 540  
CGCATACGTT ATTCCGGCAA TACCGAAAGT GGCTCCGGTC GATGGCTTCG TCTTGATGCC 600  
TTTACCGGTG GTTCGGAGAT TAGCATCGTG GATCCTACA CCGTAGTGGG CATATCTCGC 660  
AAGAATAGCG GAGGTGTGCC GGCTAACTTC GCCTGTTATT TCATCCTGCA GTCCGATACT 720  
60 CCTATGGCCG ATGTCCTGCT TGAGACAGAT ACCGGCAAGT CAGACGAAGG CACAAGGGCA 780  
TGGGCAGCCT GTCGCTTCGA TTCGCAAGAA GTTACCGTCC GGGTGGCATC TTCTTTTATC 840  
AGTGTGAGC AGGCGGAAAG AAATCTTGCG GAAGTCAAAG GGCAGAGTTT CGACCGGATC 900  
AGACTTGCCG GTCGCGAAGC TTGGAATAAG GTGCTCGGAC GCATACATGT GGAAGGAGGA 960  
ACGAAGGATG AGCGCACTAC ATTCTATTCC GCACTCTATC GCTGTCTGCT TTTTCCCGGT 1020  
CGCTTCTATG AGGAGGATGC TTCCGGCAAT TTTGTGCATT ACAGCCCTA CAATGGAGAG 1080  
65 GTACTTCCCG GTTATCTCTA TACCGATACC GATATTTGGG ACACTTTTCG AGCCCTTTTC 1140  
CCCTGCTCA ATCTGCTGTA TCCCGATGAA AACATTAAAA TTCAGGAAGG TCTGCTGAAT 1200  
GTATATCGCG AGAGTGGCTT TTTCCCGGAA TGGGCCAGTC CGGGCCATCG GGATTGTATG 1260  
GATACCCGTA CACTGATGAA CGSACTCTTG CATGCTACGA AAGCCGTCCA TCCGAAAATC 1320  
70 TCCTCCACGG GTCGCAAGG TTGGGAGTGG TACAACCTCT TAGGTTATGT TCCGGCTGAT 1440  
GCAGGCATCG ATCGCAAGTGC TGCCCGTACG CTCGAATATG CTTATAACGA TTGGTGCATC 1500  
CTCCGACTGG GSCGCACATT GGGTTGGGAT AGAGCTGCAT TGGACACGTT GGCTCATCGT 1560  
TCGATGAACCT ATCGTCATCT GTTCGATCCG GAAACCAAAC TCATGCGCGG TAGAAATCAG 1620  
GATGGTAGTT TCCGGACACC TTTTCCCCT TTCAAATGGG GAGATGTATT CACGGAGGGC 1680  
75 AATGCCTGGC ACTACACTTG GTCGGTCTTT CATGATGTGC AGGGGCTTAT CGACCTGATG 1740

SUBSTITUTE SHEET (Rule 26) (RO/AU)

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5 GGAGGAGATC GCCCGTTCGT GTCTATGCTC GATTTCGGTAT TCAATACTCC TCCTATGTTT 1800  
 GATGAGAGCT ATTACGGATT TGTCATCCAC GAAATCAGAG AGATGCAAAT AGCGGATATG 1860  
 GGCAATTATG CTCATGGCAA TCAACCCATA CAGCATATGA TATATCTGTA TAATCATGCC 1920  
 GGTTCATCCAT GGAAAGCTCA GGAGAGACTA CGCGAAGTGA TGGGGCGGCT CTATCGTCCT 1980  
 ACTCCGGATG GGTATTGCGG CGATGAAGAC AACGGACAGA CTTCGGCTTG GTACGTTTTT 2040  
 TCTGCTTTAG GCTTCTATCC TGTTACACCC GCTACGGATC AGTATGTGCT CGGTTCCGCC 2100  
 ATTTTTTCCA AGGTAATACT CTCTTTTCCC GACGGACACA AAACGGTGTT GCATGCTCCG 2160  
 GCCAACAGTG CCGATACGCC TTACATCCGC TCGATCAGCG TAGAAGGAAA AGAATGGAGC 2220  
 10 TGCAATTACC TGA CTACGA ACAGCTTCG TCTTCTGCAT CCATTCAATG GATGATGGAC 2280  
 ACGAAACCCA ATTATAATCG TGSTATGAAG GAAAGTGACA GACCTTATTC CTTCTCCACG 2340  
 GAGCAACAGC GTCGCGCTAA TCACAGTAAT 2370

15 (2) INFORMATION FOR SEQ ID NO:109  
 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 858 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular  
 (ii) MOLECULE TYPE: DNA (genomic)  
 (iii) HYPOTHETICAL: NO  
 (iv) ANTI-SENSE: NO  
 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS  
 (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...858  
 35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:109

40 ATTTGTGGCA GTAAATGAA TCTATCGGGA TTACAATCTT TCACTATGAT GAAATCCATG 60  
 CGCAGCGTGC TGTGCTACT CTTTCCATTG TCTTTGATCA CTGCTTTGGG CTGTAGCAAT 120  
 AACAAAGCTG CCGAATCGAA GTCTGTCTCT TTCGATTCCG CCTATCTCGA ACGCTACATC 180  
 CCTCTGCGGG CAGACATAGA TACGCCATCG CTGCATGTGA TGATCAGCTA CGTCTATCCT 240  
 TCGGGAGATG ATATGCTCAC AGAGATTTTC AACGGTTTGC TCTTCGGCGA CAGCCTGATG 300  
 GATTTCCTCT CGCCGGAGAA TGCCATGGAA GGCTATGCAC AGATGCTGGG AGAAGACTAT 360  
 CGCTCTAACA ATGCCGAAGC CAATCTGCAA GGGCTTCCTT CTGACCTTTT GGACTATATC 420  
 45 TACAAGCAGG AAAATACCAT CGCTTATTGC GATACGGGAT TGATCTCCAC GCGCATCAAT 480  
 ACATATACTT ACGAAGGCGG TGACACATAC GAGAATACAG TCCGGTTTGC CAACATCCTT 540  
 CGCACCACCG GCAAGGTGCT CGAAGAGCGA GATATATTCA AGATCGACTA TGCGGAAAGG 600  
 CTGTCCGCAC TCATCATAGG ACAATTGGTG CACGATTTCG GCAAGACCAC ACCTGCCGAA 660  
 TTGGATGCAA TAGGTTTCTT CAACGCAGAA GAAATACAGC CCAATGGCAA TTTTATGATC 720  
 50 GATGACAAAG GTCTCACATA CTGTTTCAAT GAGTATCAGA TAGCTGCTTA TGCCAGAGGT 780  
 GCTGTCTATG TCCGTCTCGG ATATGACGTA TTGGCTCCTT TGCTAAGGGA TGATTCCCA 840  
 CTAAGCGTT ACTTGCCG 858

55 (2) INFORMATION FOR SEQ ID NO:110  
 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1134 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular  
 (ii) MOLECULE TYPE: DNA (genomic)  
 (iii) HYPOTHETICAL: NO  
 (iv) ANTI-SENSE: NO  
 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS  
 (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...1134  
 70 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:110  
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	GGGATAATAT	CTGTTCTTTC	ACATGTGGTT	GACCGTCCAC	AATGGGGTGC	TTCTCCCGAA	60
	GCTGCTGGCA	CGCATAGTGT	GTATTTCGATT	CTACATCCCT	CCGCCGGTAT	TATCCGGATC	120
	AGGTCTATGG	GTATTATCTC	AGCCTGCCGT	ATCGCAATTC	TTGCCGGCAA	GCACCCCGGT	180
5	AGCGGTCTGT	CGAGGGGCAA	TGTAGGTATT	CTTTCGTACA	ATCCAGAAAA	CACGCCCGAG	240
	AAAAAGAGAA	AAC TGCAAGA	AAAAAATGTT	TTCTCCCAA	TCCGGCTCCG	TCAATCATTT	300
	AATAATTGTA	TACCTTCGCT	CCCATTTAGA	ATCGATAACA	CAAAAAAAT	CACTGAAATG	360
	AAAAAACTA	CTTTGACAGG	ATCGATATGT	GCTTTACTCC	TGTTTTTGGG	TCTCTCGGCC	420
	AATGCCCAAT	CGAAGTTAAA	GATCAAGAGC	ATTGAGGCAG	CTACCACTTT	CAGTTCGGCC	480
10	ACGGCCGGAA	ATGGTTTTTG	TGGCAATATC	TTCCGGCATG	ACATGAGCAT	ACGGATGAGG	540
	GTACACCACA	GCATTCTGCC	CGAAGGGTTG	GATTTTTCGG	TAGGAATACA	TGAAAGAAGA	600
	GCACACTGGG	AAGAGGCCGG	AAGTCCGAAG	CTCATGTATA	CGAATGTCCC	AAGTATCATT	660
	GGTATTGTTG	AAAAGGTAAT	AGTCTTCGAA	GACGCAGAAG	ACTTTTTTGA	CAAAAAAGCT	720
	CTCGGCCGCT	TCCTCATCAG	TTTGGGGATA	TCCTATACCA	AGCATCTGGG	AGCGTATTGG	780
15	GGATGGACCA	ATGACGCCCA	TATTCTTTTC	TCACCGGATA	CCAAGAGCAA	GGTCCACTAT	840
	GACACCTACA	CAAGAGCTGG	CAGTGACCTT	GTACTTCAGT	CCGAAGATGT	TGCCACAGTG	900
	AGCAATGGCT	TTTCACCGGG	GATCGGACTC	AAAASTTCTA	TTTGGTGGAA	AATGCCCATC	960
	AAGAGCAAAT	ATGATTTTCG	CCTCGGTTTC	AGCCTGGGCT	ATGAGTATCT	GAACCTGCTA	1020
20	TATCCGTATC	GTAATTTCAA	GCTGGATGGA	AATAAGCCGC	TTTCAGCACT	ATCTCCTCGC	1080
	ATGAACCACA	TCGGCCATGT	GGGCTTCAAC	TTTACCGTGG	GTCTTTGGAC	TAAT	1134

## (2) INFORMATION FOR SEQ ID NO:111

- 25 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 3807 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular
- 30 (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- 35 (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- 40 (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...3807
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:111

45	GTAAATGTA	TGGGCAAGTA	TAAAAGAGCT	AAGTACCGCT	ATTGGCTTTT	TCCTTCTGT	60
	TCGGATTATT	ATACCTTTGA	GGGAGTTACT	TTTTTATGCG	CATCTGACGA	TATGACAACC	120
	AAGAAACCCC	AAGCCATTTT	AGACTTAGAG	AAGGCCATATA	ACATTGAAAT	TCCTGATCTC	180
	TCCTCACAA	AAGGGATAAG	CTGGTCGGTA	AATAGATATT	TCAAGCAAGA	TTCTCCGGT	240
50	GCAGTCGTTG	AGCTTTGCTT	GCGAGAATGT	CAGATAGAAA	GCATGACTTG	GCTTATTGAT	300
	TTTCCTGTCT	TAAAAAAGCT	TGATCTATCG	TATAACCCAA	TCAGTAAGCT	AGAGGGTCTA	360
	GAACGTCTTA	CTTCGTAAAC	AAAACCTCGT	CTAAGAAGTA	ACCAAATCCG	TAACTAGAG	420
	GGCCTGGATA	GTCTCACCTC	GCTAACAAAA	CTTCTCTCT	CCGATAACCA	AATCAGTAAG	480
	CTAGAGGGTC	TGGAACGCT	CACCTCGTTA	GCGGAGCTTT	ATCTTTTGGG	TAACCAAATC	540
55	AGTAAACTAG	AGGGTCTGGA	ACGTCTCACG	TCCTTAGCAA	CGCTTGAAC	ATCGGGTAAC	600
	CAAATCCGTA	AGCTGGAGGG	TCTGGAACGT	CTCACGTCT	TAGCAACGCT	TGAACATATC	660
	GGTAACCAAA	TCCGTAAGCT	AGAGGGTCTG	GAACGTCTCA	CTTCGTAAAC	AAAGCTTCGT	720
	CTAAGAAAGTA	ACCAAATCAG	TAAGCTAGAG	GGTCTGGAAC	GTCTCACGTC	CTTAGCAACG	780
60	CTTGAACAT	CGGGTAACCA	AATCCGTAAG	CTGGAGGGTC	TGGAACGCT	CACGTCTTA	840
	GCAACGCTTG	AACTGTCGGG	TAACCAAATC	AGTAAGCTAG	AGGGTCTGGA	ACGTCTCTCT	900
	TCGTTAACAA	AGCTTCGTCT	AAGAAGTAAC	CAGATCAGTA	AACTAGAGGG	CCTGGAACGT	960
	CTCACCTGGC	TAACAAAAT	TTCTCTCTCC	GATAACCAAA	TCAGTAAGCT	AGAGGGTCTG	1020
	GAACGTCTCA	CCTCGTTAGC	GGAGCTTTAT	CTTTTGGATA	ACCAAATCCG	TAAGCTGGAG	1080
	GGCCTGGAAC	GTCTCACCTC	GTTAACAAAG	CTTCGTCTAA	GAAGTAACCA	AATCAGTAAA	1140
65	CTAGAGGGCC	TGCTAGTCT	CACCTCGCTA	ACAAAACCTT	CTCTCTCCGA	TAACCAAATC	1200
	AGTAAACTAG	AGGGCCTGGA	ACGTCTCACG	TCCTTAGCGG	AGCTTTATCT	TTTGGATAAC	1260
	CAATCCGTA	AGCTGGAGGG	TCTTGATGGT	CTTGCTTCC	TAACAAGGCT	TAGTCTAAGG	1320
	CGCAACCAAA	TCAGTAAGCT	GGAAGGACTA	GACAGACTAA	AGSTTTTGAG	AAAACCTGAT	1380
	GTTTCGGGCA	ATGATATTCA	ATCTATTGAT	GATATTAAGC	TATTGGCTCC	GATTCTGGAG	1440
70	CAAACTTTAG	AAAAACTGAG	AATCCATGAC	AATCCATTTG	TTGCATCATC	AGGCTTGATA	1500
	CTCTCTCCTT	ATGATAATCA	TTTCCCGGAG	ATTAAAGCTC	TTCTTGAAAA	AGAAAAAGAA	1560
	AAACAGAAAA	AGACTTCAGT	TGAATATCAC	CCATTTTGCA	AAGTAATGCT	ATTGGGAAAT	1620
	CATTCTTCGG	GTAACCAAC	ATTTCTTAGT	CAATACGATA	CAAATTATAC	GTATCAGAAA	1680
	AATACACATG	TGTTGTGAT	ACATCGAAGC	AATAACCTTA	ATGCGATCTT	TTACGACTTT	1740
75	GGGGGACAGG	ACTATTATCA	TGGGATTTAC	CAAGCCTTTT	TTACCACCCA	ATCGTTATAC	1800

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	CTTCTCTTTT	GGGATGCTAA	GAAGGATCGA	AACTTTGTGA	GCGTAGATGA	TAAAGAATAT	1860
	CAGACTCTTA	ATTTCAATCG	CCCCATTGG	TTAGGACAGA	TAGCCTATGC	CTGCAATCGT	1920
	TGTATGTCCG	TTGGAGGAAA	TCCTGATGGC	AAGGACACAC	CACAGACCAC	AGACGATACA	1980
5	ATTATCATTC	AGACTCATGC	CGATGAAACG	GGCGCTAAGC	AGCAAACCTT	AGGCTGTGCA	2040
	GCCGAGAATG	GAGTATTGGA	AGAAATCTAT	GTATCCTTAG	AGCCCAAGGC	GAATAGTGCC	2100
	GTACATGCCG	TCAACTATCT	GAATGAGCGG	GTGCGAGAAG	TTGTGCGAAG	CAGGAGTAAA	2160
	TCAATTGAGA	TCACAGAAAA	AGATAAGGGA	TTGTACGAAG	CTCTTCCAC	AATCGCCGGT	2220
	GATAATAAAC	ACATCCCTAT	CTCTCTCGAA	GCTCTTGGCG	CTCAATTGAA	TAAGGGAAGA	2280
10	GCTGAAAATG	ATCTTTACAC	CATAGAGTAT	CTACAGACCG	AATTGAACCA	GCTTAGTCTG	2340
	CGAGGGGAGG	TGCTTTACTA	TCGTGAGAAT	GAGAAGCTGA	ACAATTATGT	CTGTTTAGAT	2400
	CCGGCAGCTT	TTGTCCAAAT	GATTCATGGA	GAAATCCTCC	AAAAAGACAA	CATCAATAGA	2460
	GGAACAGTTC	CTAAAGACAT	TTTTGAATGC	AAACTGCATA	ATCTAAGTTC	CGGAAGTATA	2520
	TTTGAAGAAG	ATGGCCAAAA	TGGTAATATG	ATCTTGCAGC	TATTATTGGA	AGAGCTGATC	2580
15	GTATATGAAG	ATAAGGACTG	CTATGTGATA	CCGGGCTATC	TCCCTTTGCA	TTCCGATGAC	2640
	GAAGCCTATA	AATGGCTTAC	TTTGGGATTC	GAGAGGCCCA	ATTTTGTCTT	CAAATTCGAA	2700
	CGTTTTATCC	CCCTTTGGCT	GATCAACCGA	ATTATAGCCT	ACTATGGCCG	GGAAGAAGGT	2760
	GCTCTAAAGC	GGTATTGGCG	AGATCAGGTC	ATCTTCACAG	CAGGCCGTGA	GATGGATAGG	2820
	CAAACGCTTG	AGCAAGAAGA	AGAGAAAGAG	GGTTTGCCCA	AGACGAATGC	CGAGGATTAT	2880
20	CAGATCTGGA	TCAAGCTCGA	CTTTACCGAC	TTGGCCATAT	CGTATTTCAT	CAAAGAGCAG	2940
	AGAAAGACAT	CAGCTAAGSA	TATGCAGCGG	AAAGAGGCTA	CTATCCTCAG	TGATATGTTG	3000
	GATATGTATT	GGAAACAATAT	CCCTCCGAGG	GAGCAAATAG	GAGATAAGGA	TACGGAGCAA	3060
	ACGAGAAGCA	CTATTGCTGA	AACAAACAGA	AAGAAGAGAC	CCATCCAGGA	TCTCTACCTC	3120
	TCCTGTGCCC	AAGCGGATAA	ASATTTGACG	GAGTCTCATT	ATATCCATTT	GGGCACGCTG	3180
25	GACGATGAAA	GCAAGACTAC	GGCGAGGATT	GCAGCCTATC	CGTTGAAGAA	CGGCCGTTATC	3240
	GATAAAGAGC	GGGTGCGAGA	AGTATCGACT	CGTCCCTACA	AACATCTTTC	CGTCAATAAA	3300
	AATCTGGCTA	CTGCAAAACA	GATCTTTTAT	TCCTATTCCA	AAGAGGATCA	GACTGAACCTG	3360
	GAGACCTGTC	TGCAATTTT	CAAACCCCTG	GAGAAGAATG	GTCAGATCGA	GATCTACTAT	3420
	GATAAGTTGA	CTAAGTTTGA	AACACCTATT	CACCTTGAAA	TAAGAAAGCG	TATTGTGCGA	3480
30	GCCGACTGTA	TAATCGCTTT	GATCAGCCAA	CGCTATCTGG	CCACGGATTA	CATCCTGGAT	3540
	CATGAGTTGC	CTGTATTTCG	GGAGTATAAC	AAGACCATAG	TGCCGATATT	GATCAAGCCT	3600
	TGTACATTTC	AAGACGATGA	GTTCCCTCGG	GAGAAATATT	TTGCTCAGAA	AGCTCAAATA	3660
	ATCAATCTTG	GAAAAGAGGG	AAAAACCATT	AAAGCTTATG	ATAGTATTAC	GGCATCAGCC	3720
	CATCGTGATG	AAAATTGGGT	GGCAGTAGTC	AGAGAGTTCA	AAGAGAAGAT	ATTAAGAATA	3780
35	ACAAAACAGG	AGGTAATATC	AGATGAA				3807

## (2) INFORMATION FOR SEQ ID NO:112

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 693 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PORPHYROMONAS GINGIVALIS
- (ix) FEATURE:  
 (A) NAME/KEY: misc feature  
 (B) LOCATION 1...693
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:112

60	AAGTTTATGA	TGAAAAAAGC	ATTTGTTTTC	GTACTACTGG	TTTGCCTATT	CTCCTCGTTC	60
	AGCAGTTCCG	CCCAAACAAC	GACGAACAGT	AGCCGGAGTT	ATTTTACAGG	ACGAATCGAG	120
	AAGGTGAGTT	TGAACCTTAGG	GGTCCCCCCC	GTAAGCACAG	AGSTTTGGGG	AATGACCCAT	180
	GATGCGAAGC	GTCTCCCTTT	CGAAATACCT	ATCTCTTTCA	GTGCTTTCAA	CAGCCAGGGA	240
	GATATAGCTA	CCACTTATTA	CATAGCGAAT	AGCGAGGCAA	CTTTGAATGA	ATGGTGCGAC	300
65	TATGCACACC	CGGGCGGCAT	CGTGAGGATA	GAAGTCTGTT	TTTGGAAAAT	GACTTACAAC	360
	ATACCAACCT	ACAATGCAGT	CTGCACCCGG	ATTACATTGG	AAAATCAAGA	AATAGAAGGA	420
	ACGATCGTCT	TGATACCCAA	GCCCAAAGTC	TGCTGCTGTC	ATGTGTGCGA	ATCGGTGCCT	480
	TGCATCCGAA	CCGAAGCCGG	GAGGGAATTT	ATCCTTTGCG	AAGAAGACGA	CACCTTTGTG	540
70	TCTCACGATG	GTAACGAAGT	AACGATAGGC	GGTAAACCTT	TCTTGCTCAA	TACCAACGTA	600
	AAGATTGTGG	GGGACGTATC	TCAAAAGTAT	GCCGTGGGGG	TAGGAGAAAT	TCGATTCTTG	660
	CAGATTTSTG	CCCAAACAGT	ATCACAAACA	AAA			693

## (2) INFORMATION FOR SEQ ID NO:113

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(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 1689 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:  
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:  
(A) NAME/KEY: misc\_feature  
(B) LOCATION 1...1689

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:113

TCGCTAATCA	ACAATTCAAG	AGACTGGAGG	GCTCCTGTCC	GATTGAGTCT	CAAAAAAAG	60
ACAAAAACTA	TGAAGACAAA	AGTTTTACGC	AAATTCGTGG	TGGCGGCTTT	CGCCGTCGCA	120
ACCCCTCTGC	CTCTCGCCCA	AGCGCAGACG	ATGGGAGGAG	ATGATGTCAA	GGTGGTCCAG	180
TACAATCAGG	AAAAACTGGT	ACAAACGAGG	ATGAGTGTGG	CGGACAACGG	ATGGATCTAT	240
GTAATGACCC	ACAGTGGATA	CGACACCGGC	AATAGCAATG	TGAAGATCTT	CCGCTCCAAA	300
GACCAAGSTG	CCACATACCA	AAAGTTGAGG	GATTGGGATC	CATCGGATGA	TTATCAGTTT	360
CAAGACTTCG	ATATCGTGGT	AACGGGTAAG	AATGAATCCG	ACATCAAGAT	TTGGTCGGTA	420
GAGCTCATGA	ATAAGCCCGG	AGGATATAAG	AGTAGAGTTG	CGGTCTTCAG	TCGCGATGCC	480
AACGGCGAGA	ATGCGAAACT	CGTGTATAAG	GAAGACTTCT	CCAATGTGCA	GTGTACGAT	540
GTGGATATAG	CCTCCAACTA	TCGTTGCGCT	TCTTCTCTTA	ACAATGGTGG	CAACCCCTTT	600
GCTTTGGCTT	TCGCTTACAC	CGGCTTCAAC	AATACGCACA	AAATAAGTTT	TGTGGACTAT	660
GTGTTCTCTC	TGAATGGAGG	GCAAAATTTT	AATAAAACT	TACTCTTCAG	TCAAGATGGA	720
GAGAAGAAAA	TTGACAAGGT	GGATCTCTCA	TTGGGTAGCA	CCTCTGAATC	CATGGGTCAC	780
AATGCCTGGC	CGCTAATGGG	TGTGGTATTC	GAAATGAATA	AACAAGGGGG	AAAAAGCGAT	840
ATCGGTTTCT	TGTCGAACTT	TGTCGACAAT	GATCCCGAAT	TTCAGTGGTC	AGGCCCTATA	900
AAAGTGAGTG	AAAGCGACAT	GTCGTTTCA	CCCAAAATCC	AAATGTTGCT	GGACGAGGAT	960
AACAAATACG	TCAATGGGGA	GAGTTGCCAC	AACTTCATGA	TTACGTACAG	CGATTATGAT	1020
TCTGAATAT	CGGATTTGGG	CATTCGGTAT	GTATATCCCA	AGAAATCGTT	CAAGTATGAA	1080
AAAGGAAAAA	CTCCGACTAT	GGATGATCTG	GTGGAAGCTT	TCCTTACAGC	TTCGTACCAG	1140
AGTGAGACCA	ACTCGGGGCT	GGGGTATGAC	AAGAACGCCA	ATCACTACCT	GATTACATAT	1200
GCCAAAAAAG	AAGAGAACGG	TACGAACACG	CTGAAATACC	GCTGGGCCAA	TTATGACAAG	1260
ATTCATAACA	AAGATTTGTG	GAGCGACACA	TTTACGTATA	CATCATCTGC	CAATGCTCTC	1320
TACACACCTC	AAGTAGACAT	CAATCCGACC	AAGGGTCTCG	TGTGCTGGTC	ATGGGTGGAA	1380
TATCTGCCGG	GCAAACGGAT	CGTTTGGTCT	GATACGCAST	GGACCCATGC	CAACGGTGTA	1440
GAAGACATCG	TAATGCAAGA	AGGCAGCATG	AAGCTCTACC	CGAATCCGGC	TCAAGAATAT	1500
GCTGTGATTA	GCCTGCCGAC	GGCAGCAAAC	TGCAAGGCTG	TTGTTTACGA	TATGCAGGGC	1560
AGAGTAGTCG	CTGAGGCTTC	TTTCTCCGGC	AACGAATACA	GGCTGAACGT	GCAGCACTTG	1620
GCTAAGGGTA	CGTACATACT	CAAGTGCGTA	TCCGATACGG	AGCGTTTCGT	AGAGAAGCTC	1680
ATCGTGGAA						1689

(2) INFORMATION FOR SEQ ID NO:114

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 2358 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:  
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:  
(A) NAME/KEY: misc\_feature  
(B) LOCATION 1...2358

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:114

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	ATCGTTTACC	TTTGTCAC	TATGAACCAC	AGACGATCAA	AAACCATGCT	GACGATCCGA	60
	AACCTTCCTCC	TCTTTTGTG	TCTGTGCGTG	ATAGCGTTTG	CTGCCGATGC	ACAAAGCTCT	120
	GTCTCTTCGG	GTAGACGACT	GACAGAATAT	GTCAATCCCT	TTATCGGAAC	GGCCAATTAC	180
5	GGTACCACGA	ATCCGGGAGC	AGTATTGCC	AATGGGTTGA	TGAGCGTTAC	CCCTTTCAAT	240
	GTCAGCGGAT	CGACAGAGAA	TCGCTTCGAC	AAAGATTGCG	GTTGGTGGAG	TGCGCCTTAT	300
	TCGGCCGACA	ATAGTTACTG	CATCGGTTTC	AGCCATGTGA	ATCTGAGTGG	AGTAGGCTGT	360
	CCCGAACTGA	GTGGAATACT	GCTGATGGCC	ACTTCCGGCA	CATTCGATCC	TGATTACTGC	420
	TGCTATGGCT	CTTCGCTCAG	TCGAGAATAT	GCGCGCCCGG	GAGAATACAA	GGCTGTATTG	480
	GACAAATACG	GTATAGATGC	AGCCGTGACC	GTAACCGAGC	GGACTGCTTT	GACCGAATTT	540
10	GCTTTTCCCG	AAGGAGAAGG	CCATATCCTG	CTGAACCTGG	GACAGGCCCT	AAGCAATGAA	600
	TCGGGAGCCT	CTGTTCGATT	CTTAAACGAC	TCCACAGTCG	TCGGCAGCAG	GCTGATGGGG	660
	ACSTTCTGCT	ACAATCCGCA	AGCAGTTTTT	CGTCAGTATT	TCGTAATCA	GGTGAGTCGG	720
	CGACCGATCT	CTGCGGCTA	TTGGAAGAAG	CAGCCTCCTA	TGACAGTGG	AGCCCAATGG	780
	GATTCGACTG	CAGGGAAATA	TAAGCAGTAC	GACGGCTACA	AGCGTGAGAT	GAGCGGTGAT	840
15	GACATCGGTG	TCCGATTCTC	GTTCAACTGC	GATCAGGGGG	AAAAGATCTA	TGTACGATCG	900
	GCCGTTTCAT	TCGTACGCGA	AGCCAAATGCG	CTCTATAATC	TGGAAGCGGA	GCAAGAAGAG	960
	GTGTTCAAAA	GTGTGCGAGG	GAATCCGGCC	AAGGCTTTCT	CCGCTATACG	CTCTCGCGCT	1020
	ATAGAGCGTT	GGGAGGAAGC	CCTCGGTACG	GTGGAAGTGG	AAGGAGGCAC	ACCGGATGAA	1080
	AAGACGATAT	TCTATACCGC	ACTCTATCAC	TGCTGTATAC	ATCCGAATAT	CCTACAAGAT	1140
20	GCCAATGGAG	AATATCCTAT	GATGGGCAGT	GGCAAAACGG	GTAATACGGC	TCACGACCGC	1200
	TACACCGTGT	TCTCTCTTTG	GGACACGTAC	CGCAATGTAC	ACCGCGTGCT	CTGCCTCCTC	1260
	TATCCCGAGA	AGCAGTTGGA	TATGGTACGG	ACACTGATCG	ACATGTACCG	AGAGAGCGGG	1320
	TGGCTGCCGA	GATGGGAGCT	GTACGGACAG	GAGACCTGA	CGATGGAGGG	CGACCCCTCG	1380
	CTTATCGTCA	TCAATGACAC	TTGGCAAAGG	GGCCTTCGTG	CTTTCGATAC	GGCAACGGCC	1440
25	TATGAAGCCA	TGAAAAAATA	TGCTTCTTCG	GCAGGAGCGA	CCCATCCGAT	CCGTCTTGAC	1500
	AACGACGACT	ATCTCACCCCT	CGGCTTCGTA	COGCTTCGCG	AACAGTACGA	CAATTCCGTA	1560
	TCGCATGCGC	TGGAATACTA	TCTGGCCGAC	TGGAATCTGT	CCCGGTTTGC	CCACGCACTT	1620
	GGGCATAAAG	AAGACGCAGC	TCTATTGCGA	AAACGCTCGT	TGGGCTACAG	ACACTATTAT	1680
30	AATAAGGAGT	ATGGTATGCT	GTGTCCATTG	CTGCCGGATG	GATCATTCCT	CACTCCTTTC	1740
	GATCCCAAAC	AGGGTGAAAA	CTTCGAGCCT	AATCCCGGTT	TCCACGAGGG	CAGTGCTTAT	1800
	AACATATGCT	TTTTCGTTCC	CCACGATATA	CAAGGGCTTG	CCCGGCTGAT	GGGAGGAGCA	1860
	AAGSTTTTTT	CGGAAAGGTT	GCAGAAAGTC	TTGATGAAG	GATATTATGA	TCCGACCAAC	1920
	GAGCCGGACA	TCGCCTATCC	TTACCTCTTC	TCCTATTTC	CCAAGGAAGC	ATGGCGAAGC	1980
35	CAGAAATTGA	CCCGGGAGTT	GATAGACAAA	CATTTTGTGA	ATGCTCCTAA	CGGCTTGCCC	2040
	GGTAATGACG	ATGCCGGTAC	GATGAGTGCT	TGGCTTGCT	ATTCATGCT	GGGATTCTAC	2100
	CCTGACTGTC	CGGGCAGCCC	CACCTATACA	CTGACCTCGC	CGGTATTCCC	CCGAGTTAGG	2160
	ATTGCGCTCA	ATCCGAGTA	TTATCCTCAG	GGGGAGTTGA	TCATTACGAC	CAATACAGAG	2220
	AATCAACCGA	CAGATTCCAT	TTACATCCAT	ACGGTTTCTC	TTGGCAATAA	AACACTTCCG	2280
40	CATGGAACAA	GGCATATCAG	CCATGCCGAT	TTGGTGCCT	GCGGTCACCT	CCGTTACGAA	2340
	CTAAGCAATC	GTCTCCTGA					2358

## (2) INFORMATION FOR SEQ ID NO:115

- 45 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 2442 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular
- 50 (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- 55 (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- 60 (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...2442
- 65 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:115

	CCCCGTTTTC	ATCCCGGAGG	GACACACGCT	CAGCTTTGCA	GAAATGGGAG	AAGAAACCAA	60
	AAATCAAATC	AGTCATCGTG	CTTTGGCGGT	GGCACAGCTC	CGCGATTTTT	TATTATGTGC	120
	AAAATAAGAT	TCAGCCTCTT	GCAGGCTCTT	GTGCTCTGCT	TATTGTTTAC	CTCTTTTCT	180
70	CTCCAAGCTC	AAGAGGAAGG	TATTTGGAAT	ACCCTCTTGG	CTATCCACAA	GACGAAAAAA	240
	GCCGTAGAAA	CGCCCAAGAA	AGTCTTTGCC	GTAGCCAACG	GAGTACTTTA	CTCGGTGGGC	300
	AAAGAAGCTC	CCCATGAGGC	AAAGATCTTC	GACCGTATCA	GCGGACTCAG	CGATACATCG	360
	GTAAGCAGCA	TAGCCTACTC	CGAGCAACTA	AAATCCTTGG	TCATATACTA	TGCATCAGGC	420
	AATATCGACA	TCTTGGACGA	AGCAGGCCGT	GTGACCAACG	TACCTGCATT	GAAAGACAAT	480
	ATCGATCTGA	TAGACAAAC	GCTCAATCGC	CTTTTGATCG	TAGGCAACAG	GGCTTATTTC	540
75	GCAGGAGGAT	TCGGCCTCTC	CGTCTGGAT	GTGCGCGAAG	CTCGCATACC	GGCTACCTAC	600

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	GCCAAAGGGAA	CTAAGGTGAC	CGATGTGGCT	AAGTTGGACA	ATGATCGCTT	GCTGATGCTG	660
	AAAGAAGGGC	AGCTCTTCAT	CGGAAAAGAG	ACCGATAACC	TGCAAGATCC	GGCCGCATGG	720
	ACAGCCTTGT	CTTTGAATTT	GCCGATGGGC	TCGGTCACCG	GTCTGGGCAT	TGTCGGGGAA	780
5	GACATCTGTT	TCCTGCTCGC	CGATGGCCGT	GTATATGTGG	CTGCAAAACCA	ATCGTTTGAG	840
	CCGGAGCTAT	TGCTCTCTTC	CTCCGCCGAT	TCACGACTGT	ATGTGACGGA	TCGTGGTCTG	900
	TTTCATCTGT	CCGAGAATCG	AATTTATTTT	ATAGAAAAAG	GTGCAAAAC	GACACAATTT	960
	CCTATAGCCG	ACSTCCTTGG	TGTCCGTGCC	ATGAACGAAA	GCAATACGGC	ATACATAGCA	1020
	TTGGGAGAAG	AAGGTTTGGC	TTCATTCTTT	CTCGCAGAGG	GAAGTACGGC	CGAAGCCATG	1080
10	CCTGTAGCAT	TCGACGGACC	GGGGGACAAT	GATTTCTAAG	AGATGCGGTT	TAGTCACGGA	1140
	CGTCTGTATG	CAGCCAGCGG	ACTCTGGGGA	ACAAACCTGA	TGGGACATGC	CGGTATGGTG	1200
	AAGCTATACG	ACGGCAACCG	ATGGACTAAC	TTCGACAAAG	AGACCGTACA	GGAACAGTTG	1260
	GGCGCGGGAT	TCAGTTTCAA	TGATGCTATC	GATATAGCTG	TTTCCAACGG	AGACCCCGAT	1320
	CACTTTTTTG	TCGGTACATG	GGGAAACGGT	CTGTTGGAAT	TCAAGGATGG	CAAAGCGATA	1380
15	GCTCGCTATT	CGGGAAACGA	AACTGCTATC	GCAGAAATGA	ATCCCGGAGA	TGCCCGTGTG	1440
	AAAGCGATTG	CCTTTGACAA	TAAGGGCAAC	CTCTGGGGGA	CGCTCGGTGC	CGTAGGCAAG	1500
	AACATCTTCA	TGTACGATCC	GCAGAGTAGC	ACATGGCATT	CTTTCAGCTA	TCCGGATGTA	1560
	GCCAATCTGG	CCTCCTTCGG	CAATATGATT	ATCCTACCCA	ACGGAGACAA	ATGGGTAAAT	1620
	ATCCTTCACC	GTAGTGGCGG	ATCCACGCGC	AAAGGTGTCT	TGATCTTCAA	CGATCGGGGT	1680
20	ACACCGGAAA	CGACTTCGGA	CGACAGCCAT	CTTTACGTGG	AGCAGTTTGT	CAATCGCCTC	1740
	GGGCGAGCCA	TAGGACATAA	GACTATCTAT	GCAATGGCGG	TCGATCATAA	CGGCTCTGTC	1800
	TGGATGGGAT	CGGATATAGG	CATTTTCGGC	GTCTACAATG	CAGCCGGAGT	ATTGTCTCTG	1860
	ACTTCTACCC	CTATCGCTGT	TCGGCCGGTC	GGAGGAGAAG	AACCCAATTT	GTACTATGTG	1920
	CTGGACAAAG	TGAGCGTGAC	AGACATCGTC	GTGGACAAAC	TCAATCACAA	ATGGGTTGCC	1980
25	ACCCAAGGGA	CAGGACTCTA	TCTCCTTTCC	GAAGATTGCA	GTAAGATCCT	CGCGCAATTT	2040
	ACCGTAGAAA	ACAGCCCTTT	GCTTTCTAAC	AACATACTAT	CCCTGGCCTT	AAATGACGAT	2100
	AACGGACTGC	TGTACATCGG	TACGGCGGAC	GSACTGATGA	CGTTCCAAAC	GGGTACGGGG	2160
	ATGGATCAG	CTTCCGAACI	GGACGGCGTC	TATGTATAAC	CCAATCCGCT	AAGGCCGGAA	2220
	TATCCCGATG	GCGTCAACCA	TGCCGGAGTG	CAAGCCGGCT	GTAGTGTCAA	AATCACCGAT	2280
30	ACCACCGGCA	GACTGCTATA	CCAGACTGAG	AGCGTAACCA	CCGAAGTCAA	ATGGAATGCT	2340
	CGAGGTGCCG	ATGGCAATAG	GGTAGCTTCG	GGCGTATATG	CCGTTGCAGT	GTACGATCCG	2400
	GTATCGAAAA	AGTCCAAACT	AATTCGCTTC	GCAGTGATTG	GC		2442

## (2) INFORMATION FOR SEQ ID NO:116

- 35 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 3486 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
40 (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- 45 (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:  
50 (A) ORGANISM: PORYPHIROMONAS GINGIVALIS
- (ix) FEATURE:  
(A) NAME/KEY: misc\_feature  
(B) LOCATION 1...3486
- 55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:116

	GCTATTCTC	AGATGAAACG	AATACTTCCA	ATAGTCGCAT	TCCTTTCTCT	CTTCCTTGCC	60
	CTTGCTTTGC	CTGCCGAAAGC	GCAACGAGCT	ATGGGGGAAGA	CGGCCGACCG	TTCGCTAATG	120
	GCTT'CGGGA	ATTGGGTCAA	GATACGTGTC	GATGCAAGTG	GAGTGTATCG	CCTTACGGAC	180
60	GAACAGCTCC	GTGCCAATGG	CTTCTCCGAT	CGGTCCAAAG	TAGGTGTGTT	CGGTTATGGT	240
	GGAGGGGTGC	TTCGGAAGA	TCGTAGCCGG	ATCACGACAG	ACGATTTGCC	TCCGGTACCG	300
	GTA'CTCGTC	AGGGCAATGC	GCTGTATTTC	TATGCCGTGG	GCCCGGTGAC	ATGGTTCTAC	360
	AATCCGGCCA	AAACCACCAT	GGAGCATACG	GTGAATACAT	ACAGTACGCA	TGGCTACTAC	420
65	TTCCTGTGCG	ATGCTGCCGG	AGCACCTTTG	CAGATGTCCC	AATATACGGG	TGGAGGTGCG	480
	TCGGCCGAGG	CTTTGATCGA	CTACTACGAT	GAGCTGATGC	TCCATGAACA	GGAATTGTAT	540
	TCGCCCAAAG	AATCGGGACG	AGATCTGTAT	GGCGAGTCTT	TCASTGCAGT	CAATACGCGT	600
	ACGGTCAAGT	TCCCTTTGAG	GGGCAACACC	CGCTCGTCTG	GCGAATCGGG	TACCGTATTC	660
	TCATACATAG	CCAAGGCCAG	ATCGGCCGGT	GGCGCCCGTG	AGATGTGCGT	CTCGGCGAAT	720
70	GGCATTCTGA	TCTTCAGCGA	TCTTTTTC	ATGACATCGA	ATGAAGTCTC	CAATTCCCTAT	780
	TTGGCCGGGA	AGAAGCGT'CG	TCTCTATCAC	AGTACGCCGA	TGAACAGCTT	GGTCAATGAG	840
	TTCCGCTTGG	ACGCGAACTA	TAGCATGACA	GGAGATGCGG	TCAATCTGGA	TTTCATAGAG	900
	GTGGCTACAC	AGAACGACCT	CCGGTACGAT	GGCGCACCCA	TGCATATCAG	GCGGTTTTC	960
	AATTTGCCCG	TTTTGGGGGG	CGAGTCTCTG	CGGTTTCGTTA	TCASTGAGGT	GCCGAGTCT	1020
75	CTGGTGGTTT	TGCAGGCCAA	TTCTTCCCTG	ACAGCATCGC	TTGTTCCCGT	TAAGACTGTC	1080
	GGGGATAAGA	CCATTGAGTT	CGTGGCTCCG	CCGAAGGGTC	AGGATCGTAG	GACTATCAAT	1140

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	ACGTTTATATG	CCGTGGACTT	GTCACAGGCT	TCTGCTCCGG	AGATCCTCGG	AGCGGTACCC	1200
	AATCAAAACC	TGCATGGAGA	GGAAATCCCT	GATCTGATCA	TTGTCTCTAC	TCAGGCGCTC	1260
	CTCCTTGAGG	CTGATCGACT	GGCCACCTAT	CGTAGAGAGA	AAAACGGGCT	GAAGGTTTTG	1320
	GTCGTGTTGC	AGGAACAGGT	GTTCACAGAG	TTTTCGGGTG	GAATCCCGA	TGCTACAGCA	1380
5	TACCGCCTCT	TTGCCAAAT	GTTCTACGAC	AGATGGAAGG	CAATGCACC	TGTGGGAGAG	1440
	ACCTTCCCGA	TGCAAAATGCT	TCTCTTCGGT	GATGGGGCTC	ATGACAACAG	GAAGGCTCTC	1500
	GTAGCTTGGC	AGAAACCGTA	TCTCCAACAA	ACGGAGTTCT	TGCTGACATT	CCAAGCCGTC	1560
	AATTCGACGA	ACGTAAACAG	TTATGTGACG	GATGATTACT	TCGGCTTGCT	GGATGATCAG	1620
	CCGGCCTCGG	TCAATATCGG	TTGGCGCAAT	TATAATATGG	CTGTAGGGCG	ATCCCCCGTA	1680
10	CGTACTCCGG	CCGAAGCTCG	CATCGCAGTG	GACAAGACCA	TCCGATATGA	GGAGGATCGA	1740
	GAGAGTGGTG	CCTGGCGTAT	TCGTGCCTGT	TTTGGCGCAG	ACAACGGGGA	CAAGCACGCA	1800
	ACCGAGACTT	CCCCTTTGAT	CGATACCGTC	AAGCGTTATG	CTCCTGCCAT	CATGCCGGTA	1860
	GCGCCTTTTC	AGGACGTATA	TCCGCATGTC	ATCGAGAACG	GGTTGCACAG	CATTCCGGGT	1920
	GCAAAAGAAAA	AGATGCTGGA	AACCCCTTCA	TCGGGTATTA	TCCTGCTTAA	TTATGCTGGT	1980
15	CATGGCGGTC	CTGCCGGATG	GTCCGACGAG	CATTTGCTGA	CGCTCAACGA	TATACACAAA	2040
	TTCAATTATA	AGCATATGCC	CATTTGSAAT	ACTGCCACGT	GCGACTTTGC	CAACTATGAC	2100
	AGTCAGACGA	CCTCGGCAGG	GGAGGAGGTT	TTCTCTCATG	AGAAGAGTGG	CACTCCGATC	2160
	ATGTTCTCGA	CTACGCGTGT	CGTTTACAAT	ACGCAGAAATG	AGAAGATCAA	TGGTTTTATG	2220
	CTTCGCGGTA	TGTTCCGAGAA	AGCTAAGGAT	GGGCGTTATC	GTACGATGGG	CGAGATTATC	2280
20	CGATCGGCCA	AACAGGGGAT	GCTCAGTACT	GTTTTCCCGG	ATTTCGATCAA	CCAGTTGAGT	2340
	TTCTTTCTGA	TGGGTGATCC	GTCCGTGCGT	ATGAATCTTC	CTACCCACAA	AGTGCAATTG	2400
	ACCGCAATCA	ACGGGCAGGA	TCCCGAAGGG	CAGTATGGAA	CTATTATGCT	CAAGTCTTTG	2460
	GAACGGGTAG	CTCTGAAGGG	TAAGGTAACC	GATGAAAAGG	GGACATTGCA	CGAGACATTG	2520
	AGTGGCAAGG	TTTTCTCTGAC	CGTCTTCGAT	GGCAGAAAGA	AAATGACAGC	TTTGGAAGAG	2580
25	GAGGGAAACG	ATCTCTCTCT	TGTATATTAT	GACTATCCTA	ACGTGATGTA	TGCCGCTATT	2640
	GCCGAGGTGA	AAGACGGGACT	CTTCGAAACT	TCGTTTATCG	TACCCAAGGA	TGTGAACAT	2700
	TCCGAGCAGC	AAGGCCGGAT	CAATCTTTAT	GCTTATAACG	AGAGCACAAA	GGCGGAAGCC	2760
	ATGGGGGTAG	ACTTCTCCAT	CAGAGTCCAA	CCGGGTATTC	CTGATGAGGT	AACGGAAGAT	2820
	AATACACCGC	CTGAAATCAT	AAGCTGCTTC	CTCAATGACA	GTACATTCCG	ATCGGGAGAT	2880
30	GAGGTAAATC	CTACTCTCT	GTTTATGGCC	GAAGTATTCC	ACTTGAATGG	AATCAATATC	2940
	ACGGGTAGCG	GAGTAGGGCA	TGATATTACG	CTTTGTATCG	ATGGCCGTGC	CGACCTGACC	3000
	TACAACCTCA	ATGCATATTT	CACAAGTTCC	GCTACGGATG	CAGGTGTGGG	CACTATTCTC	3060
	TTCATGATAC	CGGCTTTTGGC	CGAAGGAGAT	CATACTGCCC	GACTGACGGT	TTGGGACATT	3120
	TTCAATAATG	CCGTCCATCA	TGACTTTTCA	TTCAGAGTGG	TAGATGGCAT	TGCTCCGGAT	3180
35	GTGGCTGATG	TGATTTCTATT	CCCGAATCCG	GTACGCGAGA	GTGCTACGTT	CCGAATCTTC	3240
	CACATCGGCC	CCGGAAGCGA	TTTGAACGTG	GCCGTGGAGA	TCTATGACTT	CACCGGTGCT	3300
	CTTGTAACA	GTTTGCCAGT	CAAGACCTAT	TCTCTTCTCT	ACGGAGAACC	TATAGAGATC	3360
	AAGTGGGATC	TGACCTCCAA	ATACGGAGTG	AAGATCGGAA	ACGGATTCTA	CCTCTATCGT	3420
	TGTGTGGTGA	ACTCTCCCGG	AGGACAGACG	GCCTCCATGG	CCAAGAAAAT	GATCGTGTA	3480
40	GGACAA						3486

## (2) INFORMATION FOR SEQ ID NO:117

- 45 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 2919 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: circular
- 50 (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- 55 (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:  
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- 60 (ix) FEATURE:  
(A) NAME/KEY: misc\_feature  
(B) LOCATION: 1...2919
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:117

65	TTTACACCG	GAATTGACTT	GCATATAGAA	AGCCAAATGA	AGAACTTTT	CCCATTATTA	60
	TTACTCATAT	TGTCGATTTT	GGTCGGATGT	GGAAAAAAG	AAAAACACTC	TGTAACGTAA	120
	ATCGCCCGAG	AGAAAAAGCG	TATTACTGCA	TTGCTGTACG	AAAAAGAACT	CCCCACTGAT	180
	TCTGTAAAC	AGCTTTACGA	GAACAGCGTA	CAGAACAAGA	ACCTTGTGGG	ACAAATGTTA	240
70	TTCCGATCG	AGGTCCGGCA	ACGGATGCCG	AATATGTCCC	AATACACAGA	TGCGATGCTA	300
	TATCACCAAA	AAGGGTTGAA	CGCTGCATTG	AATCTAAGGG	ACACCATCGT	AGCCGCACAA	360
	GCATGGAATC	ATCTCGGAAC	GGATAGCCGT	CGTATCGGTG	CTTTGGCAGA	AGCTTCGGAT	420
	TATCATTACA	AGGCTCTTTC	CTTGATAGAA	TCTTTTAGCG	GAAACCAGAA	TAGGCCTGCG	480
	ATCAAAGCCA	GATCGCGGCG	CCTGAACGGC	ATCGGCAACA	TCAATCTTGA	GTTAGGATAC	540
75	CATGATGAGG	CCGAAAAGAA	TTTCTGAAA	GCACTGCAAG	GTGAGAAAGA	ACTCGACAGT	600

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5	CCTCTCGGGC	AAGCTATCAA	CTATGCGAAC	CTCGGACGTA	TCTATCGACA	ACGCAAAGAA	660
	TACGACAAGG	CTCGTACCTA	CTTCCTCTTG	TCTCTGGAGC	AGAACAATAT	GGCAGAGAAT	720
	CTGATGGGTA	TCGGACTCTG	TAGCATCAAT	CTCGGAGAAG	TAGACGAAGA	AAAAGGGGAT	780
	TATCAAAAGG	CTTTGCAAGA	GTATGCCACG	GCATACAAAC	TGATGGAACA	GTTGTCCGAT	840
	CGATGSCACT	GGCTGAATTC	CTGTATCCCG	ATGGCACGTA	TCAATCTCAA	ACAAGGTAAC	900
	GAAAGGCTCT	ACCAGCATTT	CATTTCTTTG	GCCGAAGGGA	CTGCGAAAGA	AAATTAATTCG	960
	ACTTCACATC	TGATAGAAAT	ATACAATCTT	CAATACGAGA	ATCTCGAGCG	TAAAAAAGAA	1020
	TACAAACAAG	CCCTCGAAGC	ATTCTGTCTG	AGCAAGACGT	TGAGCGACAG	CATGTCCATT	1080
10	GCGCACAAGG	TCAGCAGCAT	ACAAGAAACG	CGATTCAACT	ACGAACGAAA	CAAGTCCCAA	1140
	AAAGAGCTTG	AAGAAATACA	GCAAGTAAGC	AAGGCAAAAC	AAGAGAAATC	GAAGTTTATC	1200
	CTCTTGAGCA	CTCTTTTTCG	CCTTTTCATC	TCGATTCTTT	TGATTTCTGT	TCTGACATAT	1260
	GCATACCGTC	AGGGCAAGAA	GCATAACAAG	CTGATCAAAG	AGACGGATAA	ACTTCGCTCC	1320
	GGCTTTTTC	CCGGTATTAC	ACACGAATTT	CGTACGCCTA	TCACCGTCAT	ACAAGGTTTG	1380
	AATGAGAAAA	TGAGTTCAAG	TCCTGATCTC	CAAGCATCGG	ACAGAACCGA	GCTGCACAAG	1440
15	ATAATAGACA	GACAGAGTAG	CCATATGCTG	AATTTGGTGA	ACCAGCTGTT	GGATATTTGC	1500
	AAGATCAGAA	GCGGAGTATC	CACGCCCGAA	TGGCGCAATG	GCGACATCGT	CTCCTTCGTA	1560
	CAGATTCTCA	TCGATTCGTT	TGCACCATAC	GCACAGGCTC	AAGACATAAC	CTTGAGAGCTA	1620
	CAACCCGAGA	GCAAACCTAT	TGTCGTGGAC	TTCGTCCCTT	CCTACTTGCA	AAAAATCATA	1680
20	TCCAATCTTT	TGTCCAATGC	CATCAAGTAT	TCTTTAGCCG	GAGGGAGAGT	GGTCATATCT	1740
	CTGGCAAAAA	CCAAGAATGA	AAAAAATCTG	ATCATACCGG	TTGCAGACAA	TGGCATAGGA	1800
	ATAGATAAAA	CTGATCAGGC	TCATATCTTC	GACATCTTCT	ATCGAGGACA	GTCCGCTACC	1860
	GAAAAGCATG	GATCAGGCGT	CGGACTCTCG	TTTACCAATA	TACTGGTCTG	AAACCTTCGA	1920
	GGTACGATCA	AAGTGAAAG	CCAGCCGGGG	AAAGGAAGTG	CCTTCACCAT	CAGTATTCCT	1980
25	ACACAAAACC	AGTCCCTCTT	GGCAGAGATT	CTTCCTTGGC	TACCCCTCCTC	CGATGACATT	2040
	GTCAATGCCG	TCCACATCGC	GCCCGATGAC	TCACCGACAT	CTCCGATGGT	AGCAGCTCTG	2100
	AATCATCGCT	TCGAGGACGA	ACGTCCGACC	ATACTGCTCG	TCGAGGACAA	TAAGGATATC	2160
	AACCTGCTCG	TCAAACCTACT	CCTTTGCGAT	CGCTACAATG	TGCTATCCGC	CGCAAACGGA	2220
	AAAGAGGGTA	TAGCCCTCGC	TACCGAGCAT	ATTCCCGACA	TTATCATTAC	GGATATTATG	2280
30	ATGCCGATAA	TGGATGGGAT	AGAAATGACA	ATCCGGATGA	AGCAATCGCC	TCTGCTCTGT	2340
	CACATTCCTA	TTGTGCTTTT	GACGGCCAAG	AGTACCGAAC	AGGACAGATT	GGAGGGAATC	2400
	AAAAGCGGTG	TAGTCTCTTA	TCTATGCAAG	CCATTCTCTC	CGGAGGAGCT	TTTGATGCGG	2460
	ATCGAGCAGC	TTCTGAAAGA	CCGTGAGTTG	CTCAAGAAAGT	TCTATATGCA	AAAACTCATG	2520
	CTGGATCGGA	AGCCGGAGGA	GGAGCCTCAA	CCGATAGATG	ACAGCAGTAT	GCAGTTTCTC	2580
35	CTTGCTGCCA	AAGATGCAAT	GTCCGGTGGA	ATCAAACAAA	ATCCGGATTT	TTCCGCTCAA	2640
	GACTTGGCCG	AAAAAATGTG	CATGAGTCCA	TCCCAACTCA	ACAGAAAGCT	CACGAGTGTC	2700
	GTAGGTTGCT	CCACCATCGG	CTACATACAG	CAGATCAAGA	TAAAAATGGC	CTGCAAGCTC	2760
	CTTGCCGATG	AGAGCAAAAA	CATCTCCGAC	ATTAGCATTG	AGGCAGGCTT	TTCCGATCCG	2820
	GCTTACTTCT	CTCGCACCTT	CAACGCTAC	ATGAACITGCT	CTCCCTCCCA	ATATCGGCAA	2880
40	AAACTCCTTG	CCATGCCGGG	GAGCGACAAG	GAGACAGTT			2919

## (2) INFORMATION FOR SEQ ID NO:118

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1689 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
- (A) NAME/KEY: misc\_feature
- (B) LOCATION: 1...1689
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:118

65	CATCATAAAA	CATATCAAAC	AATGAAAAAG	CTTTTACAGG	CTAAAGCCTT	GATTCTGGCA	60
	TTGGGACTCT	TCCAACCTGCC	CGCAATCGCC	CAAACGCAAA	TGCAAGCAGA	CCGAACAAAC	120
	GGTCAATTTG	CAACAGAAGA	GATGCAACGA	GCATTCCAGG	AAACGAATCC	CCCTGCAGGT	180
	CCTGTGCGTG	CTATCGCTGA	GTACGAACGC	TCTCGAGCCG	TTTTGGTACG	CTACCGTTTC	240
	GGTATCCCGA	TGGAATTGAT	CAAAGAGCTG	GCCAAGAACG	ACAAGGTGAT	TACCATTGTG	300
70	GCGAGTGAAA	GCCAAAAAAA	CACCGTTATA	ACCCASTACA	CCCAAAGCGG	TGTGAATCTC	360
	TCTAATTGCG	ATTTTCATCAT	TGCGAAAACT	GACTCTTACT	GGACACGCGA	CTATACCGGT	420
	TGGTTTCGCA	TGTACGATAC	GAACAAAGTA	GGTCTCGTGG	ACTTTATTTA	TAACCGCCCT	480
	CGTCCTAACG	ATGATGAATT	CCCCAAATAC	GAAGCACAAAT	ATCTGGGCAT	CGAGATGTTC	540
	GGGATGAAGC	TCAAGCAGAC	CGGTGGCAAC	TACATGACCG	ACGGATATGG	ATCCGCTGTG	600
75	CAGTCACATA	TCGCATATAC	GGAGAACTCC	TCTCTGTCTC	AAGCTCAAGT	AAATCAAAAG	660

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5 ATGAAAGACT ATCTCGGCAT CACACATCAT GATGTGGTAC AAGATCCGAA CGGCGAATAT 720  
 ATCAACCATG TGGACTGTTG GGGCAAGTAT TTGGCACCAG ACAAATCCT CATCAGGAAA 780  
 GTGCCTGACA ATCAACCTCA GCACCAAGCC CTGGAAGATA TGGCAGCCTA CTTGCGAGCA 840  
 CAGACCTGCG CATGGGGAAC GAAGTACGAG GTATATCGCG CTTTGGCCAC CAATGAACAA 900  
 CCGTACACGA ACTCTCTGAT TCTGAACAAC AGGGTATTG TTCTGTCAA TGGCCCGGCC 960  
 TCCGTGGACA ACGATGCTCT GAACGTCTAT AAGACGGCAA TGCCCGGTTA CGAAATTTATA 1020  
 GGTGTCAAAG GGGCTTCAGG AACACCTTGG TTAGGAACAG ATGCCCTGCA TTGTCTGTACT 1080  
 CACGAGGTAG CGGATAAGGG CTATCTCTAT ATCAAGCACT ACCCGATACT GGGCGAACAG 1140  
 10 GCAGGCCCTG ATTATAAGAT CGAAGCAGAT GTCGTCTCAT GCGCCAATGC TACTATCTCG 1200  
 CCGGTACAAT GTTACTATCG TATCAATGGT TCCGGTAGCT TTAAGGCTGC TGATATGACG 1260  
 ATGGAATCAA CAGGTCACTA TACTTATAGC TTTACAGSTC TTAACAAGAA TGATAAGGTA 1320  
 GAATACTATA TCTCTGCCGC TGACAATAGT GGTGCGCAAAG AGACTTATCC CTTTATCGGC 1380  
 GAACCTGATC CTTTCAAGTT TACGTGTATG AACGAAACCA ATACATGTAC TGTGACCGGA 1440  
 15 GCTGCCAAAG CTCTTCGTGC ATGGTTCAAC GCCGGTCGTT CAGAAGTGGC TGTTCGGTA 1500  
 AGTTTGAATA TTGCCGGCAC ATATCGGATA AAGCTTTATA ACACCGCAGG AGAAGAAGTC 1560  
 GCTGCAATGA CCAAGGAATT AGTAGCAGG ACAGTGTCT TCAGTATGGA TGTGTATTCT 1620  
 CAGGCTCCG GCACATATGT TCTGGTTGTT GAAGGAAATG GAATCCGTGA GACAATGAAA 1680  
 ATTCTCAA 1689

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(2) INFORMATION FOR SEQ ID NO:119

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1311 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PORPHYROMONAS GINGIVALIS

(ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...1311

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:119

45 ACCACAAATA GAAAACCAAA TACTAATATG AAACCTTCAT CTAAGAAAAT CTTAGCAATC 60  
 ATTGCATGCG TGACGATGGG ACATGCTGTG CAGGCACAGT TTGTTCCGGC TCCCACCACA 120  
 GGGATTCGCA TGTCTGTCAC TACAACCAAG GCCGTAGGCG AAAAAATCGA ATTGTTGGTT 180  
 CATTCCTAG AGAAGAAAGG CATCTGGATC GATCTCAATG GGGATGCCAC TTACCAACAA 240  
 GGAGAGGAAA TAACCGTATT CGATGAGGCA TACCACGAAT ACACGATCGG GACGCAAAAC 300  
 CTCACTATCT ATGGTAATAC GACCCGATTG GGCTGTGCGT CTACCGGTGC AACGGCTGTC 360  
 50 GATGTAACGA AAAACCCATA TCTGACCTAT CTCGCATGCC CGAAAAATAA TCTGAAATCA 420  
 TTGGACTTGA CGCAAAACCC AAAGCTGCTG CGAGTTTGGT GCGACTCTAA CGAAATAGAA 480  
 AGTTTGGACC TGAGTGGCAA TCCGGCTTTG ATCATCCTCG GCTGTGACAG GAATAAGCTG 540  
 ACTGAGCTGA AGACCGATAA CAACCCCAAG TTGGCCTCTC TTTGGTGTTT TGATAATAAC 600  
 CTGACGGAGT TGGAACTCAG TGCCAATCCT CGTCTCAATG ATCTTTGGTG CTTCCGTAAT 660  
 55 CGGATCACGA AACTCGATCT GAGTGCCAAT CCTCTATTGG TAACACTTTG GTGCACTGAC 720  
 AATGAGCTTT CGACCTTGGA TCTTTCCAAG AATTCCGACG TTGCTTACCT TTGGTGTTCA 780  
 TCGAACAAAC TTACATCCTT GAATCTGTCG GGGGTGAAGG GACTGAGTGT TTTGGTTTGT 840  
 CATTCCAATC AGATCGCAGG TGAAGAAATG ACGAAAGTGG TGAATGCTTT GCCCACACTA 900  
 TCTCCCGGCG CAGGCGCTCA GAGCAAGTTC GTCTTGTAG ACCTCAAGGA CACTGATGAG 960  
 60 AAGAATATCT GTACCGTAAA GGATGTGGAA AAAGCTAAAA GTAAGAACTG GCGAGTATTT 1020  
 GACTTCAACG GTGATTCTGA CAATATGCTT CCATACGAAG GAAGTCCGAC ATCGAACTTG 1080  
 GCAGTAGATG CTCCCAGTGT CAGGATATAT CCCAATCCGG TAGGAAGATA TCGCTCTGTC 1140  
 GAGATCCCGG AGTCTCTTTT AGGGCAGGAA GCTGCTTTAT ACGATATGAA TGGGGTAAAA 1200  
 65 GTCTATAGTT TCGCGGTAGA GTCTCTCTGT CAGAACATTG ACCTGACACA TCTTCCCGAC 1260  
 GGCACCTATT TCTTCCGTCT CGATAACTAT ACCACTAAGC TCATCAAACA G 1311

(2) INFORMATION FOR SEQ ID NO:120

70 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 954 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular

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(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

5 (iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:  
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

10 (ix) FEATURE:  
(A) NAME/KEY: misc feature  
(B) LOCATION 1...954

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:120

AATCATTTGA	AGACAAATAT	CAAGATGAGA	AAAACAATAA	TTTTCTGCTT	GTTGCTCGCC	60
CTATTTGGCT	GTTCTTGGGC	ACAAGAAAAG	GTCGATGAAA	AAGTATTCCT	CGCAGGAACA	120
AGTATTTTTA	GGGGCATCCT	TGAAAAGGTG	AAAGCACCGC	TTATGTATGG	AGATCGTGAG	180
GTATGGGGTA	TGGCTCGTGC	GAGCGAGGAT	TTCTTTTSTA	TACTTCCCGT	TACGGATGAC	240
CTCACTCCCG	TGCTTTTCTA	TAACCGTCTT	ACAAACGAAC	CCTGCTTTGT	GTCAGACCAA	300
GGAATAACTG	AGTATTTCAA	ATTGCTCAA	GAAGGTGATT	ACATTGAAGT	CGAAGGAAGC	360
TCTGTATTCA	TGGCGAATCT	TTTGTACTAT	CGTTTTTTCC	CGACAAGAA	TACCTCCTAT	420
AATGCTCCCA	TTGAAGGTGT	TGTGAGCAAG	ACGGGAAATC	CTGCTTTTAC	AATCCCGATG	480
CTCCCGGGGG	TTTCTGATTG	CATAGAAATC	TCAAACAACC	GCAAAGTCTT	TCTGACCAAT	540
CAATTAGGGG	TTGTAAACAT	CACGTACGGG	ATGGAACCTC	CGATTATTGC	CGGAGTCTCT	600
GCTTCCTATG	GATCTTCCGT	CCGGGTGTAT	GGTCATGTCT	CACAGCGGTG	GGACATCATA	660
GGCCATTGCT	ATTTGGATAT	CTACCCAACC	AATTGCTATC	CGCTCAGCAC	GAAACCCGTT	720
GCAGGAGACG	ATGAGGTTT	TGTCAAACAA	CAAGGCAGGC	AAATAGAGAT	CGATAGCAAC	780
AGCCCCATAG	TCCAAGTGGT	CGTATACGAT	CTTGAGGGGA	AAAGTGTTTT	TCGCAAAAGA	840
ATGACCGAAA	ACGCTTATAC	CCTATCCTTT	AGAGCACCCA	TGCTCGGCTT	TATGACCATC	900
ATGATCGAAA	CACAAAATTC	GATTATCAAT	AAAAAACTTA	ATGTTACACA	GCTA	954

(2) INFORMATION FOR SEQ ID NO:121

35 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 1383 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
40 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

45 (iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:  
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

50 (ix) FEATURE:  
(A) NAME/KEY: misc feature  
(B) LOCATION 1...1383

55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:121

AGACGGGCAG	TTAAAAATCCG	ATCACCTCCC	CATATCCACT	CATTATTTGT	ACGTAAATGT	60
CTTTTTTTCAG	ACTTTTAAATA	CTTATATTTA	TCCCGAAAAA	TTACCCAAGA	GAGATTGGGT	120
CGATTGTCGA	TCCGTCCTAA	GTCATACAAT	CCAATAATCA	TTATTGAAAT	GAAAAAACA	180
ACCATTATTT	CTTTGATTGT	CTTCGGTGCT	TTCTTTGCAG	CCGTGGGCCA	AACCAAGGAC	240
AATTCTTCTT	ACAAACCTTT	TTCGAAAGAA	GATATTGCCG	GAGGAGTTTA	CTCTCTCCCG	300
ACTCAAAATC	GTGCGCAGAA	GGACAATGCC	GAGTGGCTTC	TTACAGCGAC	CGTCTCCACA	360
AACCACTCTG	CAGATACTCA	CTTTATCTTC	GATGAGAACA	ACCGCTATAT	CGCTCGTGAC	420
ATAAAAGCCA	ATGGGGTAAG	AAAATCCACG	GACTCCATTT	ACTACGATGC	CAACGGGCGA	480
ATATCGCATG	TGGATCTTTA	TATCTCGTTC	AGTGGCGGAG	AGCCTGCACT	CGACACCCGA	540
TTCAAGTACA	CCTATGATGA	CGAGGGAAAG	ATGACCGTGA	GGGAAGTATT	CATGCTGGTA	600
ATGGATCCGA	ATACACCTAT	CTCACGCTTG	GAATATCATT	ATGATGCACA	GGGCAGACTG	660
ACCCACTGGA	TTTCTTTTGC	TTTCGGGGCA	GAATCCCAAA	AGAATACGTA	TCACTATAAT	720
GAAAAAGGTC	TGTTGGTCAG	CGAAGTGCTG	AGCAATGCAA	TGGGGACAAC	CTATTGAGAC	780
ACCGGCAAAA	CGGAATACAG	CTATGACGAT	CGAGATAATA	TGGTGAAGGC	CGAGTACTTC	840
GTCGTCCAGC	AAGGAAAGGC	ATGGCAAGTA	CTCAAAAGAG	AGGAATACAC	CTATGAGGAC	900
AATATCTGCA	TACAATATTT	GGCTATTAAC	GGTACCGACA	CAAAGGTGTA	CAAGCGAGAC	960
ATCGAGAGCG	ATAAGTCCAT	CTCCGCAAA	GTCATTGACA	TTCCGTCAAT	GCCGGAACAG	1020
ACCTGGCCTA	ATATGTACGG	ATTCAACGCA	AAGCGACTGA	AAGAGACTTA	TTCTCTCTAC	1080
GAAGGAGATG	TGGCTACTCC	TATATTCGAC	TATATCTATA	CGTACAAGGC	TCTTACCTCA	1140

SUBSTITUTE SHEET (Rule 26) (RO/AU)

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5 ATGGCAACAC CTTTCGACAGA AGCTCAGGTA GCAGTCTATC TCAATCCGTC AACGGACCGG 1200  
TTAGTGATTG TGGCCAACGG CATCACACAT CTGAGCATGT ACGACTTGCA GGGTAAGCTT 1260  
ATCCGTGATT GTGCCTTGAG CGCGGATAAG GTGGAAATGG GTGTCGGATC TTTGACCAAA 1320  
GGGACATACC TGCTTAAAGT GAATACGGAT CAGGGAGCCT TTGTGAGAAA AGTCGTGATT 1380  
CGA 1383

## (2) INFORMATION FOR SEQ ID NO:122

- 10 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 1353 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: circular
- 15 (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- 20 (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:  
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- 25 (ix) FEATURE:  
(A) NAME/KEY: misc\_feature  
(B) LOCATION 1...1353
- 30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:122

ATGGCAAAAG TTATAAAAAC AAAAAAAGGC CTGCACTTA ATCTGAAAGG AAAACCGCTG 60  
CCCGAGATGC TGGCCGAACC GGCCCAAAGT CCTACTTACG CGGTCGTGCC CGACGATTTT 120  
GAAGGTGTTA TCCCCAAGGT GACGGCTCGT CCGGGGGATA AGGTGCGTGC CGGCTCAGCA 180  
CTGATGCACC ACAAGGCATA TCCGGAGATG AAGTTTACAA GTCCGGTTAG CGGCGAAGTG 240  
35 ATCGCGGTGA ATCGCGGTGC CAAGCGCAAG GTGTTGAGCA TCGAGGTGAA ACCGGACGGA 300  
CTGAACGAAT ACGAGTCATT CCTGTGCGG GATCCGCTCG CCTCTCTGC CGAACAGATC 360  
AAGGAGCTTT TACTGTCGAG CGGTATGTGG GGTTTTATTA AGCAACGTCC TTACGACATA 420  
GTGGCTACAC CGGATATAGC TCCACGCGAC ATTTATATTA CTGCCAACTT TACTGCACCA 480  
TTGGCTCGG ACTTCGATTT CATCGTTCGA GGAGAAGAAC GCGCCCTGCA GACTGCCATC 540  
40 GATGCCTTGG CCAAATCAC GACAGGAAAG GTGTATGTGG GCCTGAAGCC GGGTTCATCT 600  
CTGGGCTTGC ACAATGCAGA AATCGTAGAA GTACACGGAC CTCATCCGGC AGGTAACGTG 660  
GGCGTGCTGA TCAATCATAC GAAGCCAATC AATCGGGGCG AAACGGTGTG GACGCTCAAG 720  
GCTACCGACC TGATCGTGAT CGGACGTTTC CTGCTTACGG GCAAAGCCGA TTTTACCAGA 780  
ATGATTGCCA TGACCGGCTC AGACGCTGCA GCTCACGGAT ACGTCCGTAT TATGCCGGGT 840  
45 TGCAATGCTT TTGCTTCCTT CCCC GGCCGA CTGACAATAA AGGAATCTCA CGAGCGTGTG 900  
ATCGATGGCA ATGTGCTGAC CGGTAAGAAG CTCTGCGAGA AGGAGCCTTT CCTGTACGCC 960  
CGGTGTGACC AGATCAGGCT GATCCCGGAA GCGGACGATG TGGACGAAC CTTCGGGTGG 1020  
GCTGCACCCC GTCTCGATCA GTACAGCATG AGCAGAGCTT ATTTCTCTTG GTTGCAGGGG 1080  
50 AAAAACAAAG ASTACGTACT CGATGCCCGS ATCAAGGGTG GCGAACGTGC TATGATCATG 1140  
AGCAACGAGT ATGACCGCGT TTTCCCGATG GACATCTATC CGGAGTATTT GCTCAAGGCT 1200  
ATTATAGCAT TCGACATCGA CAAGATGGAG GACTTAGGCA TATATGAAGT GGCTCCGGAG 1260  
GACTTTGCCA CTTGCGAATT TGTGGATACA TCCAAGATCG AGCTGCAGCG TATCGTTTCG 1320  
GAGGGCTTGG ATATGCTCTA TAAGGAAATG AAT 1353

## (2) INFORMATION FOR SEQ ID NO:123

- 60 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 585 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: circular
- 65 (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- 70 (vi) ORIGINAL SOURCE:  
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:  
(A) NAME/KEY: misc\_feature  
75 (B) LOCATION 1...585



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## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:123

5 ATGGATAAAG TGAGCTATGC TCTGGGATTG AGCATCGSTA ATAATTTCAA GTCTTCGGGC 60  
 ATCGACAGCG TCGTTATGGA TGATTTCATG CAAGGTCTGT CTGATGTACT GGAAGAAAAA 120  
 GCCCTCAGC TCTCGTATGA CGAGGCCAAG CGCGAAATAG AGGCGTATTT CATGGATTG 180  
 CAGCAGAAGG CTGTCAAACCT GAACAAAGAG GCCGGAGAAAG AATTCCTCAA GATAAATGCA 240  
 CACAAGGAAG GTGTGACGAC CTTACCGAGC GGCTTGCAAT ACGAAGTCAT TAAGATGGGA 300  
 GAGGGCCCGA AACCCACCCT TTCGGACACG GTAACCTGTC ATTATCACGG TACGCTCATC 360  
 10 AACGGTATCG TTTTCGATAG CTCTATGGAC AGGGGAGAAC CGGCCAGTTT CCCTCTAAGA 420  
 GGAGTTATAG CCGGCTGGAC GGAGATTCTT CAATTAATGC CTGTAGGATC CAAGTGGAAA 480  
 GTAACATAC CGAGCGATCT GGCSTATGGA GATCGTGSTG CCGGCGAACA TATCAAACCG 540  
 GGTAGTACGC TCATTTTAT AATCGAATTA TTGAGTATCA ACAA 585

15

## (2) INFORMATION FOR SEQ ID NO:124

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 819 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- 30 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...819

35

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:124

40 ATGAAAAAAG CATTACTTAT TGGTGCTGCT CTTTGGGAG CAGTCAGTTT TGCAAGTGCT 60  
 CAGTCTTTGA GCACAATCAA AGTACAGAAC AATTCAGTAC AGCAACCTCG TGAGGAAGCC 120  
 ACTATTCAAG TTTGTGGAGA ATTGGCAGAG CAAGTTGACT GCATTGGGAC AGGTAATTCT 180  
 GCAATCATAG CCGCTGCAGC GAAATTTGAA AGCGATGATC TCGAAAGCTA TGTGGCTGG 240  
 GAGATCATGA GTGTTGATTT CTTCCTGGA TATAAAGCGT GCAAGTACAC ATCTGCAGTC 300  
 TGGGCTGATG ATATGACCAT TTTGGGCCAA TCAGAAGATA GTGATCCCGA AATGCAGACT 360  
 45 ATCAACAATC TTGCTCTCAA GACTAGTGTC AAGATTGAAG CCGGCAAGAA TTACATAGTT 420  
 GGTATATATG CTAATACCGC AGGTGGACAT CCTATCGGAT GTGATCAGGG CCCTGCCGTT 480  
 GATGTTATG GAGATTGGT TTCTATATCA GAAGATGGTG GTGCTACTTT CCCTCCGTTT 540  
 GAATCTCTTC ATCAAGCAGT TCCTACCTTA AATTACAACA TCTATGTCGT TGTTCAATTG 600  
 AAGAAGGGTG AAGGTGTTGA GGCTGTTCTT ACCAACGACA AGGCTAATGC TTATGTTTCA 660  
 50 AATGGCGTTA TCTATGTAGC CGGAGCTAAT GGTGTCAGG TATCTCTGTT CGACATGAAC 720  
 GGTAAGGTTG TTTATACCGG CGTTAGCGAA ACGATTGCAG CTCCTCAGAA GGGCATGTAT 780  
 ATCCTCCGTG TAGGTGCTAA GAGCATCAAG CTGGCTATC 819

55

## (2) INFORMATION FOR SEQ ID NO:125

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1662 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- 65 (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...1662

75

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## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:125

5 ATGCCAAGAA TTATGAAATT AAAAATTGCA CTCAGACTGC TGCTGGCGAC TTTTGCCATA 60  
GTTTATTATTA GCCCTCTGGC CAAGGCCAG ATGGATATTG GTGGAGACGA TGTATTGATC 120  
GAGACGATGT CCACCTATC AGGATATTCA GAGGATTTT ATTACAAGAT GGCTGTGGCA 180  
GACAATGGAT GGATCTATGT GATGTTGGAT TTCTCTCGTA TTTATTTTGA TGATGTCAGG 240  
CTGTATCGTT CCAAAGACGG TGGTGCTACT TACCAAAAGT TAGGGTCTTT GGGGCTTTG 300  
GTGCCTTATG ACTTCGATGT CTCGCATTGC GATTTTATG TAACGGGAAA GGATGAAGAT 360  
GATATCAATG TTTGGACAGT CATGACAGCA TTCGAATATG TAGGTGGTAC TATTGGCAAT 420  
10 GGGGTTTTGC TGATGCATCG CCATGATGCA GATATCAATA ATACAGAGTG TGTGTACAAG 480  
AAGGATTTCC CTAATAATAG ACTGATGGGT GTAGCCATCG CCTCCAATA CCGTGCGCC 540  
TCTCCTTACG GTTTGGGGGG CGATCCTTTT GCTCTCGCTG TCGCCSTTAG TGCTCCGGA 600  
AGCGATCACA GCTTCTTGA CTATATTTT TCGTTAGATG GTGGAGTACA CTTGAGCAA 660  
AAGCGTATTT ACACAAGACC CCAAAACTG ACTATCAATA GAGTAGACCT TTCATTAGGC 720  
15 AGTACATCTC CTCTCTTGG ATTTAATACT TGGCCACTAA TGGGAGTCGT ATTCGAAATG 780  
AATAAGAAACC TTGATGGCTT CGACATTGGT TTCATTTCCA ACTTTGTGGA CTATGATCCC 840  
CGCTATGCGT GGTCTGAACC GATAATAATA GAAGAAGACT GTGGATGGAC TGATTTTAAT 900  
CCTTTGGGAG CACTAAGTAT AGAGATCCAA ATGATGTTGG ATGACAATTC GGATAATACC 960  
GTGGGTGGAG AACGCTCCCA TAACCTCCTG ATCACTTACC CGGGCCATTA CGTATATCCG 1020  
20 AAGCAATCTT TCAATTATTC TCCCGGACAT ACACCGACAA AGAAAGATCT GGTCTTTAAA 1080  
CACTGTATAG GTATTCCGGC TTTGGCATA GATAAGGAAG GCGATCGTTA TCTGACTACT 1140  
TTTCAAGATC ACAATCTAAT GAGATACAGA TGGATCAAA ACATGACAT TAACCTTTT 1200  
TATGGTTGGA GTTGGCCATA TGTATATGCA AAAGAAGCTA AAGATAAAAA GAGGCGCCGT 1260  
CCGCAAGTAG CACTCAATCC TACCAATGGA AAGGCTTGT GGTATGGCA TACTCGCAAG 1320  
25 AGCCCATATG ATGAAACCAA ACCACATCCT ACTCCTGTAA TTATTAACA TTTCCTATGG 1380  
TCCGATACGG AGTGGGTACA TGCTCTGGAC GTGGGGGACG TATTGCAGAA GGAGGGTAGC 1440  
ATGAAGCTCT ACCCAATCC TGCCAAAGAA TATGTTCTGA TCAACCTACC CAAAGAAGGG 1500  
GGGCACGAGG CACTCGTATA CGACATGCAG GGCGAATCG TGGAGAAAGT TTCATTTTCA 1560  
30 GGGAAAGAAT ATAAGCTGAA TGTGCAGTAT CTGTCCAAAG GTACGTACAT GCTGAAAGTT 1620  
GTAGCGGATA CGGAGTATTT CGTGGAAAAA ATCATTGTAG AG 1662

## (2) INFORMATION FOR SEQ ID NO:126

35 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 1650 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: circular  
40 (ii) MOLECULE TYPE: DNA (genomic)  
(iii) HYPOTHETICAL: NO  
45 (iv) ANTI-SENSE: NO  
(vi) ORIGINAL SOURCE:  
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS  
50 (ix) FEATURE:  
(A) NAME/KEY: misc\_feature  
(B) LOCATION 1...1650

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:126

55 ATGAAATTAA AAATGCACT CAGACTGCTG CTGGCGACTT TTGCCATAGT TTTATTTAGC 60  
CCTCTGGCCA AGGCCAGAT GSATATTGGT GGAGACGATG TATTGATCGA GACGATGTCC 120  
ACCCATACAG GATATTCAGA GGATTTTTAT TACAAGATGG CTGTGGCAGA CAATGGATGG 180  
ATCTATGTGA TGTGGATT TCTCTGATT TATTTTGATG ATGTCAGGCT GTATCGTTCC 240  
60 AAAGACGGTG GTGCTACTTA CCAAAAGTTA GGGTCTTTGG GGTCTTTGGT GCCTTATGAC 300  
TTGATGTCT CGCATTGCGA TTTTATTGTA ACGGGAAGG ATGAAGATGA TATCAATGTT 360  
TGGACAGTCA TGACAGCATT CGAATATGTA GGTGGTACTA TTGGCAATGG CGTTTGTCTG 420  
ATGCATCGCC ATGATGCAGA TATCAATAAT ACAGAGTGTG TGTACAAGAA GGATTTCCCT 480  
AATAATAGAC TGATGGGTGT AGCCATCGCC TCCAACCTACC GTGCGCCCTC TCCTTACGGT 540  
65 TTGGGGGGCG ATCCTTTTGC TCTCGTGTG GCGTTAGTG GCTCCGGAAG CGATCACAGC 600  
TTCTTGGACT ATATTTTTTC GTTAGATGGT GGAGTACACT TTGAGCAAAA GCGTATTTAC 660  
ACAAGACCCC AAAAAGTGC TATCAATAGA GTAGACCTTT CATTAGGCAG TACATCTCCT 720  
TCTCTTGSAT TTAATACTTG GCCACTAATG GGAGTCGTAT TCGAAATGAA TAAGAACCTT 780  
GATGGCTTCC ACATTGGTTT CATTTCCAAC TTTGTGGACT ATGATCCCCG CTATGCGTGG 840  
70 TCTGAACCGA TAATAATAGA AGAAGACTGT GGTGGGACTG ATTTTAATCC TTTGGGAGCA 900  
CTAAGSTATAG AGATCCAAAT GATGTTGGAT GACAATTCGG ATAATACCGT GGGTGGAGAA 960  
CGCTCCATA ACTTCCGTGAT CACTTACCGG GGCCATTACG TATATCCGAA GCAATCTTTC 1020  
AATTATTCTC CCGGACATAC ACCGACAAAG AAAGATCTGG TCTTTAAACA CTGTATAGGT 1080  
ATTCCGGCTT TGGCATACGA TAAGGAAGGC GATCGTTATC TGACTACTTT TCAAGATCAC 1140  
75 AATCTAATGA GATACAGATG GATCAAAATC GATGACATTA ACTCTTTTTC TGGTTGGAGT 1200

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TGGCCATATG TATATGCAAA AGAAGCTAAA GATAAAAAAG GCGCGCGTCC GCAAGTAGCA 1260  
 CTCATCCTA CCAATGGAAA GGCTTGTGG GTATGGCATA CTCGCAAGAG CCCATATGAT 1320  
 GAAACCAAC CACATCCTAC TCCTGTAATT ATTAACATT TCCTATGGTC CGATACGGAG 1380  
 TGGGTACATG CTCTGGACGT GGGGGACGTA TTGCAGAAAG AGGGTAGCAT GAAGCTCTAC 1440  
 5 CCCAATCCTG CCAAGAATA TGTCTGATC AACCTACCCA AAGAAGGGGG GCACGAGGCA 1500  
 GTCGTATACG ACATGCAGGG CCGAATCGTG GAGAAAGTTT CATTTCAGG GAAAGAATAT 1560  
 AAGCTGAATG TGCAATATCT GTCCAAAGGT ACGTACATGC TGAAAGTTGT AGCGGATACG 1620  
 GAGTATTTTC TGGAAAAAAT CATTGTAGAG 1650

10

(2) INFORMATION FOR SEQ ID NO:127

- 15 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1170 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular  
 20 (ii) MOLECULE TYPE: DNA (genomic)  
 (iii) HYPOTHETICAL: NO  
 25 (iv) ANTI-SENSE: NO  
 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS  
 30 (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...1170

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:127

35 ATGAAACGAT TACTCCCCTT TCTCCTTTTA GCAGGACTCG TAGCCGTAGG AAACGTGTCT 60  
 GCTCAGTCAC CCGAATCCC TCAAGTGGAT GTACACACTC GCATCGCAAG AAATGCCCGT 120  
 TATCGACTGG ACAAGATCAG TGTCCTGGAT TCTCGTCAGA TATTCGATTA CTTCTATAAA 180  
 GAAGAAACGA TACCCACTAA AATACAAACG ACCACAGGAG GTGCAATTAC AAGCATCGAT 240  
 TCGCTTTTCT ATGAAGACGA CAGGTTGGTT CAGGTGCGCT ATTTTGACAA TAACCTTGAA 300  
 40 TTAAACAAG CGGAGAAAGTA TGTATACGAC GGTCTAAGC TGGTCCTTCG AGAAATTCGC 360  
 AAGTCGCCGA CAGACGAAAC GCCAATAAAG AAAGTTAGCT ATCACTATCT CTGTGSCAGC 420  
 GATATGCCTT TTGAGATTAC GACAGAGATG AGCGATGCTT ATTTTGAAAG CCATACGCTT 480  
 AACTATCTGA ATGGAAAGAT TGCCCGAATA GATATCATGA CTCACAGAA CCCATCGGCC 540  
 GAATTGATCG AAACGGGTAG AATGGTATAT GAGTTTGATG CCAATAATGA TGCTGTACTG 600  
 45 CTTCGTGACA GTGTATTTCT TCCTCTTCAA AACAAAGTGGG TAGAAATGTT TACTCACCCT 660  
 TATACATAGC ACAATAAGCA TAATTGTATT CGTTGGGAAC AAGACGAATT CGGCACCTTC 720  
 ACCCTTGCCA ACAACTTCCA ATACGACACC ACTATCCCTC TGTCGTCTGT ATTGTTCCCC 780  
 ACGCATGAGG AGTTCTTCCG TCCTCTTCTT CCCAATTTTA TGAAGCATAT GCGTACGAAG 840  
 CAAACGTATT TCAATAACTC CGGAGAAGGC TTGTCAGAGG TATGCGATTA CAACTACTTC 900  
 50 TATACCGATA TGCAGGTGAA TGCACTGACC GATGTTGCCG TGAACGAATC GATCAAGATT 960  
 TATCCTCGTC CTGCCACGGA TTTCTGCGT ATAGAAGGTT CGCAACTGCT TCGCCTTTCG 1020  
 CTATTCGACA TGAACGGGAA GCTCATCAGA GCTACCGAAT TGACAGGCGA TTTGGCCATT 1080  
 ATCGGAGTTG CATCTCTTCC GAGAGGCACT TACATCGCAG AAATAACTGC TGCAACAGC 1140  
 55 AAAACCATAC GTGCAAAAGT ATCGCTCAGA 1170

(2) INFORMATION FOR SEQ ID NO:128

- 60 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1233 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular  
 65 (ii) MOLECULE TYPE: DNA (genomic)  
 (iii) HYPOTHETICAL: NO  
 70 (iv) ANTI-SENSE: NO  
 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS  
 75 (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature

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(B) LOCATION 1...1233

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:128

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5  ATGAGACAGC ATTTATCTCT ATTTCTTTT ATCTTGTTC TGCTTCTTGC CTTCTCTTAT      60
   GTCGGTTGCA GAACAGTCCG ACAAACACCT AAGCAGTCGG AACGGTACGT CGTAGTCCTG      120
   TCTTTGGACG GCTTCCGACC GGAATATACC GATCGGGCAC GTACACCGGC GTTGGATCGG      180
   ATGGCAGACG AGGGATTGAG CGGGTCGCTC CAACCATGCT TCCCCTCGCT TACATTTCCC      240
   AATCATTACA GCATGGCTAC GGGGCTTTAC CCCGATCATC ACGGTATCGT AGCCAATGAG      300
10  TTTGTGGATT CGCTACTGGG CATCTTTCGT ATATCCGACC GAAAAGCCGT GGAGACCCCC      360
   GGATTTTGGG GCGGCGAGCC GGTTTGGAAT ACGGCCGCAC GCCAAGGCAT CCGTACCGGT      420
   GTCTAGTTTT GGGTAGGATC CGAAACGGCT GTGAACGGAA ATCGGCCGTG GCGGTGGAAA      480
   AAATTCTCCT CCACCGTCC GTTTCGTGAC CGTGCCGACT CCGTCATCGC GTGGCTCGGA      540
   CTGCCCGAAA AGGAGCGACC GCGCTTGCTC ATGTGGTACA TCGAGGAGCC GGATATGATC      600
15  GGACACAGCC AAACGCCCGA AAGCCCGCTG ACACTGGCAA TGGTAGAGCG GTTGGACAGT      660
   GTGGTGGGCT ATTTCCGCAA GCGGTTGGAC TCTCTGCCCA TAGCCGCACA GACCGACTTC      720
   ATCATAGTAT CCGATCAGCG TATGGCCACG TACGAAAATG AGAAATGTGT CAATCTGTCT      780
   CATTATCTSC CTGCGGACAG TTTCCTCTAC ATGGCCACCG GGGCCTTCAC CCCTTGTAC      840
   CCGAAGCCCT CCTATACGSA GCGAGCCTAT GAGATCCTGC GGGCCATTCC ACATATATCG      900
20  GTTTACCGCA AGGGGGAGGT GCCCAAGCGT TTGCGCTGTG GCACCAATCC TCGTTTGGGC      960
   GAACTGGTCS TGATTCCGGA CATAGGCTCC ACCGCTTTT TCGCAATAAA TGAAGACGTT      1020
   CGTCCGGGAG CGGCACATGG CTATGACAA CAAACACCGG AAATGCGGGC TTTACTCGGC      1080
   GCTGTCGGAC CCGATTTCGG TCCGGGAGT AGGGTGGAAA ACCTGCCGAA TATCACCATC      1140
   TATCCGCTCA TATGAGGCT GTTGGGTATA GAGCCTGCAC CCAACGATGC GGACGAAACG      1200
25  TTGCTGAACG GCCTGATCCG AGACAAACGA CCA                                1233

```

(2) INFORMATION FOR SEQ ID NO:129

- 30 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 738 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular
- 35 (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- 40 (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- 45 (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...738

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:129

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50  ATGAAAGTAG GTTTGTTCAT CCCCTGTTAT GTCAATGCAG TGTATCCGGA AGTGGGTATC      60
   GCCACGTACA AACTGCTGAA GAGTTTGGAC ATAGATGTCG ACTACCCGAT GGATCAGACA      120
   TGTTTGGGCC AGCCTATGSC CAATGCCGGA TTCGAACAGA AAGCTCAAAA GCTGGCTTTG      180
   CGATTGGAAG AGCTGTTCGA GTCGTATGAT GTAGTCGTAG GGCCATCGGC CAGTTGCGTT      240
55  GCTTTCGTGA AAGAAAACTA TGATCATATC CTCAGACCGA CAGGACATGT CTGCAAGTCG      300
   GCAGCCAAAG TTGGGGATAT ATGCGAGTTC TTGCACGATG ACCTGAAGAT CACGAGCTTC      360
   CCTCCCGAT TCGCCCATAA GGTGAGCCTG CACAACAGTT GCCACGGTGT GCGCGAATCG      420
   CATCTGTCCA CCCCCAGTGA AGTGACCCGA CCGTACCACA ACAAGGTGCG CCGGCTATTG      480
   GAGATGGTGC AGGGCATAGA GGTATTTCGAG CCGAAGCGAA TAGACGAATG CTGCGSTTTC      540
60  GGCGGTATGT ACTCGGTGGA GGAGCCGGAG GTATCCACCT GTATGGGGCA TGACAAGGTG      600
   CTGGATCACA TATCCACAGG TGCGGAGTAC ATCAGAGGSC CGGACAGCTC GTGCCCTCATG      660
   CATATGCAGG GAGTGATAGA CAGAGAGAAA TTGCCGATCA AGACAATTCA TGCASTAGAA      720
   ATTTTAGCAG CAAACTTA                                738

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(2) INFORMATION FOR SEQ ID NO:130

- 70 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 738 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- 75

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

5 (vi) ORIGINAL SOURCE:  
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:  
10 (A) NAME/KEY: misc\_feature  
(B) LOCATION 1...738

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:130

15	ATGGATATTTG	TAAATATGGC	CGATAAAGCT	CTTGTAAGTG	AGATGAGAGA	TGTGACGCTC	60
	TGTCAGGAGG	AAAACGTCAT	TTTTCAAAT	TTGAATCTGA	CCCTTTCCGC	CGGAGACTTC	120
	GTCTATCTGA	TAGGCTCAGT	GGGATCGGGG	AAGAGCACTT	TGCTGAAGGC	TTGTATGCT	180
	GAGGTGCTTA	TCTCTGCCG	TTATGCCCGC	GTGATAGATT	ATGATCTGGC	AAAGTTGAAA	240
	CGGAAGCAGT	TGCCCTATCT	GCGCAGGAAT	TTGGGCATTG	TGTTTCAGGA	TTCCAGTTG	300
20	CTGAACGGAC	GTACTGTTC	GGAGAATTG	GATTTCTGTT	TGCGAGCTAC	GGACTGGAAT	360
	AACCGAGCG	ATCGCGAGCA	GCSTATCGAG	GAGGTTTGA	CCCGTGTGGG	AATGTCTCGG	420
	AAGGCTTATA	AGAGACCGCA	CGAACTGTCC	GGAGGGGAGC	AACAACGTGT	GGGTATAGCC	480
	AGAGCTTTGC	TGGCGAAGCC	TGCGTTGATC	CTGGCCGACG	AACCCACAGG	CAACCTCGAT	540
	TGCGTGACCG	GATTGCAGAT	CGCTTCTCTG	CTCTACGAAA	TCAGTAAGCA	GGGCACTGCA	600
25	GTACTTATGA	GCACGCACAA	CAGCAGCCTG	CTGTCGCATC	TGCCGGCAGC	GACATTGGCC	660
	GTTCGTAAGA	ATGGCGATGC	CTCCTCTTTG	GTCCGAGCTGA	GTGCAGATGC	TGTTTCAAGA	720
	AAAAATACGG	AAATAGAT					738

(2) INFORMATION FOR SEQ ID NO:131

30 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 723 base pairs  
(B) TYPE: nucleic acid  
35 (C) STRANDEDNESS: double  
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

40 (iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:  
45 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:  
(A) NAME/KEY: misc\_feature  
(B) LOCATION 1...723

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:131

55	ATGGCCGATA	AAGCTCTTGT	AGTGGAGATG	AGAGATGTGA	CGCTCTGTCA	GGAGGAAAAC	60
	GTCATTTTTC	AAAATTTGAA	TCTGACCCTT	TCCGCCGGAG	ACTTCGTCTA	TCTGATAGGC	120
	TCAGTGGGAT	CGGGGAAGAG	CACTTTGCTG	AAGGCTTTGT	ATGCTGAGGT	GCCTATCTCT	180
	GCCGGTTATG	CCCGCGTGAT	AGATTATGAT	CTGGCAAAGT	TGAAACGGAA	GCASTTGCCC	240
	TATCTGCGCA	GGAAATTTGGG	CATTGTGTTT	CAGGATTTC	AGTTGCTGAA	CGGACGTACT	300
	GTTGCGGAGA	ATTTGGATTT	CGTTTTGCGA	GCTACGGACT	GGAAAAACCG	AGCCGATCGC	360
	GAGCAGCGTA	TCGAGGAGGT	TTTGACCCGT	GTGGGAATGT	CTCGGAAGGC	TTATAAGAGA	420
60	CCGCACGAAC	TGTCCGGAGG	GGAGCAACAA	CGTGTGGGTA	TAGCCAGAGC	TTTGCTGGCG	480
	AAGCCTGCGT	TGATCCTGGC	CGACGAACCC	ACAGGCAACC	TCGATTCTGGT	GACCGGATTG	540
	CAGATCGCTT	CTCTGCTCTA	CGAAATCAGT	AAGCAGGSCA	CTGCAGTACT	TATGAGCAGC	600
	CACAACAGCA	GCCTGCTGTC	GCATCTGCCG	GCACGGACAT	TGGCCGTTCG	TAAGAATGGC	660
	GATGCCCTCCT	CTTTGGTCTGA	GCTGAGTGCA	GATGCTGTTT	CAAGAAAAAA	TACGGAAATA	720
65	GAT						723

(2) INFORMATION FOR SEQ ID NO:132

70 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 696 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: circular

75 (ii) MOLECULE TYPE: DNA (genomic)

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- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:  
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:  
(A) NAME/KEY: misc\_feature  
(B) LOCATION 1...696
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:132
- |    |  |     |
|----|--|-----|
| 15 | ATGAGAGATG TGACGCTCTG TCAGGAGGAA AACGTCATTT TTCAAAATTT GAATCTGACC  | 60  |
|    | CTTTCCGCGG GAGACTTCGT CTATCTGATA GGCTCAGTGG GATCGGGGAA GAGCACTTTG  | 120 |
|    | CTGAAGGCTT TGTATGCTGA GGTGCCTATC TCTGCCGGTT ATGCCCGCGT GATAGATTAT  | 180 |
|    | GATCTGGCAA AGTTGAAACG GAAGCAGTTG CCCTATCTGC GCAGGAATTT GGGCATTGTG  | 240 |
| 20 | TTTCAGGATT TCCAGTTGCT GAACGGACGT ACTGTTGCGG AGAATTTGGA TTTCGTTTGG  | 300 |
|    | CGAGCTACGG ACTGGAAAAA CCGAGCCGAT CGCGAGCAGC GTATCGAGGA GGTTTTGACC  | 360 |
|    | CGTGTGGGAA TGTCTCGGAA GGCTTATAAG AGACCGCAGG AACTGTCCGG AGGGGAGCAA  | 420 |
|    | CAACGTGTGG GTATAGCCAG AGCTTTGCTG GCGAAGCCTG CGTTGATCCT GGCCGACGAA  | 480 |
|    | CCCACAGGCA ACCTCGATTG GGTGACCGGA TTGCAGATCG CTTCTCTGCT CTACGAAATC  | 540 |
|    | AGTAAGCAGG GCACTGCAGT ACTTATGAGC ACGCACAAAC GCAGCCTGCT GTCGCATCTG  | 600 |
| 25 | CCGGCACGGA CATTGGCCGT TCGTAAGAAAT GCGGATGCCT CCTCTTTGGT CGAGCTGAGT | 660 |
|    | GCAGATGCTG TTTCAAGAAA AAATACGGAA ATAGAT                            | 696 |
- (2) INFORMATION FOR SEQ ID NO:133
- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 657 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:  
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:  
(A) NAME/KEY: misc\_feature  
(B) LOCATION 1...657
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:133
- |    |   |     |
|----|---|-----|
| 15 | ATGATTGAAA TCAGCAACCT CACCAAGGTT TTCAGAACAG AAGAAATAGA GACGGTAGCC | 60  |
|    | CTCGATGSCG TATCGCTCAA AGTGGACAAA GGCGAATTTA TCGCCATAAT GGGGCCTTCG | 120 |
|    | GGATGCGGTA AGTCCACTCT GCTCAATATC CTCGGCCCTC TCGACAATCC CACTTCCGGT | 180 |
| 55 | ATCTACAAGC TCGATGGGGC AGAAGTGGGC AACCTCCGGG AAAAAAGACG GACTGCCGTC | 240 |
|    | CGTAAGGGCA ATATCGGCTT CGTATTCCAG AGCTTCAACC TCATCGAAGA GATGACGGTA | 300 |
|    | AGCGAGAACG TGGAGTTGCC GCTCGTCTAT CTGGGTGTGA AGGCCTCCGA GCGGAAAGAG | 360 |
|    | CGAGTGGAGG AGGCACTGCG CAAGATGAGC ATCAGCCACC GGGCCGGCCA CTCCCCAAT  | 420 |
|    | CAGCTCTCCG GAGGACAACA GCAGCGCGTG GCTATCGCCC GTGCCGTGGT GGCCAATCCG | 480 |
| 60 | AAGCTCATCC TCGCCGATGA ACCACGGGT AACCTCGACT CCAAAAACGG AGCCGATGTC  | 540 |
|    | ATGGAACTGC TCAGAGTCT CAATCGCGAA GGTGCAACCA TCGTCATGCT GACGCACTCC  | 600 |
|    | GAGCACGATG CACGTAGTGC CGGCCGCATC ATCAATCTGT TCGACGGTAA GATTCCG    | 657 |
- (2) INFORMATION FOR SEQ ID NO:134
- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 1785 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO

SUBSTITUTE SHEET (Rule 26) (RO/AU)

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(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:  
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:  
(A) NAME/KEY: misc\_feature  
(B) LOCATION 1...1785

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:134

ATGAAAGAAT	TTTTCAAAAT	GTTTTTCGCC	TCGATCCTCG	GGGTTATAAC	GGCAGGAATC	60
ATCTTGTTC	GTATCTTCT	ATTTATCTTT	TTGCGCATCG	TAGCCGGTAT	TGCCTCCAAG	120
GCAACGGGAG	GAACCATTC	GAAGATCGAA	GCAAACCTCA	TCCTACATAT	ANACAATTCT	180
TCTTTCCTCG	AGATCGTATC	GGCCAATCCC	TGGAGCATGC	TCACAGGCAA	AGACGAGTCC	240
GTATCGCTCT	CACAGGCAGT	CGAAGCCATC	GGCCAAGCCA	AAAATAATCC	CAACATAACC	300
GGTATCTTCC	TCGATCTGGA	CAACCTTTCC	GTGCGTATGG	CATCGGCAGA	GGAATTGCGT	360
CGCGCGTTGC	AGGATTTCAA	GATGTCGGGC	AAGTTCGTGC	TATCCTATGC	CGACAGATAC	420
ACCCAAAAGG	GTTACTACCT	CTCCAGTAT	GCAGACAAAC	TCTACCTCAA	TCCGAAAGGA	480
ATGTTGGGSC	TTATCGGGAT	TGCGACCCAA	ACAATGTTCT	ACAAAGATGC	CCTCGACAAA	540
TTGCGCGTGA	AGATGGAGAT	CTTCAAGGTA	GGCACCTACA	AGGCAGCCGT	AGAGCCATTG	600
ATGCTCAACA	GGATGAGCGA	TGCCAATCGC	GAACAAATCA	CCACATACAT	AAACGGGCTT	660
TGGGACAAGA	TCACATCCGA	TATTGCAGAG	TCGCGCAAGA	CGGCAATGGA	TTCCGTGAAA	720
ATGTTTGCCG	ACAAAGGCGA	AATGTTCCGT	CTTGCCGAGA	AAGCGGTGGA	GATGAAGCTC	780
GTGGATGAGC	TGGCTTACCG	TACCGATGTG	GAGAAAGAAC	TCAAAAAGAT	GTCCCAACGC	840
GGAGAGAAAG	ATGAACCTCG	GTTCTGATCG	CTTTCTCAGG	TTCTGGCCAA	TGGCCCGATG	900
AACAAAACGA	AAGGCAGTCG	GATCGCCGTT	CTCTTTGCCG	AAGGTGAAAT	AACGGAAGAA	960
ATAATAAAGA	AGCCGTTCGA	CACTGACGGT	AGCTCCATCA	CACAAGAACT	CGCCAAAGAA	1020
ATCAAGGCAG	CAGCCGATGA	CGATGATATC	AAAGCCGTAG	TACTTCGTGT	CAATTCTCCG	1080
GGAGGTAGTG	CTTTCACTTC	CGAACAGATA	TGGAAGCAGG	TAGCCGATCT	CAAGGCCAAA	1140
AAGCCTATCG	TGGTCTCCAT	GGGCGACGTA	GCAGCCTCGG	GCGGATACTA	CATAGCCTGC	1200
GCAGCCAACA	GTATCGTGCC	AGAGCATACG	ACTCTGACCG	GCTCCATCGG	CATATTCCGG	1260
ATGTTCCCGA	ACTTCGCGGG	CGTAGCCAAAG	AAGATAGGAG	TGAATATGGA	CGTCGTACAG	1320
ACATCCAAGT	ATGCAGACTT	GGGCAACACC	TTGCTCTCGA	TGACGGTCGA	AGATCGTGCC	1380
CTCATCCAAC	GCTACATAGA	GCAGGGCTAC	GACCTCTTCC	TCACTCGCGT	ATCGGAAGGC	1440
CGCAACCGCA	CCAAGGCACA	GATCGACAGC	ATCGCTCAAG	GCCGTGTATG	GCTCGGCGAC	1500
AAAGCTCTTG	CACTCGGTTT	GGTGGATGAG	CTTGGAGSTT	TGGACACAGC	TATCAAACGG	1560
GCCGCGAAGC	TGGTCTAGCT	CGGTGGCAAC	TACAGCATAG	AGTATGGCAA	GACCAAGCGC	1620
AACTTCTTCG	AAGAGTTGCT	CTCCTCATCA	GCAGCGGATA	TGAAGTCTGC	CATCCTGAGT	1680
ACCATTCTCT	CCGATCCGGA	AATAGAAGTT	CTGCGCGAAC	TCCGCTCCAT	GCCGCCCCGT	1740
CCTTCGGGCA	TACAGGCACG	TCTCCCCTAT	TACTTCATGC	CGTAC		1785

(2) INFORMATION FOR SEQ ID NO:135

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 1767 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:  
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:  
(A) NAME/KEY: misc\_feature  
(B) LOCATION 1...1767

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:135

ATGTTTTTTC	CCTCGATCCT	CGGGGTTATA	ACGGCAGGAA	TCATCTTGTT	CTGTATCTTT	60
CTATTTATCT	TTTTCGGCAT	CGTAGCCGGT	ATTGCTTCCA	AGGCAACGGG	AGGAACCAT	120
CCGAAGATCG	AAGCAAATC	CATCCTACAT	ATAHACAATT	CTTCTTTCCC	TGAGATCGTA	180
TCGGCCAATC	CCTGGAGCAT	GCTCACAGGC	AAAGACGAGT	CCGTATCGCT	CTCACAGGCA	240
GTCGAAGCCA	TCGGCCAAGC	CAAAAATAAT	CCCAACATAA	CCGGTATCTT	CCTCGATCTG	300
GACAACTTTT	CCGTCGGTAT	GGCATCGGCA	GAGGAATTGC	GTCGCGCGTT	GCAGGATTTT	360
AAGATGTCGG	GCAAGTTCGT	CGTATCCTAT	GCCGACAGAT	ACACCCAAAA	GGGTTACTAC	420
CTCTCCAGTA	TTGCAGACAA	ACTCTACCTC	AATCCGAAAG	GAATGTTGGG	GCTTATCGGG	480

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ATTGCGACCC AAACAATGTT CTACAAAGAT GCCCTCGACA AATTCGGCGT GAAGATGGAG 540  
ATCTTCAAGG TAGGCACCTA CAAGSCAGCC GTAGAGCCAT TCATGCTCAA CAGGATGAGC 600  
GATGCCAATC GCGAACAAAT CACCACATAC ATAAACGGGC TTTGGGACAA GATCACATCC 660  
GATATTGCAG AGTCGCGCAA GACGGCAATG GATTCCGTGA AAATGTTTGC CGACAAAGGC 720  
GAAATGTTCC GTCTTGCCGA GAAAGCGGTG GAGATGAAGC TCGTGGATGA GCTGGCTTAC 780  
CGTACCGATG TGGAGAAAGA ACTCAAAAAG ATGTCCCAAC GCGGAGAGAA AGATGAACTT 840  
CGSTTCGTAT CGCTTCTCTCA GGTTCCTGGCC AATGGCCCGA TGAACAAAAC GAAAGGCAGT 900  
CGGATCGCCG TTCTCTTTGC CGAAGGTGAA ATAACGGAAG AAATAATAAA GAAGCCGTTT 960  
GACACTGACG GTAGCTCCAT CACACAAGAA CTCGCCAAAG AAATCAAGGC AGCAGCCGAT 1020  
GACGATGATA TCAAAGCCGT AGTACTTCGT GTCAATTCTC CGGGAGGTAG TGCTTTCAT 1080  
TCCGAACAGA TATGGAAGCA GGTAGCCGAT CTCAGGCCA AAAAGCCTAT CGTGGTCTCC 1140  
ATGGGCGACG TAGCAGCCTC GGGCGGATAC TACATAGCCT GCGCAGCCA CAGTATCGTG 1200  
GCAGAGCATA CGACTCTGAC CGGCTCCATC GGCATATTCC GCATGTTCCC GAACTTCGGC 1260  
GGCGTAGCCA AGAAGATAGG AGTGAATATG GACGTCGTAC AGACATCCAA GTATGCAGAC 1320  
TTGGGGCAACA CCTTCGCTCC GATGACGGTC GAAGATCGTG CCTCATCCA ACGCTACATA 1380  
GAGCAGGGCT ACGACCTCTT CCTCACTCGC GTATCGGAAG GCGGCAACCG CACCAAGGCA 1440  
CAGATCGACA GCATCGCTCA AGGCCGTGTA TGGCTCGGCG ACAAAGCTCT TGCATTCGGT 1500  
TTGGTGGATG AGCTTGGAGG TTTGGACACA GCTATCAAAC GGGCCGCGAA GCTGGCTCAG 1560  
CTCGGTGGCA ACTACAACAT AGAGTATGGC AAGACCAAAG GCAACTTCTT CGAAGAGTTG 1620  
CTCTCTCAT CAGCAGCGGA TATGAAGTCT GCCATCCTGA GTACCATTCT CTCGATCCG 1680  
GAAATAGAAG TTCTGCGCGA ACTCCGCTCC ATGCCGCCCG GTCTTCGGG CATACAGGCA 1740  
CGTCTCCCTT ATTACTTCAT GCCGTAC 1767

(2) INFORMATION FOR SEQ ID NO:136

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 939 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:  
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:  
(A) NAME/KEY: misc feature  
(B) LOCATION 1...939

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:136

50  
55  
60  
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ATGAGAGCAA ACATTGGCA GATACTTTCC GTTTCGGTTC TCTTTTCTT CGGGACAGCG 60  
ATCGGACAGG CTCAGAGTCG AAACCGTACA TACGAGGCTT ATGTGAAACA GTACGCCGAC 120  
GAAGCTATCC GACAGATGAG CCGCTACAAT ATACCGGCAA GCATCACCAT AGCACAGGCT 180  
TTGGTGGAGA CAGGAGCCGG AGCCAGTACA CTGGCCAGCG TACACAACAA TCACTTCGGG 240  
ATCAAAATGCC ACAAATCGTG GACGGGCAAG CGCACCTATC GTACCGACGA TCGGCCGAAC 300  
GAATGCTTCC GCAGCTATTC GGGCGCTCGC GAATCGTATG AAGATCATTC CCGATTCTG 360  
CTCCAACCCAC GCTATCGTCC CCTGTTCAA CTGACAGAG AAGACTATCG GGGCTGGGCT 420  
ACGGGGTTGC AACGCTGTGG CTATGCCACC AATCGGGGCT ATGCCAATCT GCTGATCAAG 480  
ATGGTGGAGC TGTATGAGCT ATATGCTTTG GATCGCGAGA AGTACCCCTC ATGGTTCCAC 540  
AAGTCTTACC CCGGGTCCAA CAAAAAATCC CATCAAACGA CCAAGCAGAA GCAGAGCGGA 600  
CTCAAGCAGC AAGCTTACTT CAGCTACGGA CTGCTCTACA TCATAGCCAA GCAAGGCGAT 660  
ACCTTCGATT CTTTGGCCGA AGAGTTCGAC ATGAGAGCCT CCAAACTGGC CAAATACAAC 720  
GATGCTCCCG TGGATTTCCT GATCGAAAAG GCGGATGTGA TCTATCTGGA GAAAAAGCAC 780  
GCATGCTCCA TCTCCAAACA CACACAGCAC GTAGTGGCTG TGGGCGATTG GATGCACAGT 840  
ATCTCCCAAC GCTATGGCAT CCGGATGAAG AACCTCTACA AGCTCAACGA CAAGGATGGC 900  
GAATATATAC CCAAGAGGGG CGATATACTG CGCTTGCGC 939

(2) INFORMATION FOR SEQ ID NO:137

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 1569 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

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(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

5 (vi) ORIGINAL SOURCE:  
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:  
(A) NAME/KEY: misc\_feature  
10 (B) LOCATION 1...1569

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:137

15	ATGGACGGAC	GTCGATATTC	GGATGGCCTC	CATCAGGCTA	TCGAAGCCAA	AGAGCATGTG	60
	AAAGTAGAGG	CTGCCGACACA	GACATTTGCA	ACTATCACTT	TGCAGAACTA	TTTCCGCATG	120
	TATCATAAGC	TGGCAGGGAT	GACCGTACT	GCTGAACTG	AAGCGGGAGA	GCTTTGGGAC	180
	ATCTACAAAC	TGGACGTTGT	AGTTATTCCG	ACAAACAAGC	CTATCGCCCG	TAAGGATATG	240
	AATGATCGTA	TCTATAAGAC	GGCACGTGAA	AAATATGCAG	CAGTTATCGA	AGAGATTSTA	300
20	CGTCTTGTG	AAGAGGGCAG	ACCTGTACTT	GTCGGTACTA	CTTCGGTGGA	AATATCCGAA	360
	TTGTTGAGCC	GTATGTTACG	CTTGCGTGSC	ATCCAACACA	ATGTACTCAA	TGCCAAATTG	420
	CATCAGAAGG	AGGCCGAGAT	TGTAGCTCAG	GCCGGTCAGA	AAGGAACTGT	TACCATCSCA	480
	ACGAACATGG	CCGGTCGTGG	TACCGACATC	AAGCTCTCTG	COGAGGTTAA	GAAAGCCGGG	540
	GGTTTGGCTA	TCATTGGTAC	GGAAAGGCAC	GAATCCAGAC	GAGTGGACAG	ACAGCTTCGT	600
	GGTCGTTCCG	GCCGTCAGGG	TGATCCCGGT	TGCTCCATAT	TCTATGTTTC	CCTTGAAGAT	660
25	CATCTGATGC	GCCTCTTTGC	CACAGAAAAG	ATTGCATCAT	TGATGGATCG	TTTAGGTTTC	720
	AAGGAAGGAG	AAGTGCTCGA	AAACAACATG	CTGAGTAAGT	CCGTGGAGCG	TGCTCAAAAG	780
	AAGGTGGAAG	AGAACAACCT	CGGTATCCGT	AAACATCTGC	TTGAGTACGA	TGATGTAATG	840
	AATTGCGAGC	GTGAAGTCAT	TTATACCCGT	CGCCGTCATG	CTTTGATGGG	AGAGCGTATC	900
	GGTATGGAATG	TACTCAATAC	CATATACGAC	GTATGTAAGG	CTCTGATTGA	CAATTATGCA	960
30	GAAGCCAATG	ATTTGGAAGG	CTTCAAGGAA	GATCTGATGC	GTGCACTCGC	GATAGAATCT	1020
	CCTATCACGC	AAGAAATATT	CAGAGGTAAG	AAAGCAGAAG	AGCTGACCGA	TATGCTTTTC	1080
	GATGAAGCTT	ACAAGTCTTT	CCAACGTAAG	ATGGATCTGA	TCGCAGAAST	GGCCCCCCTT	1140
	GTGGTTCATC	AGGTATTCGA	GACCCAAGCC	GCCGTGTACG	AGCGCATTC	AATCCCCATT	1200
35	ACGGATGGTA	AACGTGTCTA	TAACATAGGA	TGCAATTTGC	GTGAAGCGGA	TGAAACTCAA	1260
	GGGAAAAGCA	TCATCAAAGA	ATTTGAGAAA	GCTATCGTAC	TGCATACTAT	CGATGAGTCT	1320
	TGSAAGAAGC	ATCTGCGTGA	GATGGACGAG	CTTCGTAATT	CCGTCAGAA	TGCCAGCTAC	1380
	GAAGACAAAG	ATCCACTACT	TATCTATAAA	CTCGAATCTT	ACGAACGTGT	CCGCAAGATG	1440
	GTAAGAAGCA	TGAACCGTAA	GACCGTAGCG	ATCCTAATGC	GTGCTCGGAT	ACCGGTACCG	1500
40	GAGGCTCCTT	CCCAAGAAGA	GCTGGAACAC	AGGCGGCAAA	TAGAAATCCG	ACATGCAACC	1560
	CAACAACGT						1569

(2) INFORMATION FOR SEQ ID NO:138

45 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 1125 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
50 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

55 (iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:  
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:  
(A) NAME/KEY: misc\_feature  
60 (B) LOCATION 1...1125

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:138

65	ATGAATTTCT	TAAAAAAGA	ACCGTTTAAA	ATATTCTCTA	TGATTTATCT	GCTGTTAGAT	60
	ACAATAACAA	ACCGTGCCGG	TACAGAACGC	GCCGTGATCA	ACTTGCTTAA	CAACCTGCAT	120
	GCCAATGGTC	ATCGCGTATC	ATTAGTCAGC	GTTTGTACAA	AAGAAGGAGA	GCCTTCCTTC	180
	CAAGTAGAAA	AAGGAATAGA	AGTACACCAT	CTCGGAATTA	GGCTTTATGG	CAATGCATTA	240
70	GCCCGCAAAA	CAGTATATTT	CAAGGCTTAT	CGAAGGATAA	AAGCCCTATA	CAAGAAGCGT	300
	GAACCGGTTT	TATTGATAGG	GACTAATATT	TTTATCAATA	CAATTTTGTC	TCAGATCAGT	360
	AACAGAGGCA	GAATATTTAC	GATCGGATGC	GAACATATCT	CTTATGATAT	TGCCCGCCCT	420
	ATTACAAAAC	GCATAAGGGG	GTTTCTGTAT	TCAGGGCTTG	ATGCCGTTGT	AGCACTGACA	480
	AAAAGAGATC	AGCAATCGTT	CGAGGCAATC	TTACGTGGAC	GCTCTAAAGC	ATATGTCATA	540
75	CCCAATCAAG	TTTCATTTAC	TACAGTCCAA	AGAGATGCTA	CTACTCACA	ACAAATGTTG	600

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5 GCGATTGGCA GGCTTACCTA CCAGAAGGGT TTTGAATTCA TGATAGAAGA TGCATCACGA 660  
 GTGCTGCGAG AAAGGCCTGA TTGGAAGCTT ATCATAGTCG GAGATGGCGA AAATGAATCG 720  
 ATGCTACGTA AAGAAATTGC ATCTCGCAAT ATGGAGTCGC AAATAGAAAT ACATCCATCT 780  
 ACACCGGAAA TTCGCAAATA CTACGAATCA TCTGCTATTT ATCTAATGAC GTCCCGTTTC 840  
 GAAGGACTAC CAATGGTACT TCTCGAAGCA GAAGCATATG CACTACCTAT AATCTCATAC 900  
 GATTGTCCGA CCGGCCCGAG GGAAGTATC GAAAACGGTC GCAATGGTTT CCTTGTGCCA 960  
 ATGGAAGCAC ATGAAGACTT CGCGGATAAG TTACGCTTAT TGATGGATGA TGAAACTCTT 1020  
 CGTAAGAAAA TGGGACAAGA ATCAGAGTTG ATGGTCAAAT CCTACTCTCC GGCAAATATC 1080  
 TATGAATGTT GGAAGAAACT ATTCGTCGAA ATCGGCTACA TGAAT 1125

(2) INFORMATION FOR SEQ ID NO:139

- 15 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1086 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular
- 20 (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- 25 (iv) ANTI-SENSE: NO
- (v) ORIGINAL SOURCE:  
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- 30 (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...1086

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:139

35 ATGATTTATC TGCTGTTAGA TACAATAACA AACCGTGCCG GTACAGAACG CGCCGTGATC 60  
 AACTTGGCTA ACAACCTGCA TGCCAATGGT CATCGCGTAT CATTAGTCAG CGTTTGTACA 120  
 AAAGAAGSAG AGCCTTCCTT CCAAGTAGAA AAAGGAATAG AAGTACACCA TCTCGGAATT 180  
 AGGCTTTATG GCAATGCATT AGCCCGCAAA ACAGTATATT TCAAGGCTTA TCGAAGGATA 240  
 AAAGCCCTAT ACAAGAAGCG TGAACCGGTT TTATTGATAG GGAATAATAT TTTTATCAAT 300  
 40 ACAATTTTGT CTCAGATCAG TAACAGAGGC AGAATATTTA CGATCGGATG CGAACATATC 360  
 TCTTATGATA TTGCCCGCCC TATTACAAAA CGCATAAGGG GGTTCCTGTA TTCAGGGCTT 420  
 GATGCCGTTG TAGCACTGAC AAAAAGAGAT CAGCAATCGT TCGAGGCAAT CTACGTGGA 480  
 CGCTCTAAAG CATATGTCAT ACCCAATCAA GTTTCATTTA CTACAGTCCA AAGAGATGCT 540  
 ACTACTCACA AACAAATGTT GCGGATTGGC AGGCTTACCT ACCAGAAGGG TTTTGAATTC 600  
 45 ATGATAGAAG ATGCATCACG AGTGCTGCGA GAAAGGCCTG ATTGGAAGCT TATCATAGTC 660  
 GGAGATGECG AAAATGSAATC GATGCTACGT AAAGAAATTG CATCTCGCAA TATGGAGTCG 720  
 CAAATAGAAA TACATCCATC TACACCGGAA ATTCGCAAT ACTACGAATC ATCTGCTATT 780  
 TATCTAATGA CGTCCCGTTT CGAAGGACTA CCAATGGTAC TTCTCGAAGC AGAAGCATAT 840  
 GCACCTACCTA TAATCTCATA CGATTGTCCG ACCGGCCCGA GGGAACTGAT CGAAAACGGT 900  
 50 CGCAATGSET TCCTTGTGCC AATGGAAGCA CATGAAGACT TCGCGGATAA GTTACGCTTA 960  
 TTGATGGATG ATGAAACTCT TCGTAAGAAA ATGGGACAAG AATCAGAGTT GATGGTCAAA 1020  
 TCCTACTCTC CGGCAAAATAT CTATGAATGT TGGAGAAAC TATTCGTGCA AATCGGCTAC 1080  
 ATGAAT 1086

(2) INFORMATION FOR SEQ ID NO:140

- 60 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1920 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular
- 65 (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- 70 (v) ORIGINAL SOURCE:  
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...1920

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## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:140

	ATGGGAAAAA	TCATTGGAAT	TGACTTAGGC	ACAACGAACT	CTTGTGTCTC	TGTATTGGAA	60
5	GGTAACGAAC	CTATCGTTAT	TACAAACAGT	GAGGGCAAGC	GCACAACGCC	CTCGGTAGTG	120
	GCTTTTGTGG	ATGGTGGCGA	GCGTAAGGTG	GGCGATCCGG	CCAAGCGTCA	GGCCATCACC	180
	AATCCGACCA	AGACGATATA	CTCTATCAAA	CGCTTCATGG	GCGAAACTTA	CGATCAGGTT	240
	TCCAGAGAAG	TGGAGAGAGT	GCCATTCAAG	GTAGTACGTG	GGGACAATAA	TACTCCGCGC	300
	GTAGATATAG	ACGGTCGTCT	CTATACGCCG	CAGGAAATTT	CGGCCATGAT	CCTTCAGAAG	360
10	ATGAAGAAGA	CGGCCGAAAG	CTACCTCGGT	CAGGAAGTAA	CGGAGGCCGT	GATCACTGTG	420
	CCCGCATACT	TCAACGACGC	TCAACGTCAG	GCAACGAAAG	AAGCAGGAGA	GATCGCCGGC	480
	CTGAAAGTTC	GCCGATTGTT	GAACGAGCCT	ACGGCAGCTT	CTCTGGCCTA	CGGTCTGGAC	540
	AAGTCCAATA	AGGATATGAA	GATCGCTGTC	TTGACTTGG	GTGGCGGTAC	CTTCGATATC	600
	TCTATCTTGG	AATTGGGCGA	CGGCGTTTTC	GAAGTGAAAT	CGACCAACGG	TGATACGCAC	660
15	CTCGGAGGAG	ACGACTTCGA	CCACGTGATC	ATTGACTGSC	TGGCAGAAGA	GTTCAAGTCT	720
	CAGSAAGGTG	TGGATCTTCG	CCAGGATCCT	ATGGCTATGC	AGCGTCTGAA	AGAAGCTGCC	780
	GAAAAAGCCA	AGATAGAGCT	CTCCAGCACT	TCATCTACGG	AGATCAACCT	CCCCATATATC	840
	ATGCCCGTGA	ACGGCATCCC	CAAGCACTTG	GTGATGACGC	TTACAAGGGC	TAAGTTCGAG	900
	CAGTTGGCCG	ATCGTCTGAT	TCAGSCATGT	GTGGCACCCCT	GCGAAACGGC	CTTGAAAGAT	960
20	GCCGGTATGT	CACGTGGCGA	TATCGATGAA	GTGATTCTCG	TAGGTGGTTC	CACACGTATT	1020
	CCTGCTATTCT	AGGAGATTGT	GGAGAAGATC	TTGCTTAAGG	CTCCGTCCAA	GGGTGTGAAT	1080
	CCCGACGAAG	TGGTAGCTGT	GGGTGCCGCT	ATTCAAGGCG	GTGTTCTGAC	CGGTGAGSTA	1140
	AAGGATGTCT	TGCTGTTGGA	CGTTACCCCT	TTGTGCTCTG	GTATCGAGAC	TATGGGAGGC	1200
	GTGATGACTG	GCTTGATCGA	TGCCAATACC	ACTATCCCGA	CGAAGAAGAG	CGAAATCTTT	1260
25	ACCACAGCAG	TGGACAATCA	ACCTTCGGTA	GAGATTCTATG	TACTTCAGGG	TGAGCGTTCT	1320
	TTGGCTAAGG	ACAATAAGAG	CATCGGCCGT	TTCAACTTGG	ACGGTATTGC	TCCGGCGCCC	1380
	CGTCAGACAC	CGCAGATCGA	AGTAACGTTT	GACATCGATG	CCAACGGTAT	CCTGAATGTA	1440
	ACGGCTCATG	ACAAAGCTAC	CGGCAAGAAG	CAGAATATCC	GCATCGAAGC	CTCCAGCGGT	1500
	TTGTCCGATG	ATGAGATCAA	GCGCATGAAG	GAAGAGGCGC	AGGCCAATGC	CGAAGCAGAT	1560
30	AAGAAAGAGA	AAGAACGTAT	CGACAAGATC	AATCAGGCCG	ACAGCATGAT	CTTCCAGACG	1620
	GAAAAGCAGT	TGAAGGAGTT	GGGAGACAAA	TTCCCGGCCG	ACAAGAAGGC	TCCGATCGAT	1680
	ACCGCTCTCG	ACAAACTGAA	AGAAGCACAC	AAAGCACAGG	ATGTAGCTGC	TATCGATACA	1740
	GCCATGGCCG	AACTGCAAAAC	CGCTCTTTCC	GCAGCGGGCG	AAGAGCTTTA	CAAGAATGCC	1800
	GGAGCAGCCC	AAGGTGGCGC	ACAACCCGGT	CCGGACTTCG	GCGGTGCTCA	AGGTCCCTCT	1860
35	GCCGGTGATC	AGCCCTCTGA	CGACAAGAAC	GTACAGACG	TAGACTTCGA	GGAAGTGAAG	1920

## (2) INFORMATION FOR SEQ ID NO:141

40 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1347 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular

45 (ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

50 (iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

55 (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...1347

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:141

60	ATGCGCTACG	ACTTAGCTAT	CATCGGTGGA	GGGCGGCCG	GTTATACGGC	TGCCGAACGT	60
	GCTGCCAAAG	GTGGCCTGAA	AACCTCCTA	ATTGAGAAGA	ATGCTCTCGG	TGGTGTATGC	120
	CTCAACGAAG	GATGTATACC	GACCAAGACG	CTACTCTACT	CGGCCAAAGT	GCTACATCAA	180
	ATTGCTACGG	CATCTAAATA	TGCAGTAAGT	GGAACGGCCG	ATGGAATTGA	CCTCGGCAAG	240
65	GTGATTGCCA	GAAAAGGTAA	AATCATTCGC	AAGCTGACTG	CAGGCATCCG	TTCACGCCCTG	300
	ACAGAGGCCG	GAGTAGAGAT	GGTGACGGCA	GAAGCTACCG	TAACGGGGAT	CGATGCAGAC	360
	GGCATCATCG	GCATTACTGC	GGGCGAAGCA	CAGTACAAAG	CTGCCAACCT	GCTACTATGT	420
	ACCGGTTCCG	AGACGTTTAT	TCCACCCATC	CCCGGAGTGG	AGCAGACAGA	GTATTGGACA	480
	AACCGTGAAG	CTCTACAGAA	CAAAGAGATT	CCGACCTCTC	TCGTATCAT	CGGTGGTGGA	540
70	GTGATCGGAA	TGGAGTTCCG	TTCTTTCTTC	AACGGTATCG	GTACGCAAGT	GCACGTGGTG	600
	GAGATGCTGC	CGGAAATACT	CAACGGTATC	GATCCCGAAC	ATGCAGCTAT	GCTACGCGCT	660
	CACTATGAAA	AAGAAGGAAT	CAAATTCTAC	CTCGGGCACA	AAGTAACATC	GGTTCGCAAC	720
	GGAGCTGTTA	CGGTAGAATA	CGAAGGAGAA	AGCAAAGAGA	TGGAAGGAGA	ACGTATCCTG	780
	ATGAGTGTGG	GACGTCGCCC	CGTGCTGCAA	GGATTGAGT	CGCTCGGATT	GGTGCTTGCC	840
75	GGCAAAGGTG	TAAAGACTAA	TGAGAGGATG	CAAACCTCCC	TGCCCAATGT	CTATGCTGCA	900

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5	GGTGATATTA	CAGGCTTCTC	GCTTTTGGCA	CATACGGCTG	TACGGGAAGC	AGAGGTAGCA	960
	GTAGATCAGA	TTTTGGGGCA	AACAGACGAA	ACGATGAGCT	ACCGTGCCGT	ACCAGGTGTG	1020
	GTGTACACCA	ATCCCCAGGT	CGCCGGTGTG	GGAGAGACGG	AAGAAATCGCT	TCGCAAAGCA	1080
	GGACGTGCCT	ACACTGTTCG	TCGCCTTCCT	ATGGCCTTCT	CCGGTCGATT	TGTAGCAGAA	1140
	AACGAACAAG	GCAATGGAGA	GTGCAAACTA	CTACTTGATG	AAGAGAACC	CTTGATCGGA	1200
	GCACACCTCA	TTGGCAATCC	GGCCGGCGAA	CTCATCGTAA	CCGCTGCCAT	GGCCATCGAG	1260
	ACCGGCATGA	CGGATCGACA	AATCGAACGA	ATCATATTCC	CTCATCCGAC	TGTAGGCGAA	1320
	ATCCTAAAAG	AAACTCTCGC	CGGAGGT				1347
10	(2) INFORMATION FOR SEQ ID NO:142						
	(i) SEQUENCE CHARACTERISTICS:						
	(A) LENGTH: 2823 base pairs						
15	(B) TYPE: nucleic acid						
	(C) STRANDEDNESS: double						
	(D) TOPOLOGY: circular						
	(ii) MOLECULE TYPE: DNA (genomic)						
20	(iii) HYPOTHETICAL: NO						
	(iv) ANTI-SENSE: NO						
25	(vi) ORIGINAL SOURCE:						
	(A) ORGANISM: PORYPHYROMONAS GINGIVALIS						
	(ix) FEATURE:						
30	(A) NAME/KEY: misc feature						
	(B) LOCATION 1...2823						
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:142						
35	ATGGAATTGA	AAAGATTTT	ATCACTTGGT	CTTCTGCTTG	TGGGATTCAT	TCCGATGAAG	60
	CTTTCTGCCC	AACAGGCTCA	GCCACTCCCT	ACAGATCCGG	CTGTTCTGTG	CGGTAAGTTG	120
	GACAACGGAT	TGACTTATTT	CATCCGTCAC	AACGAGAACC	CGAAAGATCG	TGCGGATTTT	180
	TTTATCGCAC	AAAAGGTAGG	TTCTATTCTT	GAAGAAGATA	GCCAGTCCGG	TTTGGCTCAC	240
	TTCTTGGAAC	ACATGGCTTT	CAACGGTACG	AAGAACTTCC	CCGGTAAGAA	CTTGATCAAC	300
	TATCTCGAAA	CGATCGGTGT	ACGTTTCTGG	CAGAACCTGA	ACGCTTCTAC	CGGATTCGAC	360
40	AAGACGGAA	ATACGATAAT	GGATGTGCCG	ACTACACGTC	AGGGAATCAT	CGACTCCTGC	420
	TTGCTTATCC	TGCATGATTG	GAGTAACAAT	ATTACCCCTG	ACGGGCATGA	GATCGACGAG	480
	GAGCGCGGTG	TGATCCAGGA	AGAGTGGCGT	GCTCGTCCGG	ATGCCAACCT	TCGTATGTTT	540
	GAGGCTATAC	TTGCCAAGGC	TATGCCGGGT	AATAAATATG	CAGAACGCGT	GCCCATC3GT	600
	CTGATGGACG	TCGTGCTCAA	CTTCAAGCAT	GATGAGCTGC	GCAACTATTA	TAAGAAATGG	660
45	TATCGTCCCG	ACCTGCAAGG	TCTGGTGATC	GTGGGAGATA	TCGATGTGGA	CTATGTGGAG	720
	AACAAGATCA	AAGAAGCTTT	CAAGGACGTT	CCTGCTCCCG	TGAATCCAGC	AGAGCGTATC	780
	TATACGCCGG	TAGAGGACAA	CGATGAGCCT	ATCGTAGCCA	TTGCTACCGA	TGCTGAGGCT	840
	ACTACCACGC	AGCTCTCCAT	CAGCTTCAAG	AGCGACCCCA	CTCCTCAAGA	AGTGCGAGGA	900
	TCGATATTCT	GACTTGTGGA	AGACTATATG	AAACAGGTGA	TCACTACAGC	CGTGAATGAG	960
50	CGTCTGTCCG	AGATTACTCA	CAAGCCTAAC	GCTCCTTTCC	TCAGTGCAGG	AGCTTTCTTC	1020
	TCTAACTTCA	TGTACATCAC	CCAGACTAAG	GACGCATTCA	ATTTTGTGTC	CACGGTTCGT	1080
	GAGGGTGAAG	CGGAGAAAGC	GATGAACGCA	TTGGTGGCAG	AGATAGAAAG	CCTCCGTCAG	1140
	TTCCGGTATCA	CCAAAGGCGA	ATACGATCGT	GCACGCACGA	ATGTGCTCAA	GCGATACGAG	1200
	AATCAATACA	ACGAAAGAGA	CAAGCGTAAG	AACAATGCTT	ATGCCAATGA	ATACTCCACC	1260
55	TACTTCACCG	ATGGCGGCTA	TATCCCGGGT	ATTGAGGTGG	AATATCAGAC	GGTGAATGCT	1320
	TTTGCTCCTC	AGGTTCTCTT	GGAAGCATTC	AATCAGGCTA	TTGCCCAAAT	GATCGATCCG	1380
	GTGAAGATG	CTGTCTGTAC	CCTCACCGGT	CCTTCAAAGG	CTGAAGCCAA	GATTCCGAGC	1440
	GAAGCAGACT	TCCTCGCTGC	TTTCAAAGCT	GCTCGTCAGC	AGAAAGTAGA	AGCCAAGAAA	1500
	GACGAAGTCT	CCGACCAAAA	ATTGATGGAG	AAAGCTCCTA	AGGCCGGAAG	GATCGTTTCC	1560
60	GAGAAGAAAG	ATCAGAAGTT	CGGTACCACG	GAACTTACCC	TTAGCAATGG	CATCAAAGTA	1620
	TACCTCAAAG	AGACCGATTT	CAAACTCAAAC	GAAATCCTGA	TGAGTGCTCT	CAGCCCGGGT	1680
	GGTATCTCTT	CCGGAAAGCA	TGCTCCCAAC	CAATCTGTGA	TGAATTCGTT	CATGAACGTG	1740
	GGTGGCTTGG	GCAACTTCGA	TGCTATCCAG	CTGGATAAGG	TGCTGACAGG	TCGCTCTGCT	1800
	TCCGTATCTC	CCTCTTTGTC	TCTGCTCAGT	GAAGGTCTTT	CGGGCAAAAC	GACTGTAGAA	1860
65	GATATGGAAG	TTTCTTCCCA	GTTGATCTAT	CTCCAAATGA	CTGCTAACCG	CAAGGATCCC	1920
	GAAGCGTTCA	AGGCCACACA	GGAAAAGTTG	TACAAATACT	TGAAAATCA	GGAAGCCAAC	1980
	CCGATGGCTG	CGCTTATGGA	CTCTATCCGT	CATACCATGT	ACGGCGATAA	TCCGATGATG	2040
	AAACCCATGA	AAGCTGCTGA	CGTGGAGAAA	GTAAATTACG	ATCAGGTAA	GGCTTTCTAC	2100
	AATGAGCGAT	TGCTGATGTC	CGGCGACTTT	ATGTTCTTCT	TTATCGGTAA	TCTGGATGAA	2160
70	GCCAAGATGA	AGCCATTGAT	CGAACTTAT	CTTGCTTCAT	TGCCCCAACCT	CAAGCGTGGC	2220
	GATAAGATGA	ATAAGGCTCA	GGTACCGGCT	GCCCCGTCCG	GAAAGATCGA	TTGCAAGTTC	2280
	GAGAAGGAAA	TGGATACTCC	TTCGACTACT	ATATTCTGATG	TCGTGTCCGG	AAATGTGGAA	2340
	TATACGCTCA	AGAACAGTCT	CCTGCTGGAA	GTCTTCTCAG	CCGTAATGGA	TCAGGTGTAC	2400
	ACGGCTACCG	TTCCGAGAAA	GGAAAGCGGT	GCATACAGTG	TGGCTGCATT	CGGCGTCTCT	2460
75	GAGCAATATC	CTCAGCCCAA	GGCTCTGATG	CAGATCTATT	TCCCCACGGA	TCCTGCTCGT	2520

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5 GCGGAGGAAA TGAATGCTAT CGTTTTTGCT GAGTTGGAGA AGCTTGCCAA GGAGGGCCCC 2580  
 AATGTGGAAT ACTTTAAGAA GACTATCGAA AACCTGAATA AGCAGCACAA AGAAAGTCTG 2640  
 CGTGAGAATC GTTTCTGGCT CGAAGCCATG AAGGCGTCTT TCTTCGAAGG AAATGACTTC 2700  
 ATCACAGACT ACGAATCCGT ACTGAACGCT CTTACTCCTG CTGAATTGCA AAAGTTTGCG 2760  
 GCAGACCTCT TGAAGCAGCA GAATCGGGTT GTTGTCTATG TGGCTCCTGT TGCAAAGGCT 2820  
 CAA 2823

## (2) INFORMATION FOR SEQ ID NO:143

10

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2052 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular

15

## (ii) MOLECULE TYPE: DNA (genomic)

## (iii) HYPOTHETICAL: NO

20

## (iv) ANTI-SENSE: NO

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

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## (ix) FEATURE:

- (A) NAME/KEY: misc feature  
 (B) LOCATION 1...2052

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## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:143

ATGAGTAAGA AAGGAACAAT CGGGGTAACG AGCGACAATA TATCCCCGT CATCAAAAA 60  
 TTCCTGTACA GCGACCATGA GATATTCCTG CGTGAGATCG TCTCCAATGC CGTGGATGCT 120  
 ACGCAGAAGC TGAAAACGCT TACATCCGTC GCGCAATTCA AAGGCGAGAC GGGTGACCTC 180  
 35 CGCGTAACGG TCAGCGTGGA TGAAGTGGCA CGCACGATCA CGGTACGCGA CCGCGCGGTA 240  
 GGGATGACCG AAGAGGAGST GGAGAAGTAC ATCAATCAGA TTGCTTTCTC CAGTGCGGAA 300  
 GAGTTTCTTG AAAAGTACAA AGACGACAAAG GCCGCCATTA TCGGCCACTT CGGACTCGGA 360  
 TTTTACTCGG CTTTTCATGGT GTCCGAGCGA GTGGACGTGA TCACGCGCTC TTTCCGAGAA 420  
 GATGCTACGG CGGTGAAATG GAGCTGCGAC GGATCGCCCG AATACACGCT CGAACCTGCG 480  
 40 GACAAGGCTG ACCGTGGCAC CGACATCGTG ATGCACATCG ATGAGGAGAA TAGCGAGTTC 540  
 CTCAAAAAAG AAAAGATAGA GGGGCTCCTC GGCAAAATACT GTAAGTTCTT TACCGTGCCG 600  
 ATCATTTTCG GCAAGAAGCA GGAATGGAAA GACGGCAAGA TGCAAGATAC GGACGAGGAC 660  
 AATCAGATCA ACGACACACA TCCTGCCTGG ACCAAAAAGC CTGCCGACCT CAAGGACGAA 720  
 GACTATAAGG AATTTTACCG TTCGCTCTAT CCCATGTCCG AAGAGCCTCT CTTCTGGATC 780  
 45 CACCTCAATG TGGACTATCC GTTCAATCTG ACAGGTATCC TCTATTTCCC GAAGATCAAA 840  
 AACCAACTGG ATCTGACGG CAACAAGATT CAGCTCTACT GCAATCAGST TTACGTACCC 900  
 GATGAAGTAC AGGGTATCGT GCCGGACTTC CTCACCTCCG TGCACGGGGT CATCGATTCC 960  
 CCGGATATTC CCCTCAACGT ATCGCGCTCC TATCTGCAGA GCGATGCCAA TGTGAAGAAG 1020  
 ATCTCGTCTC ATATACCAA GAAGGTGGCA GACCGTCTGG AAGAAATTTT CAAAAACGAC 1080  
 50 CGCCCCACAT TCGAGGAGAA ATGGGATAGT CTGAAGCTCT TCGTCGAATA CGGTATGCTG 1140  
 ACGGATGAGA AGTTCTATGA GCGTGCAGCC AAATTCCTCC TTTTCACCGA TATGGACGGA 1200  
 CACAAGTACA CGTTTCGACGA ATACCGAACG CTCGTGGAAG GTGTACAGAC GGATAAGGAC 1260  
 GGACAGGTAG TGTATCTCTA TGCTACGGAC AAGCATGAC AGTACAGCCA CGTGAACGCT 1320  
 GCATCCGACA AAGGCTACAG CGTGATGCTG TTGGATGGTC AGTTGGATCC GCATATCGTG 1380  
 55 AGCCTGCTGG AGCAAAAGTT GGAGAAGACA CACTTTGTCC GTGTGATAG CGATACGATC 1440  
 AACAACTGTA TCCGCAAGGA GGAAGAGGCC GAAGTGAAC TGTCCGATAC GGAGCGCGCC 1500  
 ACTCTCGTGA AGCTGTTGTA AGCAGCCTG CCACGGGACG AGAAGAAGCA CTTCAATGTA 1560  
 GCTTTTGAAT CGCTCGGAGC CGAAGGTGAA GCCATCCTTA TCACACAAGC CGAATTCATG 1620  
 CGCCGTATGC GCGATATGGC ACAGCTGCAG CCGGGAATGA GCTTCTACGG CGAACTCCCC 1680  
 60 GATTCTGACA ATCTGGTACT TAATACCGAT CATCCGCTCA TCGACAGGGT ACTCTCCGGT 1740  
 GAGAAAGAAT CGGTAGAGCC TTCGCTCACA GAGCTTAGAG CGAAAATCSC CGAGCTGAAA 1800  
 GCGGAAGAGG CCAAGCTGCT CGATGAGGAA AAAGGGAAGA AACCGGAGGA AATCCCTGTT 1860  
 GCCACGAAGG AAGCCAAGGA GAACAACGCC GTCGAACAGG CCAAAACCGA AGGCAGTATC 1920  
 AACGATCAAC TGACCAAATA TGCTCAGGAC AACGAGCTGA TAGGTACGCT CATCSACTTG 1980  
 65 GCTCTGCTCG GAAGCGGATT GCTGACGGGA GAGGCTTTGG CCGAATTCAT TCGTCGACGC 2040  
 CAGCGCTTTC TC 2052

## (2) INFORMATION FOR SEQ ID NO:144

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## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1392 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular

75

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(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:  
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:  
(A) NAME/KEY: misc feature  
(B) LOCATION 1...1392

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:144

ATGGA	AAAAAC	TGATC	GATAT	TTTGG	TCGTA	GACGAT	GATG	TGGCAG	TCTG	TGCCG	CACTG	60
CGTCT	GGTGC	TCAAG	CGAGC	GGGCT	TATAAT	CCCGT	TATAG	CCAAC	AGTCC	CGACG	AAAGCT	120
TTGTCC	ATAA	TGCGG	AATCC	TGATG	GGCGGC	TGTAAG	CCCG	CTGTG	ATTCT	GATGG	ATATG	180
AATTTCT	CCC	TTTCG	ACCTC	CGGCAG	GGAA	GGATT	GGAAC	TACTGG	GAGAA	GATGC	CAGATA	240
TTCACTT	CCT	GGCCT	GTCTAT	ACTGAT	GACG	GCTTG	GGCTT	CGATT	CCACT	GGCAG	TGGAG	300
GGATG	AGGC	TTGGAG	CTTT	CGACTT	CATA	GGCAAG	CCAT	GGGACA	AACGA	TCCGT	CCTT	360
CGTACC	ATAG	ATACGG	CCCTT	GCATCT	GGCT	GCTCCC	TCAG	CTGTGG	CGAA	TCCAT	CGGAA	420
CAGTCT	GACA	GAGATA	CAGC	CCGTC	AGCCG	AAAGCT	TACAG	TCCAAG	GAGAA	TGACCC	CTGT	480
GCCCAT	ATCA	TAGGCC	CGAG	CGATG	CCATC	TGTAAG	ATCA	AGGAAC	CGGAT	ACGCC	GCATA	540
GCTCCC	ACCC	ATGCCT	CTGT	GCTGAT	CACG	GGCGAG	AGCG	GTACGG	GGCAA	AGAGTT	GTATA	600
GCCGAAG	CTC	TGCAC	CGTGG	GAGCAA	AACGA	GCCTC	AGCCC	CATTCG	TCAA	GGTCA	ATTTG	660
GGTGGG	ATT	CCGAA	AGTTT	GTTCG	AAAGT	GAGCT	GTTCG	GACATA	AAGAA	AGGAG	CTTTT	720
ACCAAT	GTCT	TTTCC	GACAG	GAAAG	GACGG	TTCGAG	CTGG	CTGAT	GGCGG	CACGAT	CTTTT	780
CTGGAC	GAAA	TAGGC	GAACT	ACCGG	TCGGC	AACCA	AGTAA	AACTG	CTGCG	AGTGCT	ACAG	840
GAACAG	ACAT	TCGAG	CCCTT	GGCGG	AGAGC	GTCTC	CCACC	GAGTG	GACAT	CCGTG	TGGTA	900
TCGGCT	ACGA	ATGCTT	CCCTT	GGAGC	GAAATG	GTAGC	CGAAG	GACGT	TTTCA	AGAGG	ACCTC	960
TACTAT	CGAA	TCAAC	CTGAT	ACATCT	GCAT	CTGCCT	CCGC	TGCGT	GAGCG	TCAGG	AGGAT	1020
ATACAG	CTGC	TGGTG	GAAAGC	CTTCAG	TGAA	GCCTT	TGCC	AATCGA	ACGG	ATTGCC	CCAT	1080
GCCGTT	TGGA	GTGCG	GAAAGC	TATGCG	AGCT	ATCTGT	TGCCA	TGCCC	CTACC	GGGCA	ATGTA	1140
CGCGAA	CTGA	AAAAC	GTAGT	GGAGC	GTACG	CTATTG	CTCT	CGGGAT	CGAG	AGAAAT	CAGT	1200
GCCCGG	GATG	TGGCT	GACTT	CGGTT	CGCAG	GTGAC	CGCAG	CAGAC	CACTC	CGACG	AACGG	1260
GCTTTG	ACCG	ACATG	GAGGA	AGCTG	CTATC	CGAGAG	ACGC	TGACTA	AAATA	CAACG	GCAAC	1320
GTTAGT	CTGT	CTGCAC	GAGC	CTTGG	GATTG	AGCCG	GGCAG	CTCTT	TACCG	GCGAAT	TGSAG	1380
AAATAC	GGGAC	TG										1392

## (2) INFORMATION FOR SEQ ID NO:145

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 750 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:  
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:  
(A) NAME/KEY: misc feature  
(B) LOCATION 1...750

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:145

ATGCTT	AAGA	TAAAG	AACCT	CCACG	CCACA	GTACAG	GGSCA	AAGAG	ATATT	GAAAG	GGAATC	60
AATCTG	GGAGA	TCAAT	GCCGG	AGAGAT	TCAT	GCTAT	CATGG	GGCCG	AAACGG	ATCGG	GGGAAA	120
AGTACG	CTCT	CTTCC	GTTT	GGTGG	GACAT	CCCTC	CTTTG	AAGTC	ACGGA	AGGAG	AGGTG	180
ACATCT	CAATG	GAATC	GACCT	GCTCG	AACTC	GAACCG	GGAAG	AACGT	GCACA	CCTCG	GACTC	240
TTTCTC	CAGTT	TCCAAT	ATCC	GGTCG	AGATC	CCGGG	CGTCA	GCATG	GTGAA	TTTCAT	GAGG	300
GCAGCT	GTCA	ATGAAC	ATAG	GAAAG	CGATC	GGAGC	AGAAC	CCGTAT	CGGC	AAGCG	ACTTC	360
CTCAAG	ATGA	TGGAG	AGAA	GCGTG	CCATT	GTGGAG	CTGG	ACAAC	AAATT	GGCCAG	CCGT	420
TCTGTG	GAACG	AAGGCT	TTCTC	CGGTG	GAGAA	AAAAA	GAGGA	ACGAA	ATCTT	CCAAAT	GGCT	480
ATGCTC	GAAC	CCAGCT	GGC	TATTT	TGGAC	GAAAC	CGATA	GCGGG	CTCGA	TATCG	ACGCT	540
CTCCGC	CATCG	TAGCAG	GGCG	GGTAA	ACCGA	CTCCG	CTCTC	CGGAG	AATGC	TGCTAT	TGTG	600

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ATCACACACT ATCAGCGTTT GCTCGAGTAC ATCAAGCCGG ACTTCGTACA CGTCCTTTAC 660  
AAGGGGCGCA TCGTCAAGTC GGGAGGAGCC GAGCTGGCTC TCACGCTCGA AGAAAAAGGC 720  
TACGACTGGA TCAAGGAAGA GATAGGAGAA 750

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(2) INFORMATION FOR SEQ ID NO:146

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 1383 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: circular

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(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

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(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc\_feature

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(B) LOCATION 1...1383

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:146

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ATGGCTAAGG AGAAAACGAT CTACGTCTGC CGTTCGTGCG GAACCAAATA CGCCAAATGG 60  
CAAGGCAACT GCAATGCCTG TGGAGAGTGG AACTGCATTG ATGAGGAGAA GGTGCCGGCA 120  
CGGSCATCGG GCAAGCATGC AGCCAAGAGT TTTATGCCTC GGGAGCAGGA CAACCGGCCA 180  
AGACTCTTAC AGGATGTGGA GTCCGGCGAT GAAGAGCGTA TTCGCCTCGG CGATGAAGAG 240  
TTTCGACCGCG TACTGGGTGG AGGAATTGTC AAAGGAGCAT TTGTCTTGCT TGGCGGCGAG 300  
CCGGGAATCG GTAAGTCCAC GCTTATCCTC CAGACGGTGC TGGCTCTGCC GCAGTTGCCG 360  
ACGCTCTATG TGTCGGGCGA AGAAAGTGCC CGACAACCTGA AGATGCGCGC CGAACGACTG 420  
GGGCAAGCCA TGAATGGGTG CTACGTATAC TGGCAAACGA ATATAGAGAG GATACTCTCC 480  
CGTGCGAGAA AACTCACACC CGATCTCCTC GTGATAGACT CTATACAGAC GGTCTATACC 540  
GAGGAAATGG AAAGCTCGGC CGGCAGCGTG GGGCAGATCC GCGAATGTGC CGCCTTACTG 600  
CTCAAATACT GCAAGACTAC GGGTATCCCC GTCATCGTCA TCGGACACAT CACCAAAGAA 660  
GGTAGCATAG CCGGACCGAA GGTGCTGGAG CATATAGTGG ATACGGTGCT TCTCTTCGAC 720  
GGGGATAAGC ATCATCTCTA CCGGATACTC CGAGGACAGA AGAACCGCTA TGGCAGTACT 780  
TCCGAGCTGG GGATATACGA GATGCGGCAG GACGGTCTGC GTGGCGTGGA GAATCCGAGC 840  
GAACATCTCA TCACACGCAA TAGGGAAGAC CTCAGTGGCA TAGCCATAGC CGTAGCGATG 900  
GAGGGCATTC GCCCGATACT CATCGAAGCG CAGGCTTTGG TCAGCTCGGC CATTATATGCC 960  
AATCCGCGAG GTTCGGGCCAC GGGCTTCGAT ATTCCGGCGGA TGAACATGCT CTTAGCCSTA 1020  
CTGGAGAAAC GTGCCGGCTT CAAGCTCATA CAGAAGGATG TGTTTCTGAA CATGCGCGGA 1080  
GGTATCAAAA TAGCCGATCC GGCTACGGAT CTGGCCGTTA TCTCGGCAGT GCTGGCGTCG 1140  
AGTCTGGACA TCGTTATCCC GCCGGCCGTA TGATGACCG GCGAGGTCGG ACTCTCCGGA 1200  
GAGATACGTC CCGTGAGCCG CATCGAGCAG CGCATAACGG AAGCGCGTCG CATAGGGTTC 1260  
AAAGAGATAT TGGTACCGGC CGATAATTTT CCGCAGGAGG ATGCCGGCCG CTTGGGTATT 1320  
CGGCTCGTGC CGGTGAGAAA GGTGGAGGAA GCCTTCGGCC ATCTGTTCTC GAAAGGAAGA 1380  
GAA 1383

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(2) INFORMATION FOR SEQ ID NO:147

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 813 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: circular

60

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(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

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(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc\_feature

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(B) LOCATION 1...813

100/ 490

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:147

5 ATGAATAGCA GACATCTGAC AATCACAATC ATTGCCGGCC TCTCCCTCTT TGTACTGACA 60  
TTGGGCGGCT GCTCCGTAGC CCAACAAGAT ACGCASTGGA CTCTCGGCGG AAAGCTCTTT 120  
ACTTTCGGCGT GGATACAACG TTCGGCCGAA TATCAAGCGC TTTGCATTCA GGCATACAAC 180  
ATCGCTACGG AAAGAGTGGG CGCTCTACCG GCAGAACGTA AACAGGAGA TAGGCCTTAT 240  
GCCATCGTAA CGGACATAGA CGAAACCATT TTGGACAATA CGCCTAACTC CGTGTATCAG 300  
GCTCTCAGGG GCAAGGATTA TGATGAAGAG ACTTGGGGGA AATGGTGTGC ACAGGCGGAT 360  
10 GCCGACACAC TGGCAGGAGC TTTGTCTTTC TTCTCCATG CAGCGAACA GGGGATCGAG 420  
GTCTTTTACG TCACCAACCG CAGAGACAA CTGCGCGAAG CAACTCTTCA GAACCTTCAG 480  
CGTTACGGAT TCCCTTTTGC CGATGAAGAA CATTTGCTTA CGACCCATGG GCCATCCGAC 540  
AAAGAACCCC GTCGGCTCAA AATACAAGAA CAGTATGAAA TAGTATTGCT CATAGGAGAC 600  
AACTTGGGCG ACTTCCACCA CTTCTTCAAT ACGAAAGAAG AGTCCGGACG CAAACAGGCT 660  
15 CTGGGCGCTGA CAGCCGGGGA GTTTGGCCGG CACTTCATCA TGCTGCCCAA TCCCAACTAC 720  
GGATCTTGGG AACCAGCATG GTACGGCGGG AAGTATCCGC CACTGCCCGA AAGAGACAAA 780  
GCACTTAAAC AACTGCACTC ACAGAACAGC AGA 813

## (2) INFORMATION FOR SEQ ID NO:148

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## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1251 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
25 (D) TOPOLOGY: circular

## (ii) MOLECULE TYPE: DNA (genomic)

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## (iii) HYPOTHETICAL: NO

## (iv) ANTI-SENSE: NO

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

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## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature  
(B) LOCATION 1...1251

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## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:148

ATGAGCACCA ATATAGATGT ACAACAGATC AAACAGCGTT TCGGCATCAT CGGTAGCAGT 60  
CCGCTGATGG AACATGCCAT ACGAGTGGCA GCACAGGTGG CTCCTACCGA CATGTCCGTC 120  
45 CTCGTGACGG GGGAGAGCGG TTCGGGGAAA GAGTTCTTCC CACAGATAAT CCACTACTAC 180  
AGCGCCCGGA AACATCATAG CTACATTGCA GTCAATTGGG GAGCCATCCC CGAAGGAACC 240  
ATCGATTCCG AGCTGTTCGG ACACCGCAA GGTTCCTTTA CCGGAGCCGT ATCGGATCGC 300  
AAGGGGTACT TCGAAGAAGC ATCGGGCGGC ACGATCTTTC TGGACGAAGT GGGCGAACTG 360  
CCTTTGCCCA CGCAGGCGAG GCTGCTGAGG GTGCTGGAGA CGGGCGAGTT CATCCCCGTA 420  
GGAGCCAGCC AGTCGCAGAA GACGGATGTC CGTATCGTAG CGGCGACGAA TGTGAACCTC 480  
50 AAGGAGGCGG TAGCGAACGG GAAGTTCCGG GAAGACCTCT TCTTCCGGCT CAATACGGTA 540  
CCGATCGAGG TGCCTGCGCT GCGTATGCGA CCGGACGACG TGCCCTTGCT TTTTCGCCGA 600  
TTCGCCCGCG ACAGCGCCGA GAAGTATCGG ATGCCCTCCG TGCGCCTATC GGACGAAGCC 660  
CGTACCATAT TAATGCGTTA CCGCTGCGCC GGCAATGTGC GAGAGCTGCG CAATATAACC 720  
GACAGGCTGA GCATCCTGGA GGAGGAGCGG ACGGTATCGG CAGAGACCAT CACTCGCTAC 780  
55 CTGGACGCTG AGGGGATGCA AGACCTCCAC CCGTCTGTA TCCGACGGAA CGAAACGACC 840  
GAAGCGGACA AACAAATCCC CCATTACGAG CGGAAATCA TCTACCAGGT GCTATACGAT 900  
ATGAAGAAAG AGATAGCCGA TTTGAAGGGG ATGATGAACC GCCTGGCGCA CCACGAACAG 960  
CCCTCATGGC CTGTAGGGTC GGACGTCTGG GGCAACGACG ACAAGCGCAC CGCAGATCCG 1020  
AAGTGGGCGC TCAGCACGCA CAAGGCCCCC ATCGCGAAGC CGGCAGAACG CGTGGAGCCG 1080  
60 ATACAGGAAG CCAGCGAATA CACCGAGGAT CCGGTTTCGC TGGAGGAGGT AGAGAAGAAA 1140  
ATGATTTCCC TTGCATTGGA ACGCCACGGC GGAAGGCGCA AGCAGACAGC CGAGGAAGT 1200  
AAGATTTCCG AGCGGACACT ATACCGTAAA ATCAAGGAGT ATGGACTGGA A 1251

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## (2) INFORMATION FOR SEQ ID NO:149

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1806 base pairs  
(B) TYPE: nucleic acid  
70 (C) STRANDEDNESS: double  
(D) TOPOLOGY: circular

## (ii) MOLECULE TYPE: DNA (genomic)

75

## (iii) HYPOTHETICAL: NO



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(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:  
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:  
(A) NAME/KEY: misc\_feature  
(B) LOCATION 1...1806

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:149

ATGATCCTAC	TCTTCGGCGG	TACTACGGAA	GGCCGTGCCG	CAGCTCGCGT	GCTGGATGAA	60
GCGGGAAGTC	CGTTTTTCTA	CTCCACCAAA	GGCAATCTGC	AAGAGATCCA	GAGTAGCCAC	120
GGCCATCGTC	TGACAGGAGC	CATGACGGTT	GCCGACATGG	TTTCGTTTTC	TCGGAAAGAA	180
GAGATCCGAC	TGATCGTGGA	CGCCGCTCAT	CCTTTCGCGG	AAGAATTGCA	CGCTTCAGTG	240
GCAGAAGCCT	CTGAACAAAC	AGGTATCCCC	GTAGTAAGAT	ACGAGAGACA	ATACCCTCCA	300
CGCGAAGAAG	GTATCGTCTG	GTGTGCAAAC	TACGATACGG	CTGCCGAGCG	GATGCTTGSC	360
GATGGCGTGC	AGCGTCTGCT	GATGCTCACA	GGAGTGAATA	CGATCCCCAA	GCTGGCTGCT	420
TTCTGGAAAG	AGCGCACCCAC	CTTTTGCCGC	ATATTGAAGC	GAGACGAATC	GGTTGCTTTG	480
GCAGAGAAGA	ACGGCTTTCC	TGCGGAGCGC	ATCGTTTTCT	TOGAACCGCA	TGCGGACGAG	540
GAGCTGATGC	AAGCCGTTCG	CCCCGATGCC	ATTATCACAA	AAGAAAGCGG	AGAGAGCGGT	600
TACTTCCGAG	AAAAGATAGA	AGCTGCCCGA	CGGATGGGCA	TCCGTATATA	TGCCGTGTA	660
CGTCCCCCTT	TGCCTCCTTC	ATTCATTCCC	GTAGGCGGGC	CTGTCCGTTT	GAGACGGGCG	720
GTAGAAGGCC	TCGTGCCGGG	ATTCTTTTCA	CTCCGAAGCG	GATTCACTAC	CGGCACCACA	780
GCTACCGCTG	CAGTAGTAGC	AGCCATGTAC	CGATTGATGG	GGCTTGGCTC	TCTCGCCGAA	840
GCTCCCGTAG	AATTGCCCTC	GGGCGAAATA	GTCACTCTGC	CCATAGCGGA	AATTCGAGAG	900
GAAGAAGATG	CTGTCTGTATC	CGCAGTCCTG	AAAGATGCAG	GTGATGATCC	GGATGTGACC	960
AATGGCATGG	CGGTATGCGC	TACGATCAGG	CTCAATCCCG	AACATGAGGA	AGTCCGCTTC	1020
CTGCAGGGTG	AAGGGGTGGG	GGTAGTGACG	CTCCCCGGCC	TCGGTCTGGA	GGTCGGAGGT	1080
CCGGCTATCA	ACCTCGTACC	TCGACGAATG	ATGACAGCAG	AGGTACGCCG	ACTCTATGCG	1140
CAGGGAGGTG	TGGATATTAC	GATTAGCGTA	CCCGAAGGCC	GAGAGGCTGC	TACCCAGACA	1200
TTCAATCCCC	GACTCGGCAT	ACGGGACGGC	ATCTCTATTA	TCGGAACATC	GGGAGTCTGT	1260
AAACCTTTT	CGGCCGAAGC	GTTCGTTGGT	GCCATCCGTA	AGCAAGTGGG	TATTGCCACC	1320
GCCTTGGGAG	CCAATCATAT	CGTCTCAAT	TCGGGAGCCA	AGAGTGAGCG	TTATGTAAAA	1380
GGAGCCTATC	CGGCACCTAC	TCCACAGGCC	TTTGTGCAGT	ATGGCAATTT	CGTCGGCGAA	1440
TCAGTCAGTT	GTGTAGCTTC	CTTCCCTTCT	GTCCGTTCCG	TAACGGTAGG	AATCATGCTC	1500
GGCAAAGCAG	TGAAACTCGC	CGAAGGCTAT	CTGGATACGC	ACAGTAAAAA	GGTAGTGATG	1560
AATCGGGATT	TCCTGCACGA	ACTGGCTCGT	CAGGCAGGTT	GTTCGGGAAGA	CATCCATGCC	1620
ATAATAGACA	ACGTGAATTT	GGTCTGTGAG	CTATGGACTA	TGCCGAGTGC	GGAGGACAGC	1680
GATCGACTGC	TACGAAAGAT	TGCCGAACGA	TCTTGGGAAA	CTTGCCGCCC	ATCGGTACCA	1740
TCGGCCGAAT	TAGAACTCCT	GCTGATCGAT	GAGTCCGGAG	CGATTGCTTT	TCGTATCGGT	1800
GGAGAA						1806

(2) INFORMATION FOR SEQ ID NO:150

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 1329 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:  
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:  
(A) NAME/KEY: misc\_feature  
(B) LOCATION 1...1329

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:150

ATGTTGAGGA	CTTTCGGAAT	CGGTGGTATT	CACCCCCCGG	AAAACAAGTT	GTCGGCAGGC	60
AAGCCCGTAG	AGGTGTTGCC	TATCCCTCA	CAGGTAGTCA	TCCCTCTTGG	TCAGCACATC	120
GGTGCACCGG	CAACTGCCAC	GGTCAAGAAA	GGGGATGAAG	TTAAGGTCGG	GACTATCATT	180
GCTCAGGCCG	GAGGATTCTG	ATCAGCTAAT	ATCCACTCAT	CTGTGTCGGG	TAAGGTGCTG	240
AAGATCGATA	ACGTATACGA	CTCAAGCGGC	TATCCCAAGC	CCGCACTCTT	CATTAGCGTA	300
GAAGGTGACG	AATGGGAAGA	GGGCATCGAT	CGCTCACCAG	CCATCGTCAA	AGAATGCAAT	360
CTGGATGCAA	AAGAAATCGT	AGCCAAAATT	TCTGCAGCCG	GTATTGTGGG	TCTTGGCGGT	420

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5 GCTACCTTCC CTACCCATGT GAAGCTGTCC CCTCCTCCGG GCAACAAAGC TGAGATCCTG 480  
ATCATCAACG CCGTAGAGTG CGAGCCTTAT CTGACGAGCG ACCATGTCCT TATGCTGGAG 540  
CACGGCGAAG AGATCATGAT CGGCGTGAGT ATCCTGATGA AAGCCATTCA GGTAACAAG 600  
GCCGTCATCG GAGTTGAGAA TAATAAGAAA GATGCTATTG CTCACCTCAC CAAACTGGCC 660  
ACTGCATATC CGGGCATAGA GGTAAATGCCG TTGAAGGTGC AATATCCTCA AGGCGGTGAG 720  
AAGCAGCTGA TCGATGCAGT GATCCGCAAG CAGGTAAAAA GCGGTGCCTT GCCTATCAGC 780  
ACAGGTGCCG TAGTACAAAA CGTGGGTACG GTATTGCGCG TGTACGAAGC AGTACAGAAG 840  
AACAAGCCTC TGGTCGAGCG CATCGTGACG GTTACAGGAA AAAAAGTGTG TCGTCCGTCT 900  
AACCTCCTCG TTCGTATAGG TACTCCTATT GCGGCTTTGA TCGAAGCAGC AGGTGGCTTG 960  
10 CCGGAGAATA CGGGCAAGAT CATCGGCGGA GGTCGGATGA TGGGACGCGC TCTGCTGTCA 1020  
CCGGATGTGC CTGTGACCAA AGGCAGCTCC GGAGTATTGA TTCTCGATAG AGAAGAGGCA 1080  
GTTGCAAGC CTATGCGCGA CTGTATCCGA TGGCCCAAGT GCGTCGGAGT GTGTCCGATG 1140  
GGACTCAATC CGGCTTTCTT TATGCGCGAC ACCTTATATA AGAGCTGGGA AACAGCGGAA 1200  
AAAGGCAACG TGGTTGACTG TATCGAATGC GGTTCTGTGA GCTTCACCTG TCCGGCCAAC 1260  
15 CGTCCTCTG TGGATTATAT CCGCCAAGCC AAGAAGACTG TGATGGGTAT CCAAAGAGCA 1320  
CGTAAGCAA 1329

## (2) INFORMATION FOR SEQ ID NO:151

20

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1437 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: circular

25

## (ii) MOLECULE TYPE: DNA (genomic)

30

## (iii) HYPOTHETICAL: NO

## (iv) ANTI-SENSE: NO

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

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## (ix) FEATURE:

- (A) NAME/KEY: misc feature  
(B) LOCATION 1...1437

40

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:151

ATGAAAAGAA TACAATAAC TCTTATCGCT CTCTTCGCGG CTGTTGCCGG TTTGGTCGCT 60  
CAAATAGCTT ACGAGGGAGT AATTTTCATAT AAAATTTCTG TGGACAAAAC CGGAAACAAG 120  
45 GTTGTACTGA ATGGTGCGGC AGATATGAGT AATTTAAAGC TCAAGAGCAC TCAGATGATC 180  
ATTGTTACGC CTATTCTTCG TTCAGAAAGT GGTACCAGCC GGGTGGAATT TCCTTCGGTA 240  
GTCATTACAG GCCGCAATAG AACAAAAGCT CTCAAGCGTG AAATCGCATT TAGTTCGGCT 300  
TTGCCCCAAG CAAAACATGC AGCTCAATAC ATTGCGCGTC ATAATGGGAA GAGCGAGCAG 360  
TTTGCTTTTA CAGGAGAACA TGCTTATGCA TCATGGATGA TGGATGCCAA GTTTGTGGTT 420  
CGTGAGGAGG TACGAGGTTG TGCTAAATGC CCTGTAGGTC TCTCGAGTAA TATTGTTCTT 480  
50 TTTGATCCAC TCTTCAATCC GGCAGAGGCT CCTTATTTGT TGGCACACAT TACTCCGGCA 540  
GAAGAAGTGG AAAACACAGC AGAGTCCAGC TTCGATGCTT ATATCAACTT CAAAGTCAAT 600  
AAGGCAGATG TCCTTCCTGA GTATCGCAAC AATAAGGCGG AGTTAGAGAA AATCAAAGAA 660  
TTTGTAAGCA CCGTTAAGGC TAATCCAAAC TATTCGGTCA ATAAATGAT CATCGAAGGG 720  
TTTGCTTCTC CCGAGGCTTC AATAGCCAC AATAAGGCTT TGTGCGAGCG CCGTGTCTAA 780  
55 AGACTCGCGG AAGAATTGGT GCGTAAGTAT GGCAAAACAT TGCCGAATAT AACCCTGAA 840  
TTCGGCGGTG AAGATTGGAA GGGGCTGAAA CTGGCTATCG AAAAGAGTGA TATAGCCGAT 900  
CGTGACCGCG TATTGGAGAT AATCAACTCC GATAAATATG CCGATGATGA TGCACGTGAA 960  
CAGGCTCTGA AGCAACTTTC GTCTTATCGT TATATCTTGG ATCAGATCTA TCCGAATTTG 1020  
CGTCGCAATA CGATAACCAT GGGGTATATC GTTCGTGATT ATACCCTCGA AGAAGCTCGT 1080  
60 GAAATCATTA AGACTGCTCC GAAAGAACTT AGTGAGGCGG AAATGTACCG TGTGGCAATG 1140  
TCTTATCCTG AGGGGCACCA AGAGCGTTG TTTGCTCTGA ATACGACCCT TAAGTATTTT 1200  
CCTGAAAGTG TAACGGGCGG AATCAATTTG GCTGTAGCCG CTTTTAATGG TGGAGACGTT 1260  
CAACAGGCAA TTGCTCTGTT GAGTCCGATT CAGACAGAAA AGGGTGTAAG CAATATCCTT 1320  
GGAGCTGCTT ATGCTCGTAC GGGAGATTTT GTCGTGCGG AAACCTTCTT CCGTAAGGCC 1380  
65 GTTGCAAGAAG GAGATGCAAA TGCGCAGCGC AACCTCGATA TGCTGCTTGG CAAAAAG 1437

## (2) INFORMATION FOR SEQ ID NO:152

70

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1149 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: circular

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(ii) MOLECULE TYPE: DNA (genomic)  
(iii) HYPOTHETICAL: NO  
5 (iv) ANTI-SENSE: NO  
(vi) ORIGINAL SOURCE:  
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS  
10 (ix) FEATURE:  
(A) NAME/KEY: misc\_feature  
(B) LOCATION 1...1149  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:152  
15  
ATGGCAGAAA AAAGAGACTA TTACGAAGTC CTCGGTGTAT CGAAGAATGC CACCGACGAT 60  
GAACTGAAAA AAGCATATCG CAAGAAGGCT ATCCAATACC ATCCTGATAA GAACCCCGGT 120  
GACAAGGAGG CCGAAGAGCA CTTCAAAGAG GTAGCTGAAG CCTACGACGT ATTGAGCGAT 180  
CCGCAGAAAG GCAGTCAATA TGACCAAGTTC GGCCATGCCG GATTGGGCGG AGCTGCCGGT 240  
20 GGAGGTTTCA GCGGAGGCGG TATGTCCATG GAGGATATTT TCAGTGGCTT CCGTGATCTA 300  
TTCGGTGGGT TCGGCGGTTT CGGCGGATTC TCCGATATGG GCGGTGGCAG TCGCAGACGT 360  
GTTCCGAGAG GGTCTGACCT GCGAGTACGA GTGAAGCTTT CTTTGGCCGA TATAAGTAAA 420  
GGTGTGGAGA AGAAAGTGAA GGTAAGAAAG CAGGTAGTGT GCAGCAAAATG TCGTGGCGAT 480  
GGCAGGGAAG AAGCCAATGG CAAGACTACC TGCCAGACCT GCCATGGAAC CGGCGTGGTT 540  
25 ACACGTGTGA GCAACACTTT CCTTGGGGCC ATGCAGACCC AGAGCACTTG TCCCACTTGC 600  
CACGGAGAGG GTGAGATCAT CACGAAGCCA TGCTCCAAGT GTAAGGGCGA AGGTGTGGAG 660  
ATCGGCGAAG AGGTGATCTC ATCCACATC CCTGCCGGTG TAGCCGAAGG AATGCAAAATG 720  
TCCGTGAACG GCAAGGGAAA TGCCGCGCCC CGAGGAGGCG TGAATGGCGA CTTGATAGTC 780  
GTGATCGCCG AGGAACCGGA TCCGAATCTG ATCCGCAATG GCAACGATCT GATATACAAT 840  
30 CTGCTTATAT CGGTTCGGTT GGTATAAAA GGAGGTAGTG TGGAGTGCC GACGATAGAC 900  
GGACGAGCCA AGATCCGCAT CGAGGCGGGG ACACAACCCG GCAAGATGCT GCGTTTGGCG 960  
AATAAGGGGT TGCCAGCGT AAACGGCTAT GGCATGGGAG ACCAACTGGT GAATGTCAAT 1020  
GTCTATATCC CCGAATCGAT CGATGCCAAA GATGAGCAGG CTATCGCAGC GATGGAAAAC 1080  
TCGGACAGCT TCAAACCTAC CGATGCTGCT CGTAAGGATA TAGACAAGAA ATACAGAGAG 1140  
35 ATGCTGGAT 1149

(2) INFORMATION FOR SEQ ID NO:153  
40 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 879 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: circular  
45 (ii) MOLECULE TYPE: DNA (genomic)  
(iii) HYPOTHETICAL: NO  
50 (iv) ANTI-SENSE: NO  
(vi) ORIGINAL SOURCE:  
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS  
55 (ix) FEATURE:  
(A) NAME/KEY: misc\_feature  
(B) LOCATION 1...879  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:153  
60  
ATGAAAAAAC TGATTTTAGC GACTTTGGGA CTTATGGCCA TTGCCATGCT CTCATGTTCA 60  
AGCAACAACA AGGATTGGA GAACAAAGGG GAGGCTACTC TTTTGGTAAC GTTTGGTAGC 120  
TCCTATAAAG CTCACGCGCA AACCTATGCG AAGATTGAGA AGACTTTTGC CGCAGCTTAT 180  
CCCGATCAAA GGATAAGCTG GACATACACG TCTTCTATTA TCCGAAAGAA ACTGGCTCAG 240  
65 CAGGGTATTT ATATCGATGC TCCGGATGAG CTTTGGAGA AATTGGCTCG TCTGGGTTAT 300  
AAGAAGATCA ATGTACAGAG TCTTCATGTG ATCCCGGCC GAGAAATGA TGAGATGATC 360  
GACTTTGTCA ATAAGTTTAA GGCAGCACAT AGTGATATTA CTGTGAAGGT AGGGGCTCCG 420  
CTTTTCGATA CCGATGAAGA TATGCGCGAG GTGGCAGAGA TCTTGACAAA GCGTTTTCAG 480  
CAAACGATAG AGAAAGGTGA AGCTATTGTA TTCATGGGAC ACGGCACCGA GCATGCTGCC 540  
70 AATGACAGGT ATGCCCGTAT CAATAAGATC ATGAAGAACT ATAGCAAGTT CATGATCGTC 600  
GGAACCGTCG AGTCCGATCC CTCTATCAAT GATGTTATTG CCGAACTGAA AGAAACCGGT 660  
GCCACGGCCG TAACAATGAT GCCGCTGATG AGTGTGGCAG GCGACCATGC TACGAATGAT 720  
ATGGCCGGAG ATGAGGACGA TAGCTGGAAG ACGTTGCTGA CCAATGCCGG CTACACAGTT 780  
TCTATAGACA AGCTGGACAA TGCCAATTTT TCAGCTCTTG GAGATATAGA AGAGATCCGG 840  
75 AATATCTGSC TCAAGCATAT GAAAGCCACC TCTGCTCGC 879

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## (2) INFORMATION FOR SEQ ID NO:154

- 5 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 1068 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: circular
- 10 (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- 15 (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:  
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- 20 (ix) FEATURE:  
(A) NAME/KEY: misc\_feature  
(B) LOCATION 1...1068

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:154

25 ATGACATCCG TCAGCCACTT ACGTACAATT TCTGTGCGCAG GTATCCTGGC TGCCTGGGA 60  
GGGGCTGTAC TCATTCTCTT CGGGGTTAAT CTCTTCCTCG GCTCGGTGGC TATTCCGATG 120  
AGCGAGATCT TCCGACATCT TTTTTCAGAT CGTCCCGAAG GAGGAGAAGC ACTCGTGAC 180  
TACAATATCC TATGGAAATC CCGCCTGCCC GAAGCCCTCA CGGCTGCTTT TGCCGGCGCA 240  
30 GGTTTATCCG TTAGTGGCTT GCAGATGCAG ACCGTCTTTC GCAATCCTTT GGCCGGTCCG 300  
TCCGTTCTCG GCATCAGCTC CGGTGCCAGT TTGGGTGTTG CTTGGTCCG TCTGCTGAGC 360  
GGCTCGCTGG GAGGAGTGGC ATTGAGTAGC CTGGGTATA TGGGCGAGGT GGCCATGAAT 420  
ATAGCCGCTG CCGTAGGCTC GCTGGCAGTA ATGGGGCTGA TCGTTTTTGT CAGCACCAAG 480  
GTGCGCAGCC ACGTTACGCT GCTCATTATC GGCGTTATGA TCGGATATGT AGCCACTGCC 540  
35 GTCATCGGGG TATTCAAGTT TTTCAGTATC GAAGAAGATA TTCGGGCATA CGTAATTTGG 600  
GGGTTGGGCA GCTTTTCCCG TGCCACGGAT TCGCAACTGA GTTTCCTTGC CATTCTGATG 660  
TTGATCTTFA TTCCGGCCGG TATGCTCCTT GTCAGCAGT TGAATCTCTT ATTGCTGGGA 720  
GAAAGCTACG CACGTAATCT GGGACTGAAT ACTCGTCGGG CACGGCTGCT CGTGATCTCT 780  
TCCGCGGGTT TGCTCATCGC TACCGTCACG GCCTATTGCG GTCCCATCGG CTTTTTGGGG 840  
40 ATGGCTGTGC CACACTTGGC ACGGGTTATC TTTACACAT CGGATCATCG GATCCTGATG 900  
CCTGCTACCT GTTTGATTGG AAGTGCTCTG GCTCTTTCT GCAATATCAT TGCTCGTATG 960  
CCGGGGTTTG AGGGGGCTTT GCCCGTCAAT TCCGTAACGG CTTTGGTGGG AGCACCTATT 1020  
ATCGTCACCG TTTTGTTCGG GCGCAGACGC TTCAAGGAAG AAACCGAC 1068

## (2) INFORMATION FOR SEQ ID NO:155

- 50 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 2271 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: circular
- 55 (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- 60 (vi) ORIGINAL SOURCE:  
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:  
(A) NAME/KEY: misc\_feature  
(B) LOCATION 1...2271

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:155

70 ATGCGGACAA AAACATCTT TTTTGCATT ATCTCTTTTA TTGCTCTATT GTCGTCTTCT 60  
CTGTCGGCTC AGAGCAAAGC CGTTTAAACC GGTAGTGTGT CGGATGCCGA AACCGGAGAG 120  
CCTCTTGCCG GTGCTCGAAT CGAAGTCAAA CACACCAACA TAGTAGCCGG TGCCGATGCC 180  
GGCGGACATT TCGAGATCAA GAACCTGCCG GCAGGGCAGC ATACTATTAT ATGTTCTGTT 240  
GGGGGGTATG GACAGAAAGA GGAGGTGGTT GCCATCGAAG CCGACAGAC CAAAACGATC 300  
TCTTTTGCAT TCGCACTGCG AACGAACAAC TTGGAGGAAG TCGTCGTTAC CGGTACCGGT 360  
75 ACACGTTACC GCTTGGTCTG TGCTCCTGTG GCAACGGAAG TCCTTACC GC TAAGSACATA 420

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5 GCCTCTTTCT CGGCTCCTAC TTCGGAGGCC TTATTGCAGG GGCTGAGTCC GTCTTTTGAC 480  
 TTCGGCCCCA ATCTGATGGG CTCTTTTCATG CAGCTGAACG GCCTTAGCAG TAAGTATATC 540  
 CTCTATCCTTA TCGATGGTAA GCGTGTGTAC GCGGTCAGGC CGATTGAGT 600  
 CGTATTTCTC CTGATCAGAT CGAACGGATC GAACCTGGTGA AAGGTGCTTC GAGTTCGCTC 660  
 TACGGATCCG ATGCCATCGC CGGGGTAAATC AATGTGATCA CAAAAAGAA TACGAATCGA 720  
 CTGAGTGCAT ATACGTCACA TCGCATATCG AAGTACAACG ATCGGCAAAAC CAATACTTCG 780  
 CTGGATATAA ACATCGGTAA GTTCAGTAGC AATACCAACT ATTTCTTCTA CCATACGGAT 840  
 GGCTGGCAGA ATAGTCCGTT CGAAAAATAA AAGAAAAAAG GATCCGGCGA ACCGGTCTTG 900  
 GAGGAAACGT ATAAGAAAAC TTTTCGTGCA CAGGAAAATC AGGGTGTAA GCAATCGCTT 960  
 10 TCCTATTATG CAACTAACAA TCTTAGCTTC AGCGGAAATG TGCAGTACAA TAAACGTCAG 1020  
 ATCTTCACTC CGACTTTTTC CGAAAAGAAG GCCTATGACA TGGATTATCG TGCTTTGACG 1080  
 GCTTCACTCG GTACGAACTA TCTTTTCCCC AATGGTCTGC ATACGCTTTC TTTTCGATGCC 1140  
 GTCTACGATC GCTTCCGTTT CGGATATTTG TATCATGACA AGGACAGCAG TGAGAGCCTG 1200  
 ATCAACAAAC AAGGTCAGAC CGAGCAACCC ACATTCCTTC CGGGTCAGCT ACGCAATAAA 1260  
 15 AACGATCAGA TCCGATACAC GGCAGAGGCT CGCGGTGTAT TTACTACTGCC TTATGCGCAG 1320  
 AAACTGACCG GCGGTTTGGG GTATTTCGGT GAGGAATTGA TCTCTCCCTA TAATTGATT 1380  
 ACCGACAAAG CAGATGCTTC CACGCTCTCT GCTTATGTAC AAGATGAATG GAAACCGCTC 1440  
 GATTGGTTCA ATATGACAGC CGGTTTCCGT CTGGTACACC ATCAGGAGTT CGGTACACGA 1500  
 ATGACGCTTA AGGTATCCAT ACTCGCCAAG TATGGGCGCG TGAACCTCCG CGCTACGTAT 1560  
 20 GCTAACGGCT ATAAGACTCC CACGCTGAAA GAGCTTTTTG CACGGAACGA ACTCACCCT 1620  
 ATGGGTTCGC ACAATCTCTA TCTCGCAAT GCGGATCTTA AGCCACAGAT GTCGATTAT 1680  
 TATGCTTTGG GCTTGGAGTA CAATCAAGGC CCTATCTCGT TCAGTGCAAC GGTATTATGAC 1740  
 AATGAATCTC GCAATCTGAT CTCTTTATG GATATACCGA CCTCACCCGA GCACGAAGCT 1800  
 25 CAGGGAATCA AGAAAAACCA GCAGTATGCC AACATAGGAA AAGCTCGCAG CCGCGGCCCT 1860  
 GATGTCCTAT GTGATGCCTC TATCGGTTGG GGTATCAAGT TAGGAGCCGG ATACAGCCTC 1920  
 GTGGAAGCTA AGAATCTCCA GACGGATGAG TGGCTGGAAG GAGCTGCACG TCATCGTGCC 1980  
 AATGTGCACG CCGATTGGGT TCACTACTGG GGTCASTATA GACTTGGGCT GAGCCTTTTC 2040  
 GGCCGTATTC AGAGCGAGCG TTACTACAAA GACGGCAATG CTCGGACTA TACCTTGTGG 2100  
 CGACTCGCCA CATCGCATCG TTTCTGCTCAT TTCCGCCACA TCATCTTGA TGGAACGCTC 2160  
 30 GGTATAGACA ACCTGTTTGA CTACGTGGAT GATCGTCTTA TGGGTGTCAA TTATGCTACC 2220  
 GTAACGCCGG GACGTACTTT CTTTGCTCAA ATAGCGATTG GATTCAACAA C 2271

## (2) INFORMATION FOR SEQ ID NO:156

- 35 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 993 base pairs  
 (B) TYPE: nucleic acid  
 40 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular  
  
 (ii) MOLECULE TYPE: DNA (genomic)  
  
 45 (iii) HYPOTHETICAL: NO  
 (iv) ANTI-SENSE: NO  
 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PORPHYROMONAS GINGIVALIS  
 50 (ix) FEATURE:  
 (A) NAME/KEY: misc feature  
 (B) LOCATION 1...993  
 55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:156

ATGACGGACA ACAAACAACG TAATATCGTA TTCCCGGCGT TTCTCCTCTT GCTGGGAGTC 60  
 ATCGCAGATG TGACGATCGT TGGTTTTTTC ATGCTCAGAC CGGCCGAGGA GATTATCCAA 120  
 GGACAGATTG AAGTGACCGA ATACCGAGTG TCCAGCAAAG TGCCCGGGCG CATCAAGGAA 180  
 60 CTAGGGTAT CCGAGGGACA GCAGGTGCAG GCCGCGGATA CCTCGCTGT CATCGAAGCC 240  
 CCCGACGTAG CGGCTAAGAT GGAGCAGGCA AAGGCTGCGG AAGCAGCTGC ACAGGCTCAG 300  
 AACGCCAAGG CTCTCAAAGG AGCACGCAGC GAACAGATAC AGGCAGCCTA TGAGATGTGG 360  
 CAGAAAGCTC AGGCCGCGGT AGCCATAGCG ACCAAGACAC ACCAGCGCGT GCAGAACCTC 420  
 65 TATGACCAGG GAGTGGTACC GGCTCAGAA GGTGACSAAG CCACTGCCCA GCGCGATGCG 480  
 GCCATCGCTA CGCAAAAAGC GGCCGAAGCC CAGTACAATA TGGCTCGCAA CGGTGCCGAA 540  
 CGCGAAGACA AGCTGGCAGC TTCTGCCCTC GTCGATAGAG CGAGAGGAGC CGTCCGCGAG 600  
 GTGGAGTCGT ACATCAACGA AACCTACCTC ATCGCCCCAC GGGCAGGCGA AGTGTCCGAG 660  
 ATATTCCCCA AAGCCGGCGA ACTCGTAGGT ACCGGCGCAC CTATCATGAA TATCGCCGAG 720  
 70 ATGGGCGATA TGTGGGCCAG CTTTGCCGTT CGTGAGGATT TCCTCAGCAG CATGACCATG 780  
 GGAGCCGTTT TGGAGACTGT GGTGCCGGCT CTGAATGAAG AAAAAAGTACG CTTCAGATC 840  
 ACATTCTATC AGAACATGGG TACCTATGCT GCCTGGAAAG CGACCAAGAC AACAGGGCAG 900  
 TACGACCTGA AGACCTTCGA GGTAAAGGCC ACCCTTGGCG ATAAAGACAA GGCACAAAAG 960  
 CTACGCCCGG GTATGTCCGT GATCATACGC AAG 993

75

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## (2) INFORMATION FOR SEQ ID NO:157

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 801 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...801
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:157

25 ATGCGTATTG TCAGTAATTT TTTGTTTCGTC TCTTTTTCGG TTTTGCTTTT TGCATCATGC 60  
 CGTTCCCGAGC GAGAAAAGGT CGTTTACCTG CAAGATATCC AAACTTTAA TCGGGAGATT 120  
 ATCGCTAAAC CATATGACGT AAAAATTGAG AAGGACGATG TGCTGAACAT CCTTGTGAGC 180  
 AGTAGAGACC CGGAGCTTTC AACGCCCTAC AACCAAGTGT TGACCACTCG TGCCTGGGCC 240  
 CGCAACGGCT ATGGAACGAA CTGGAACGAA GGCTTCTCGG TCGATTCGAA AGGGTACATC 300  
 AATTATCCTA TTTTAGGCCA GATCTATGTA GAGGGCCTTA CTCGTACCGA ACTGGAGAAG 360  
 30 GAGATACAGA AGAGGATTAT TTCCAGTGGA TTTATCAAGG ATCCTACGGT AACGGTGCAG 420  
 CTTCAAAATT TCAAGGTGTC GGTTTTGGGA GAGGTGAATC ATCCGGGTTT GATGTCGGTA 480  
 AAAGGAGAGC GAATAACTCT TTTGGAAGCG ATCGGAATGG CCGGAGACCT GACAATCTAT 540  
 GGTCGCCGCG ATCGGGTTT TGTGATTAGA GAAACCGATG GGCATCGCGA GGTTTTCCAG 600  
 ACGGATCTCA GAAAGGCCGA CTGCTCGCA AGCCCCGTGT ACTATCTGCA TCAGAACGAC 660  
 35 GTCATCTATG TGGAGCCGAA CGACAAGAAA ACACAGATGA GCGAGATCAA CCAGAATAAT 720  
 AACGTAAACG TATGGCTGAG TGTTACCTCC ACTTTGGTAT CCATTTCCAC GCTGACGATT 780  
 ACGATAATAG ATAAGACCAA A 801

## 40 (2) INFORMATION FOR SEQ ID NO:158

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1707 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...1707
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:158

65 ATGAAAAAGA CCAATCTGTT TTTATCTCTG CTGGTGATCT TTATCACCGG TAGTTTATG 60  
 ACTGCCCTGTG CACAGAAGTC CAAGACGAAC AAACCTACCG AAGAAGATCG GAGCCGCAAT 120  
 GAGTATGTAC AGTCGATGGA TGTGCTTAGC AATATTATCG GTAACGTCAG GCTGTATTTC 180  
 GTCGATACCA TAAGTATCAA ACATATGACT CGGCGTGGA TAGATGCGAT GTTGGGCGGG 240  
 CTTGACCCCT ATACCGAATA CATTCCTTAC GAGGAAATGG ATGAAGTGA ATTGATGACT 300  
 ACGGGAGAGT ATGCCGGAGT CGGAGCTATC ATATCGCAGC GCCCGGATAG TGCTGTGATT 360  
 ATCCAGAGAC CTATGGAAGG TATGCCCGCA GACGAAGCAG GATTGATAGC AGGCGACCGC 420  
 70 ATCCTGACTA TCGATGGGAA AGACTTCCCG AAATCCACCA CACCGAAAGT AAGCCAAGCA 480  
 CTGAAAGGGA TAGCCGGTAC TGTGCAAGG GTGACAGTAA TGCCTATGG CGAAACCAAA 540  
 CCTCGTACTT TTTCCGTGAA ACGTCAAAA GTGATTATGA ATTCCGTAC TTACAGCGGA 600  
 ATGCTCGATG GCTCGATAGG ATATATCCCG TTGAACAAC TACGGACAA AAGTGCAGAA 660  
 GAGGTGCGCA CGGCTTGTG GGATCTCGT GACAAACAAG GAGCGAAAG TCTCATTTTG 720  
 75 GATTTAAGAG GCAATGGTGG CGGACTGATG CAGGCTGCTA TCGAGATAGT CAATCTGTTC 780

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5 GTCCCTAAGG GCAAAGAGGT GGTAACGACC AAAGGTCGCA TTGCAGAGTC GGCGTCCGTA 840  
 TTTTCGCACAT TGACTGAACC GATCGACACG AAACCTCCCGA TAGTAGTCCT GATCGATGGA 900  
 CAATCGGCAT CTTCCTCGGA GATTGTAGCC GGAGCACTGC AGGATATGGA CAGGGCTGTA 960  
 CTGATGGGAC AAAAGAGCTA TGGCAAAGGG CTTGTACAAA CGACTCGTCA GCTACCATAC 1020  
 AACGGCGTGA TCAAATTGAC TACGGCCAAAG TACTACATCC CAAGCGGACG TTGTATTGAG 1080  
 CGTTTGGACT ACAGCCGCAC CAATCGGACA GGTATGGCAA CGGCCATTCC TGACAGTCTG 1140  
 CACAAATCT TTTACACTGC TGCCGGAAGA CGGTAGAAAG ATGCAGGAGG AATCCTGCCT 1200  
 GACATCGAGG TCAAACAAGA TACAGCTGCG ACATTACTTT ATTATATGGC CATCAATAAT 1260  
 GACGTTTTCG ATTTTCGTAC AGGTTATGTG CTCGAAGCATA AAACGATTGC CAAGCCGGAG 1320  
 10 GATTTTTCCTA TAACGAACGA GGAATATGCA GCTTTCTGCA AGATGATGGA AGAAAAGAAA 1380  
 TTTGACTATG ATCGCCAGAG TGGCAAGATG CTTGACAAAC TGGAGGAACT GGCTAAGATA 1440  
 GAAGGCTACC TGCCGGAAGC CAACTCGGAG CTTAAAGCAC TACGCGAAAA GCTAAAACCC 1500  
 AACCTGTCGC GTGATCTGCT ACGATTCAAA AAGGAGATAA CAAACTATCT CAACAATGAG 1560  
 ATTGCTACTC GCTATTATTA TGAGCGAGGC AGTATCCGCC AGAGTTTGCC GGAAGATAAG 1620  
 15 GTAGTCAAAG AAGCTATTAA GCTGCTGAAG GACCATCCGG AACAAATTCG ACAGATCCTT 1680  
 GCAGCTCCGA AAGCAGAGAA TAAAGGG 1707

20 (2) INFORMATION FOR SEQ ID NO:159  
 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 2943 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 25 (D) TOPOLOGY: circular  
 (ii) MOLECULE TYPE: DNA (genomic)  
 (iii) HYPOTHETICAL: NO  
 (iv) ANTI-SENSE: NO  
 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS  
 35 (ix) FEATURE:  
 (A) NAME/KEY: misc feature  
 (B) LOCATION 1...2943  
 40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:159

ATGCAAAACA AAGGATTGT GATTGTTATC ACATCGGCTC TGGCCATCAT CTGTGCGTTT 60  
 TACCTGTTCAT TCTCTTTTCG TACGAAACCGT TACGAAAAGA AGGCTAAGGC GATGGGCGAT 120  
 GTTGCCGGAA TGGCCTATCT TGATTCCATG TCGAATGAGA AGGTCTGGTT CGGCTACACG 180  
 45 CTGAAGAAG CTCAAGCCCA GCAAAATTGGT CTTGGCCTTG ACTTAAAGGG GGGTATGAAC 240  
 GTTATCTTGA AACTTAACGC AAGCGATCTG CTTGTAACC TCTCTAACAA AAGTTTGGAT 300  
 CCCAACTTCA ACAAAGCTCT GGAGAATGCT GCCAAGAGCA CGGAGCAATC CGACTTCATC 360  
 GATATTTTCG TGAAGGAATA TCGCAAGCTC GATCCCAACG GTCGCTTGGC CGTTATCTTC 420  
 GGTTCGGGTG ACCTTCGCGA CCAGATTACC GCAAAGTCTA CGGATGCAGA CGTAGTGCCT 480  
 50 CTGCTCAAAG AAAAATATAA TAGTGCTGTA GAAGCTTCGT TCAATGTGCT CCGTGCTCGT 540  
 ATCGATGCTT TCGGTGTGGT TGCACCTAAT TTGCAGCGAT TGAAGGGCA AGGGCGTATC 600  
 CTTGTGCAAG TCCCGGAGT GAAAGACCCCT GAGCGTGTTC GTACCCTTTT GCAACGCAST 660  
 GCCAACCTAC AGTTCTGGCG TACATACAAA TTCGAAGAGG TCAGCGGAGA CTTGATCGCT 720  
 GCCAATGATC GTCTGAGCGA ATTGGCTATG AACCAACACG ATGCTACCCC GGAAACAGAG 780  
 55 CCTGCAACTA CTGACTCTGT AGCTGCAACA GCCGATTCTG CTGCTGTACA AGCTGTAGCT 840  
 GATTCTGCTA CTGTAGCACA AAAAGAGGCC AAGGATGCTA CTCGTAAAGA CGCACTCTTC 900  
 TCTCTGCTTA CTCCCCTGAA TCGTGGCGGT GCAAGTAGTG GTGTGGCTCG TCGTGCTAAT 960  
 ATGGCTCAGA TATCTGAAAT GCTCCAGCAA GCTCACGATC TGAAGTTAC ACCTGAAGAT 1020  
 60 GTGCTTTTCC TCTGGGGTGC TAAAGCAATC GAAGACCCCG AAACCAAAAA GGAGACCGAC 1080  
 CTCTACGAAC TCTATGCTAT TCGTACCAAT CGTACGGGAG ATCCTGATT TGGAGTGAT 1140  
 GTAGTGACTT CCGCCAAGAG TGATATCCAA AATGACTTCG GTCGTTCGA ACCGATCGTT 1200  
 TCGATGACGA TGAATGAAGA AGGTGCTCGT AAATGGGCGC GTATCAGAAA GGATAACGTG 1260  
 GGACGGGCAA TCGCTATCGT TTTGGATGGT GTGGTTTATT CTGCTCCGAA CGTGAATGAT 1320  
 65 GAGATCACGG GCGGTCGCTC TCAGATCTCC GGGCACTTCA CCGTGGAGGA GGCCGGTGAC 1380  
 CTTGCCAACG TACTCAACTC CGGTAAAATG GATGCTACGG TAAGCATCGA ACAGGAAAAC 1440  
 GTGATTTGGT CTAAGCTGGG TGCCGAGTCC ATTAAGCCCG GATTCTTGTC GTTCTGCTC 1500  
 GCTTTGGTTA TCCTGATGTG TTACATGTGT CTGGCTTACG GTTCTTGCC GGGTCTTATC 1560  
 GCAACCGGCG CATTGATTGT AAACAGCTTC TTCACATTGG GCGTATTGGC TTCTTTCCAT 1620  
 70 GCCGTGCTGA CCCTCTGGGG TATCGCAGGT TTGGTGTCTG CGCTGGGTAT GCGTGTGGAT 1680  
 GCCAACGTAC TTATCTTCGA GCGTATCAAA GAAGAGCTTC GTGCCGGTAA GACTCCGATT 1740  
 CGTGCCGTTA CGGATGGTTA TGGCAACGCT TTCTCTGCCA TCTTCGACTC GAACGTTACG 1800  
 ACTATTATTA CCGGTATCAT CCTATTCCTC TACGGGACGG GGCCGATTCT GCGTTTGGCC 1860  
 ACTACGTTGA TTATCGGTCT TATCGCTTCT TTCATTACGG CTGCTTCTT GACTCGTATC 1920  
 75 GTCTTCGAGA AACTGGCGAA AAAAGGTCGT TTGGATAAGA TTACATTAC TACGAGCATT 1980  
 ACTCGCAATC TCCTTGTCAA TCCCTCATAC AACATCTTGG GTAAGCGCAA GACCGGCTTT 2040

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5 ATCATTC0033 TGATTATCAT CGTTTTGGGA CTTATAGCTT CATTTACAAT CGGTCTCAAT 2100  
 AGGGGTATTG AATTCTCCGG AGGACGTAAC TACGTAGTTA AATTCGACCA GCCTGTATCT 2160  
 TCCGAAGCCG TTGCGTTCGGC CTTGTCTTCT CCCCTGCAGG AAAAGGTATT GGTACCTCC 2220  
 ATCGSTACTG AAGGGACAGA GGTGCGTATA TCTACGAAC ATAGATCCA GGAGGAAAGC 2280  
 GAAGAACTG AAGCAGAGAT TACTGACAAA TTGTATCAGA GCCTGAAAGG TTTCTACACC 2340  
 CAGCAGCCTA CTGCTGATCA GTTCTTGGAC AATAICATTA GCTCTCAGAA AGTAAGTCCC 2400  
 AGTATGTGCA GTGACATCAC GAGAGGTGCT ATTTGGGCTG TGCTGTTATC GATGATCTTC 2460  
 ATGGCCATTT ATATTCTGAT TCGCTTCCGT GACATTTCTT TCTCTGCCGG GGTATTCGTA 2520  
 TCTGTGGCCG CTAATACATT CTGCATTATT GCTCTGTATG CGTTGCTGTG GAAGATTCTG 2580  
 10 CCCTTCACCA TGGAGATCGA TCAGAACTTC ATCGCTGCTA TTCTGGCTAT CATCGGTAC 2640  
 TCGCTCAATG ACACCGTGGT TGTATTGAC CGTATCCGAG AGACGATGAA ATTGTACCCC 2700  
 AACAGAGATC GCTATCAGGT GATCAACGAT GCCCTTAAT CAACATTGGG TCGAACATTA 2760  
 AATACGTCTT TGAATACGTT TATCGTTATG TTGGTAATCT TCATCTTTGG AGGTGCTACG 2820  
 15 ATGCGTAGTT TCACGTTCTC GATCCTGCTC GGTATCGTTA TCGGTACATA CTCTACGCTC 2880  
 TTTGTTGCTA CACCCCTTGC CTACGAGATC CAAAAGCGCA AGCTCAACAA AGCAGCTAAG 2940  
 AAA 2943

## (2) INFORMATION FOR SEQ ID NO:160

20

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 3051 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

25

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

30

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

35

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc feature

(B) LOCATION 1...3051

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:160

ATGAAAAGAA TGACGCTATT CTTCTTTGCG TTGCTGACGA GCATTGGGTG GGCTATGGCC 60  
 CAGAATAGAA CCGTGAAGGG TACAGTTATC TCCTCCGAGG ATAATGAGCC CCTGATCGGC 120  
 45 GCGAATGTCG TGGTTGTCGG AAACACCACT ATCGGTGCTG CAACCGACTT GGATGGCAAC 180  
 TTCACGCTTA GCGTGCCTGC CAATGCCAAA ATGTTGAGAG TGTCCTATTC CGGTATGACT 240  
 ACCAAAGAGG TCGCCATCGC TAATGTGATG AAGATCGTAC TGGATCCGGA CTCTAAGGTT 300  
 CTGGAGCAGG TAGTTGTATT GGGTTACGGT ACGGGACAGA AACTCAGCAC TGTTTCCGGT 360  
 TCTGTGGCCA AAGTGTCCAG CGAAAAGCTC GCGGAAAAGC CCGTTGCCAA TATCATGGAT 420  
 GCCCTCCAAG GTCAGGTAGC CGGTATGCGA GTTATGACTA CATCCGGTGA CCCTACTGCC 480  
 50 GTCGCTTCTG TGGAGATCCA TGGTACAGGG TCGTTGGGGG CAAGCTCTGC ACCATTGTAT 540  
 ATCGTGGATG GTATGCAAAC TTCTTTGGAT GTTGTGGCTA CGATGAATCC GAATGATTTT 600  
 GAATCTATGT CCGTTTGTGA AGATGCTTCT GCAACATCTA TTTATGGAGC TCGTGTGCA 660  
 AACCGAGTCT TTTTCATTCA AACGAAGAAA GGTAAAATGA GCGAGAGAGG TCGTATTACC 720  
 TTTAATGCCA GTTACGGGAT TTCTCAAATC CTGAATACTA AGCCCCCTGA TAATATGATG 780  
 55 ACTGGAGATG AATTGCTGGA TTTTCAGGTG AAGGCAGGTT TTTGGGGGAA CAATCAAACC 840  
 GTTCAGAAGG TTAAGATATG GATCCTTGCC GGAGCTGAAG ATTTGTATGG CAATTATGAT 900  
 TCTTTGAAAG ATGAGTATGG TAAGACATTC TTCCAGTGG ATTTTAATCA TGATGCAGAC 960  
 TGGCTCAAGG CTTTGTTTAA AACAGCACCC ACCAGTCAAG GTGATATTTT TTTCTCCGGA 1020  
 GGGTCTCAGG GAACCTCATA TTATGCCTCT ATAGGCTACT TCGATCAGGA AGGTATGGCT 1080  
 60 CGTGAACCGG CAAATTTTAA GCGCTATAGT GGCCGGCTCA ACTTCGAAAG TCGTATCAAT 1140  
 GAATGGCTGA AAGTTGGTGC AAATTGTCTT GGTGCGATAG CGAATAGACG ATCTGCCGAC 1200  
 TATTTTGGAA AGTATTATAT GGGGTCAGGT ACTTTCGGTG TGTAAACGAT GCCTCGTTAT 1260  
 TATAACCCCT TTGATGTGAA TGGGGATTTA GCAGATGTCT ATTACATGTA TGGAGCTACC 1320  
 AGACCTTCTA TGACAGAACC GTACTTCGCA AAAATGAGAC CGTTCAGTTC CGAATCACAT 1380  
 65 CAGGCCAATG TAAATGGTTT CGCCAGATT ACTCCGATCA AAGGCCCTAC TTTAAAGGCA 1440  
 CAGGCTGCTG TTGATATTAC TAATACTCGC ACTTCTTCTA AGAGAATGCC CAATAATCCG 1500  
 TATGATTTCT CTCCTTTGGG GGAAAGAAGA GAAAGAGCTT ATCGAGATGT TAGCAAGTCT 1560  
 TTTACAAATA CGGCTGAATA TAAAGTTTCA ATGATGAAA AACATGATCT TACAGCATTG 1620  
 ATGGGGCATG AATATATTGA ATATGAAGGG GATGTTATTT GGGCATCTTC TAAAGGATTT 1680  
 70 GAAAGTGATA AGTTGATGTT ACTGAGCCAG GGAAAAACCG GAAATAGTTT GTCTTTGCCT 1740  
 GAACACAGAG TCGCTGAATA TGCCATTATT TCTTTCTTTA GTCGTTTAA TTACGGTTTT 1800  
 GACAAATGGA TGTATATAGA TTTCTCTGTT CGTAATGACC AATCCTCTCG ATTCGGATCC 1860  
 AATAATAGAA GCGCGTGGTT CTATCTGTCT GGTGGAATGT TTGACATATA TAATAAATTC 1920  
 ATTCAGAAAA STAATTGGCT CAGTGATCTT CGACTGAAAA TGAGTTATGG TACAACGGGT 1980  
 75 AACTCGGAGA TTGGTAATTA CAACCACCAA GCACTCGTTA CTGTGAACAA TTATACTGAA 2040

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	GATGCTATGG	GGCTTAGCAT	TTCTACAGCA	GGCAATCCCG	ACCTCTCGTG	GGAAAAGCAG	2100
	TCTCAGTTCA	ACTTCGGTTT	GGCTGCAGGG	GCTTTCAATA	ATCGCTTATC	TGCAGAGGTA	2160
	GATTTCTATG	TCCGCACTAC	GAATGATATG	TTGATTGATG	TCCCGATGCC	TTATATCAGT	2220
	GGTTTCTTCT	CACAGTATCA	GAATGTAGGC	TCTATGAAAA	ATACGGGTGT	AGACCTTTCT	2280
5	CTTAAGGGGA	CGATCTACCA	AAATAAGGAC	TGGAATGTAT	ATGCTTCTGC	GAATTTCAAC	2340
	TACAATAGAC	AGGAAATAAC	AAAGCTTTTC	TTCCGGTCTCA	ATAAGTACAT	GTTGCCTAAT	2400
	ACCGGTAATA	TATGGGAAAT	TGGGTACCCC	AATTCGTTCT	ATATGGCTGA	ATATGCTGGA	2460
	ATCGACAAAA	AAACCGGTAA	GCAGTTGTGG	TATGTTCTTG	GTCAAGTCTGA	TGCGGATGGT	2520
	AATAAAGTTA	CAACAAGCCA	GTACTCAGCT	GACTTGGAGA	CACGAATTGA	TAAGTCTGTT	2580
10	ACTCCTCCTA	TTACAGGTGG	TTTCTCCTTA	GGTGCTTCTT	GGAAAGGACT	TTCTTTAGAT	2640
	GCTGATTTTG	CCTACATCGT	TGGTAAATGG	ATGATCAATA	ATGACCGTTA	CTTTACAGAG	2700
	AATGCAGGTG	GATTGATGCA	ATTAAATAAA	GATAAAATGC	TATTGAATGC	CTGGACAGAG	2760
	GATAATAAAG	AAACAGATGT	TCCAAAATTG	GGACAGTCTC	CTCAGTTTGA	TACGCATTTG	2820
	TTGGAGAATG	CTTCTTTCTT	GCGTTTGAAG	AATCTCAAAC	TCACCTATGT	ACTCCCAAT	2880
15	AGTCTTTTGT	CTGGGCAGAA	TGTGATTGGT	GGAGCTCGTG	TCTATTTGAT	GGCGCGCAAT	2940
	CTGTTAACTG	TTACGAAGTA	TAAAGGCTTT	GACCTGAAG	CAGGGGGGAA	TGTGGGAAAA	3000
	AATCAATATC	CTAATTCTAA	GCAGTACGTT	GCGGGTATTC	AGTTGTCTTT	C	3051
20	(2) INFORMATION FOR SEQ ID NO:161						
	(i) SEQUENCE CHARACTERISTICS:						
	(A) LENGTH: 3042 base pairs						
	(B) TYPE: nucleic acid						
25	(C) STRANDEDNESS: double						
	(D) TOPOLOGY: circular						
	(ii) MOLECULE TYPE: DNA (genomic)						
30	(iii) HYPOTHETICAL: NO						
	(iv) ANTI-SENSE: NO						
	(vi) ORIGINAL SOURCE:						
35	(A) ORGANISM: PORYPHYROMONAS GINGIVALIS						
	(ix) FEATURE:						
	(A) NAME/KEY: misc_feature						
40	(B) LOCATION 1...3042						
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:161						
	ATGACGCTAT	TCTTCTTTTG	CTTGCTGACG	AGCATTGGGT	GGGCTATGGC	CCAGAATAGA	60
	ACCGTGAAGG	GTACAGTTAT	CTCCTCCGAG	GATAATGAGC	CCCTGATCGG	CGCGAATGTC	120
45	GTGGTTGTGC	GAACACCCAC	TATCGGTGCT	GCAACCGACT	TGGATGGCAA	CTTACCGCTT	180
	AGCGTGCCCTG	CCAATGCCAA	AATGTTGAGA	GTGCTCTATT	CCGGTATGAC	TACCAAAGAG	240
	GTCGCCATCG	CTAATGTGAT	GAAGATCGTA	CTGGATCCGG	ACTCTAAGGT	TCTGGAGCAG	300
	GTAGTTGTAT	TGGGTTACGG	TACGGGACAG	AAACTCAGCA	CTGTTTCCGG	TTCTGTGGCC	360
	AAAGTGTCCA	GCGAAAAGCT	CGCGGAAAAG	CCCGTGGCCA	ATATCATGGA	TGCCCTCCAA	420
50	GGTCAGTAG	CCGGTATGCA	GGTTATGACT	ACATCCGGTG	ACCCTACTGC	CGTCGCTTCT	480
	GTGGAGATCC	ATGGTACAGG	GTCGTTGGGG	GCAAGCTCTG	CACCATTTGA	TATCGTGGAT	540
	GGTATGCAAA	CTTCTTTGGA	TGTTGTGGCT	ACGATGAATC	CGAATGATT	TGAATCTATG	600
	TCCGTTTGA	AAGATGCTTC	TGCAACATCT	ATTTATGGAG	CTCGTGCTGC	AAACGGAGTC	660
	GTTTTTCATTC	AAACGAAGAA	AGGTAAAATG	AGCGAGAGAG	GTCGTATTAC	CTTTAATGCC	720
55	AGTTACGGGA	TTTCTCAAA	CCTGAATACT	AAGCCCTTG	ATAATATGAT	GACTGGAGAT	780
	GAATTGCTGG	ATTTTCAGGT	GAAGGCAGGT	TTTTGGGGGA	ACAATCAAAC	CGTTCAGAAG	840
	GTTAAAGATA	TGATCCTTGC	CGGAGCTGAA	GATTGTGATG	GCAATTATGA	TTCTTTGAAA	900
	GATGAGTATG	GTAAGACATT	GTTCCAGTGC	GATTTTAATC	ATGATGCAGA	CTGGCTCAAG	960
	GCTTTGTTTA	AAACAGCACC	CACCACTCAA	GGTGATATTT	CTTTCTCCGG	AGGGTCTCAG	1020
60	GGAACTTCAT	ATTATGCCTC	TATAGGCTAC	TTCCGATCAGG	AAGGTATGGC	TCGTGAACCG	1080
	GCAAAATTTTA	AGCGCTATAG	TGGCCGGCTC	AACCTCGAAA	GTCGTATCAA	TGAATGGCTG	1140
	AAAGTTGGTG	CAAATTTGTC	TGGTGCGATA	GCGAATAGAC	GATCTGCCGA	CTATTTTGGGA	1200
	AAGTATTATA	TGGGGTCAGG	TACTTTCGGT	GTGTTAACGA	TGCCTCGTTA	TTATAACCCCT	1260
	TTTGATGTGA	ATGGGGATT	AGCAGATGTC	TATTACATGT	ATGGAGCTAC	CAGACCTTCT	1320
65	ATGACAGAAC	CGTACTTCGC	AAAAATGAGA	CCGTTCAAGT	CCGAATCACA	TCAGGCCAAT	1380
	GTAATAGGTT	TCGCCAGAT	TACTCCGATC	AAAGGCCTTA	CTTTAAAGGC	ACAGGCTGGT	1440
	GTTGATATTA	CTAATACTCG	CACCTCTCTT	AAGAGAATGC	CCAATAATCC	GTATGATTCT	1500
	ACTCCTCTTG	GGGAAAGAAG	AGAAAGAGCT	TATCGAGATG	TTAGCAAGTC	TTTTACAAAT	1560
	ACGSGTGAAT	ATAAGTTTTC	AATTGATGAA	AAACATGATC	TTACAGCATT	GATGGGGCAT	1620
70	GAATATATTG	AATATGAAGG	GGATGTTATT	GGGGCATCTT	CTAAGGAGTT	TGAAAGTGAT	1680
	AAGTTGATGT	TACTGAGCCA	GGGAAAAACC	GGAAATAGTT	TGCTTTTGCC	TGAACACAGA	1740
	GTCGCTGAAT	ATGCCTATTT	GTCTTTCTTT	AGTCGTTTTA	ATTACGGTTT	TGACAAATGG	1800
	ATGTATATAG	ATTTCTCTGT	TCGTAATGAC	CAATCCTCTC	GATTCCGATC	CAATAATAGA	1860
	AGCGCGTGGT	TCTATTCTGT	CGGTGGAATT	TGTGACATAT	ATAATAAAT	CATTCAAGAA	1920
75	AGTAATTGGC	TCAGTGATCT	TCGACTGAAA	ATGAGTTATG	GTACAACGGG	TAACCTCGGAG	1980

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5 ATTGGTAATT ACAACCACCA AGCACTCGTT ACTGTGAACA ATTATACTGA AGATGCTATG 2040  
 GGGCTTAGCA TTTCTACAGC AGGCAATCCC GACCTCTCGT GGGAAAAGCA GTCTCAGTTC 2100  
 AACTTCGGTT TGGCTGCAGG GGCTTTCAAT AATCGCTTAT CTGCAGAGGT AGATTTCTAT 2160  
 GTCCGCACTA CGAATGATAT GTTGATTGAT GTCCCGATGC CTTATATCAG TGGTTTCTTC 2220  
 TCACAGTATC ASAATGTAGG CTCTATGAAA AATACGGGTG TAGACCTTTC TCTTAAGGGG 2280  
 ACGATCTACC AAAATAAGGA CTGGAATGTA TATGCTTCTG CGAATTTCAA CTACAATAGA 2340  
 CAGGAAATAA CAAAGCTTTT CTTCGGTCTC AATAAGTACA TGTTCCTAA TACCGGTACT 2400  
 ATATGGGAAA TTGGGTACCC CAATTCTGTC TATATGGCTG AATATGCTGG AATCGACAAA 2460  
 10 AAAACCGGTA AGCAGTTGTG GTATGTTCCCT GGTCAGATCG ATGCGGATGG TAATAAAGTT 2520  
 ACAACAAGCC AGTACTCAGC TGACTTGGAG ACACGAATTG ATAAGTCTGT TACTCCTCCT 2580  
 ATTACAGGTG GTTCTCTCCT AGGTGCTTCT TGGAAAGGAC TTTCTTTAGA TGCTGATTTT 2640  
 GCCTACATCG TTGGTAAATG GATGATCAAT AATGACCGTT ACTTTACAGA GAATGCAGGT 2700  
 GGATTGATGC AATTAAATAA AGATAAAATG CTATTGAATG CCTGGACAGA GGATAATAAA 2760  
 15 GAAACAGATG TTCCAAAATT GGGACAGTCT CCTCAGTTTG ATACGCATTT GTTGAGAAT 2820  
 GCTTCTTTCC TGGCTTTGAA GAATCTCAAA CTCACCTATG TACTCCCAA TAGTCTTTT 2880  
 GCTGGGCGCA ATGTGATTGG TGGAGCTCGT GTCTATTGTA TGGCGCGCAA TCTGTTAACT 2940  
 GTTACGAAGT ATAAAGGCTT TGACCTGAA GCAGGGGGA ATGTGGGAAA AAATCAATAT 3000  
 CCTAATTCTA AGCAGTACGT TGGGGTATT CAGTTGTCTT TC 3042

20

(2) INFORMATION FOR SEQ ID NO:162

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 2463 base pairs  
 25 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular  
  
 (ii) MOLECULE TYPE: DNA (genomic)  
 30 (iii) HYPOTHETICAL: NO  
 (iv) ANTI-SENSE: NO  
 35 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS  
 (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 40 (B) LOCATION: 1...2463  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:162

45 ATGAAGAAAA ASAATTTTTT GCTTCTTGGC ATTTTCTGTTG CTTTGCTGAC TTTCATCGGC 60  
 AGCATGCAGG CACAACAGGC CAAAGATTAT TTCAACTTTG ACGAACGGGG CGAGGCCTAC 120  
 TTCTCATTTCA AAGTGCCTGA TAGGGCGGTT CTACAAGAGC TGGCTCTGAT CATGTCCATC 180  
 GACGAGTTTG ACCCGTAAC CAATGAAGCC ATTGCCTATG CCAGCGAAGA GGAGTTCGAG 240  
 GCATTCCCTGC GCTATGGGCT CAAGCCTACA TTCTTGACTC CTCCATCCAT GCAGCGCGCT 300  
 GTCCGAGATGT TCGACTACCG CTCAGGAGAA AAATACGAAT GGAATGCTTA CCCACCTAT 360  
 50 GAAGCCTATA TCAGCATGAT GGAAGAGTTC CAAACAAAGT ATCCATCACT TTGTACTACT 420  
 TCCGTCAATG GCAAGTCCGT AAAGGATCGT AAAGTATGTA TTTGCAAGCT GACGTCTCTT 480  
 GCCAATACAG GGAAGAAAGCC TCGCGTGCTC TATACTTCTA CGATGCACGG AGACGAAACG 540  
 ACCGGATATG TGSTACTGCT CCGACTCATA GACCATCTGC TGTGAACTA CGAATCCGAT 600  
 CCGAGGATTA AGAATCTCT GGATAAAACG GAAGTATGGA TCTGCCCTTT GACCAATCCG 660  
 55 GACGGAGCAT ACAGAGCCGG AAACCAACCC GTACAAGGAG CTACTCGCTA CAATGCCAAC 720  
 AATGTGCAAT TGAACCGTAA CTTCAAGGAT GATGTAGCCG GTGATCACCC CGATGGAAAA 780  
 CCTTGGCAGC CGGAGGCAAC TGCATTATG GATTGTGAAG GAAACACCTC TTTCGTGCTC 840  
 GGTGCCAATA TACATGGAGG AACAGAGGTG GTGAACATAT CATGGGATAA TAAAAAAGAA 900  
 AGACATGCAG ACGATGAGTG GTACAACTG ATCAGTCGCA ACTACGCAGC CGCTTGTCAG 960  
 60 AGTATTTCCG CCAGCTACAT GACCTCCGAA ACCAATTCGG GAATCATCAA CGGTTCAGAC 1020  
 TGGTATGTAA TTGCGGGAAG TCGTCAGGAC AATGCAAAAT ATTTCCATCG TCTGCGAGAA 1080  
 ATTACCTTTG AAATCAGCAA CACGAAGTTG GTGCCGGCCT CTCAACTTCC AAAGTATTGG 1140  
 AATCTGAACA AAGAATCTCT GCTTGCTCTG ATCGAAGAAAT CCTTATACGG CATCCATGGT 1200  
 ACATGACATT CCGCTCGGAA CGGACAGCCT CTCAAATGCC AGATCTTGAT AGAAAACCAT 1260  
 65 GACAAGCGCA ACTCCSATGT TTAATCCGAT GCTACACAG GCTACTACGT ACGTCTTATC 1320  
 AAAGCCGGGA CTTATACGGT GAAATACAAA GCGGAGGGTT ATCCTGAGGC AACTCGTACC 1380  
 ATTACGATCA AGGACAAAGA AACCGTCATC ATGGACATTG CATTTGGCAA CTCGGTTTCT 1440  
 CTGCTGTATC CCGATTTTAC AGCTTCTCCT ATGACCATCT CAGTAGGCGA AAGCGTCCAA 1500  
 TTCCAAGATC AAACGACAAA TAACCCACAG AATTGGGAGT GGCAGTTTCA AGGCGGACAG 1560  
 70 CCTGCCATGA GTACAGAGCA GAATCCGCTC GTATCCTATA GTCAATCCCG TCAGTACGAC 1620  
 GTTACGCTCA AASTGTGGAA TGCAAGTGGT TCCAACACGA TTACGAAAGA AAAATTTCATC 1680  
 ACTGTCAATG CCGTTATGCC TGTAGCTGAA TTCTGCTGTA CCCCAGCGGA AATAGAAGAG 1740  
 GGCAGACGG TATCTTTCCA AAACCAATCC ACCAATGCCA CCAACTACGT ATGGATATTC 1800  
 75 GATGCGGCA CTCCCGCTAC CAGTGAAGAC GAAACCCGA CTGTGCTTTA CAGCAAAGCC 1860  
 GSCCAATACG ATGTACGCT CAAGGCGATC AGTGCTTCCG GTGAACCGGT GAAGACGAAA 1920

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5 GAAAAATACA TCACTGTCAA GAAAGCTCCG GTCCCTGCTC CGGTAGCCGA CTTCGAAGGA 1980  
 ACACCTCGAA AAGTAAAGAA AGGCGAGACA GTTACTTTCA AAGACTTGTC TACGAACAAT 2040  
 CCGACTTCAT GGCTTTGGGT GTTCGAAGGC GGCTCTCCTG CCACCAGCAC GGAGCAAAAC 2100  
 CCGGTGGTCA CCTACAATGA AACAGGCAAG TACGATGTCC AGCTGACTGC CACCAACGAG 2160  
 10 GGCGGAAGCA ATGTGAAGAA AGCAGAAGAC TACATTGAGG TTATCCTCGA TGACAGTGTC 2220  
 GAGGACATAG TGGCACAGAC GGGTATCGTC ATTCGTCCGC AAAACGGAAC GAAGCAGATC 2280  
 CTCATAGAAG CCAACGCTGC TATCAAAGCG ATCGTTCTCT ATGACATCAA TGGACGGGTC 2340  
 GTAATCAAAA CTACTCCGAA TCAGCTCCGC TCGACCGTAG ATCTTTCCAT CCTGCCCGAA 2400  
 GGAATCTACA CCATCAATAT CAAACGGAA AAATCCGCTC GCACGGAAAA GATCCATATC 2460  
 15 GGG 2463

## (2) INFORMATION FOR SEQ ID NO:163

15 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 228 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular  
 20 (ii) MOLECULE TYPE: DNA (genomic)  
 (iii) HYPOTHETICAL: NO  
 25 (iv) ANTI-SENSE: NO  
 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS  
 30 (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...228  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:163

35 ATGCGACTGA TCAAGGCTTT TCTCGTGCAA CTCTTACTGC TCCCCATTTT CTTCTACAAG 60  
 CGGTTTATAT CGCCGCTTAC ACCGCCTTCA TGCCGGTTTA CCCCCTCATG TTCGTCTAT 120  
 GCCATCGAAG CCTTACGTAA ATATGGCCCG GGCAAAGGAC TATTGCTGAG CATCAAGCGT 180  
 40 ATTTCCCGCT GTCACCCGTG GGGTGAAGT GGCTATGACC CCGTTCCG 228

## (2) INFORMATION FOR SEQ ID NO:164

45 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 2577 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular  
 50 (ii) MOLECULE TYPE: DNA (genomic)  
 (iii) HYPOTHETICAL: NO  
 (iv) ANTI-SENSE: NO  
 55 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS  
 (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...2577  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:164

65 ATGGCATAAG ACTTTACACA AACATTCGCG AACAGCCTGG AGTACAGCTA TCAGGAAGCA 60  
 ACCCGTCTCG GCGTCGTAGC CGTGACGCAA GATATGCTCG TACTCGGTAT CATTCGCGAC 120  
 GGAGACAATG GCGCGATCGA CATCATGCGG CACTATGGGA TCAACTTGTA CGAACTCAAA 180  
 CGGTTGATCG AGTTGGAAGC CATCGCCGAG AGTTTGCTTG CTTGCGCTGA GGGATCGCCC 240  
 ATCTTCACCC CTTCGGCTCG GGAGGCTATC GATGATGCCA CAGACATCTG TGCCGACATG 300  
 70 GAGGACGAGG CCGTCAGCCC GGTCCATCTG TTGCTGAGTA TCCTCAACTC GACACAGGAG 360  
 AGCTTAGTAC AAAAGATAT TATGAAACAA GGTATAAAAT ACGACACCAT CCTGTCGGAT 420  
 TACTTCGGAC AGCGCAACCC CTCCGAAGGG AAGTCTCCCT CCGAAATGGA GATCCTCGAC 480  
 GGGTACCAAG ACAACGACTT CGACGACGAA GAGGACGAAT CCTCTCCGCC TTCCGGGAAT 540  
 AGCGGGACAG GCGGAGGCTC CGGCGACGCC CCCGAACAGA ATACCGGCGG AGGCGATACT 600  
 75 ACCACCACGA CACGGAGTGG AGGCGACACG CCTGCACTGG ACACCTTCGG CACCGACATC 660

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5 ACTGCCATGG CGSCAGCAGG CAAGCTCGAC CCGGTAGTGG GTCGGGAGCA GGAGATCGAA 720  
 AGGGTGATAC AGATACTCAG CCGGCGCAAA AAGAACAATC CGGTGCTCAT CGGCGAACCC 780  
 GGTGTAGGCA AGAGTGCCAT CGTGGAAGGA CTGGCCGAAC GCATCGTGAA CAGGAAGGTG 840  
 AGCCGTATTC TTTCGACAA GCGGATCATC AGCCTCGATT TGGCTCAGAT GGTAGCCGGC 900  
 ACCAAATATC GCGGACAGTT CGAAGAGCGG TTGAAAGCCG TGCTCGATGA GCTGAAGAAG 960  
 AATCCGCAGA TCATCCTCTT CATCGACGAG ATACATACCA TCGTGGGAGC AGGCTCTGCA 1020  
 GCCGGATCGA TGGATACGGC CAATATGCTC AAACCCGCTC TTGCCCGTGG ACAGGTACAG 1080  
 TGATCGGAG CCACTACGCT GGATGAGTAT CGTAAGAACA TAGAAAAGGA CGGAGCACTC 1140  
 GAACGCCGCT TCCAGAAGGT GCGGATAGCC CCCTCGACTG CAGAAGAAAC GCTGACCATC 1200  
 10 CTGCAAAACA TCAAAGAGAA ATACGAGGAC TATCACGGTG TACGCTATAC GGACGAAGCG 1260  
 ATCAAAGCGG CAGTGSAACT GACCGATCGC TATGTATCCG ATCGTTTCTT CCCAGATAAG 1320  
 GCGATAGATG CCGTGGACGA GGCCGGCGCG AGCGTCCATA TCACCAATGT GGTGGCTCCG 1380  
 AAAGAAATCG AGTACTGGA GGCCGAATTG GCATCGGTGC GAGAGAACAA GCTCTCGGCC 1440  
 GTAAAGGCTC AGAACTACGA ACTGGCTGCC TCCTTCCGCG ATCAGGAGCG GCGCACTCAG 1500  
 15 CAGCAGATAG CCGAAGAGAA GAAAAAATGG GAAGAGCAGA TGTCCAAGCA CCGCGAGACG 1560  
 GTGGACGAGA ATGTAGTGGC GCATGTAGTG GCGTTGATGA CAGGCGTTCC GGCTGAGCGG 1620  
 CTGAGCACGG GCGAAGGCGA ACGTCTGCGC ACGATGGCAG ATGATCTCAA GACCAAAGTA 1680  
 GTAGGTGAGG ACACAGCCAT CGAAAAGATG GTGCATGCCA TCCAGCGCAA TCGTCTGGGA 1740  
 CTTCGCAACA AAAAGAAACC GATCGGTTCT TTCCTTTTCC TCGGCCCCAC GGGGGTAGGC 1800  
 20 AAGACCTATT TGGCCAAGAA GCTCGCCGAA TACCTGTTCC AGGATGAGAA TGCCATGATC 1860  
 AGGGTGGATA TGAGCGAGTA TATGGAGAAG TTCTCCGTTT CCGCTCTCGT GGTGCCCCCT 1920  
 CCGGATATG TGGGCTATGA AGAAGGCGGC CAACTGACGG AGCGCGTAAG ACGCAAACCC 1980  
 TATTCGGTGG TTCTCTTGA TGAGATCGAA AAGGCGCATG CCGATGTCTT CAATCTGCTC 2040  
 TTACAGGTGA TGGACGAGG TCAGCTGACC GACAGTCTGG GACGGCGCGT GAATTTCAAG 2100  
 25 AACACCGTGA TCATCATCAC CTCCAACGTG GTTACACGCC AGCTCAAAGA CTTCGGGCGAG 2160  
 GGTATCGGGT TCCGTTCGGA AAAAGACGAG GAAGCGAACA ASGAGCATAG CCGTTCCGTG 2220  
 ATCCAAAAAG CTCTGAACAA GACGTTTCAG CCCGAATTTC TCAACCGTTT GGACGATATC 2280  
 ATCCTCTTGG ACCAACTGGG CAAGACGGAG ATTGCGCGGA TGGTGGACAT AGAGCTTAAA 2340  
 GCGTCTTGG CCGCATCCA TCGTGCCGGA TACGACCTCG TCCTTACCGA TGAAGCCAAAG 2400  
 30 GATGTGATAG CGACGAAGGG ATACGACCTC CaATACGGAG CACGACCGCT CAAGCGCACA 2460  
 CTCCAGAACG AAGTGGAGGA TCGCCTCACG GATCTTATCC TCTCGGACA GATCGAGAAA 2520  
 GGGCAGACGC TTACGCTCTC TGCTCGCGAT GCGGAGATCA TCGTACAAGA ACAAGCA 2577

- 35 (2) INFORMATION FOR SEQ ID NO:165  
 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1251 base pairs  
 40 (B) TYPE: nucleic acid  
 (C) STRAINEDNESS: double  
 (D) TOPOLOGY: circular  
 (ii) MOLECULE TYPE: DNA (genomic)  
 45 (iii) HYPOTHETICAL: NO  
 (iv) ANTI-SENSE: NO  
 (vi) ORIGINAL SOURCE:  
 50 (A) ORGANISM: PORYPHYRONAS GINGIVALIS  
 (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 55 (B) LOCATION 1...1251  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:165

60 ATGAATTACC TGTACATACT GATTACACTT TTAATCTCCG GCTTTTTTTC CCGTGCTGAG 60  
 ATTGCTTTCC TTTCTTCGGA CAAACTGCGT CTTGAGTTGG ACAGGAATAG AGGCGATCTC 120  
 ACAGGCAGAG CGTTAAACTT GCTGTATCGA CATCCGGACC AACTGGTGAC TACTCTCCTT 180  
 GTGGGTAATA ATATCGTTTT GGTAGTCTAT GGTCTGCTGA TGGCGGGATT GCTGGCCGCA 240  
 CCTTTGGCGC AATGGATTGA TAACGATGCT ATGATCGTGC TTCTCCAATC TGTCTTATCC 300  
 ACTATCATCA TACTGTTTAC CCGGGAATTT CTACCCAAAG CCATTTTCAA GACCAATGCC 360  
 65 AATATGATGA TGAGGGTATT CGCCCTCCCT ATCGTAGCGA TCTATTATCT GCTTTATCCT 420  
 CTGTCTAAAC TCTTCACCGG TTTATCTCGC TCTTTTATTC GTCTGGTGGA CAAGAATTAT 480  
 GTGCCTACAA CAGTAGGGTT GGGGCGCGTA GATCTCGATC ATTATTTGGC AGAAAATATG 540  
 TCCGGAGAAA ACGAACAGAA CGACTTGACT ACCGAAGTGA AAATCATCCA GAATGCGCTG 600  
 GATTTTTCGG GTATTCAGGT GCGAGACTGC ATGATCCAC GCAATGAGAT GATAGCATGT 660  
 GAGTTGCAAA CGGATATTGA AGTACTCAA ACGACTTTTA TCGATACCGG TTTGTCCAAG 720  
 70 ATCATTATCT ACAGACAGAA CATAGATGAC GTAGTAGGAT ATATCCATTC GAGCGAAATG 780  
 TTTCGTGGGC AAGACTGGCA AAAACGTATC AATACTACTG TATTCGTACC CGAAAGCATG 840  
 TATGCCAATA AACTGATGCG ACTACTCATG CAGCGCAAGA AAAGCATTGC GATCGTCAATC 900  
 GATGAATTG GAGGTACGGC CGGAATGGTC ACATTAGAGG ATTTGGTAGA AGAATTTTTC 960  
 GGTGACATTG AGGACGAACA CGAAGCTCGC AAGATCATAG CCAACAGCT CGGCCCTCAT 1020  
 75 ACCTATCTGG TCAGTGCTCG TATGGAATA GATGATGTA ACGAACGTTT TGGSTTGTCC 1080

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TTGCCTGAGT CTGACGACTA CCTTACCGTG GCCGGATTTA TCCTGAATAG CCATCAAAAT 1140  
ATCCCACAGG CCAATGAGGT CGTGGAGATT GCTCCTTATA CTTTACCAT TCTCAGATCT 1200  
TCTTCCACCA AGATCGAACT GGTGAAAATG TCCATCGACG ACCAATCGAA C 1251

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(2) INFORMATION FOR SEQ ID NO:166

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 879 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: circular

10

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(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

20

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

25

(A) NAME/KEY: misc feature

(B) LOCATION 1...879

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:166

30 ATGAAACAGA ACTACTTCAA AAGAGTCTGC TCACTGCTTT GGCTGGTTTT ACCCATGCTT 60  
ATTATGCCAT TGGGAAGTAG AGCTCAAGAG ATTATTCCGA ACGAAGAGGT GTTGGGAATCA 120  
TTGACTTTCTG TTGCACCGGT TGAGGAGACA GACGCAATAG AGGCAGAGGT AGAAGCTCTG 180  
CAGGAGATAG TCCTACTGA GGAGATTGCG GAGCAGGCTG TTCGTTCTTA TACCTACACG 240  
GTCTATCGTG ATGGCGTGAA GATTGCTTCA GGATTGACTG AGCCCACTTT TCTCGATGAA 300  
35 GATGTTCTCTG CCGGCGAACA TACCTACTGC GTAGAAGTAC AGTATCAGGG AGGCGTATCC 360  
GACAAAGTAT GCGTGGAGCT AGAGGTGAAG GACTTCAAAC CGGTTACCAA TCTCACCGBA 420  
ACTGCTTCCA ATGACGAAGT TTCTTTGGAC TGGGACGGTG TGGGAAGAGAA AGCTGAAGAG 480  
CCGGCAAGTG ATAAAGCAGT CAGCTACAAC GTCTACAAGA ATGGAACCTT GATCGGTAAT 540  
ACAGCTGAAA CTCATTATGT GGAGACCGGT GTAGCCAATG GTACATACAT CTACGAAGTG 600  
GAAGTAAAGT ATCCTGACGG TGTATCTCCG AAGGTGGCTG TAACCGTGAC CGTGACCAAC 660  
40 AGCTCATTTGA GCAATGTAGA TGGACAGGCT CCTTACACAT TGCGAGTAGA AGGCAAGAAG 720  
ATTATTGCGG AAGCCCATGG TATGATCAGC CTCTACGACA TCAACGGACG TACCGTGGCC 780  
GTAGCCCCGA ATCGATTGGA ATACATGGCG CAAACCGGTT TCTATGCAGT GCGCTTCGAT 840  
GTGGGGAATA AACACCATGT ATCGAAAATA CAAGTAAGA 879

45

(2) INFORMATION FOR SEQ ID NO:167

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 936 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: circular

50

55

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

60

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

65

(A) NAME/KEY: misc feature

(B) LOCATION 1...936

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:167

70 ATGATTCCTC TAAGCGAGAG TTTTGAATCA GGTATTCCAG CTATATGGAA GACCATGAC 60  
GCAGATGGCG ATGGCTATAA TTGGATGCAT TTGACCAATT TCACGGGACA GAGTGGTCTC 120  
TGTGTCTCTT CGGCTTCATA CATAGGCGGC GTCGGAGCTT TGACTCCGGA CAATTATCTG 180  
ATAACACCCG AATTAAAACT ACCACAGAC GCGTTGGTGG AAATAATCTA TTGGGTATGT 240  
ACTCAAGATC TCACTGCTCC ATCGGAGCAC TATGCCGTTT ATTCCTCTTC TACAGGCAAT 300  
AATGTGCTG ACTTTGTAA TCTCTTATAT GAAGAGACTT TGACTGCCAA ACGGATACAA 360  
75 TCCCCGAGT TGATCCGCGG AAATCGGACA CAAGGTGTTT GGTATCAAAG AAAGGTGTA 420

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CTCCCTAACG ATACTAAATA TGTTGCTTTC CGCCATTTTA ATTCCACGGA TAATTCTGG 480  
 CTCAATTTGG ATGAAGTATC TATCCTGTAT ACCCTCTTTC CCCGAAGAGC TCCGTGTCCG 540  
 CATCCGGGTG GTTACACTTA TTCTGTATTC CGTGATGGAC AAAAGATAGC GAGTGGATTG 600  
 TCGGCATTGG CATATATCGA TACGGATGTA CCGTATGGGA CTCGAAGACTA TTGTGTCCAA 660  
 5 GTCAATTATC TGCAAGGAGA CTCGTATAAA GTCTGCAAAA ATATAGTGGT GGCAAAATCT 720  
 GCAAACATCT ATGGGGCGGA TAAGCCTTTT GCGTTGACCG TGGTTGGCAA GACCATTGTA 780  
 GCGAGTGCTT TCAAAGGAGA GATCACTCTT TATGACATTC GTGGCCGGCT GATAGCTTCC 840  
 GGCTGCGATA CGCTTAGGTA CAAAGCGGAA AATGGTTTTT ACCTCATTA AATACAGGTA 900  
 10 AACGGAACGT TCTATACTGA GAAATCCAA ATCCAA 936

(2) INFORMATION FOR SEQ ID NO:168

- (i) SEQUENCE CHARACTERISTICS:  
 15 (A) LENGTH: 2529 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular  
 20 (ii) MOLECULE TYPE: DNA (genomic)  
 (iii) HYPOTHETICAL: NO  
 (iv) ANTI-SENSE: NO  
 25 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS  
 (ix) FEATURE:  
 30 (A) NAME/KEY: misc feature  
 (B) LOCATION 1...2529  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:168

35 ATGAAAAAAA GTTTCTTTT AGCCATAGTA ATGCTCTTTG GCATTGCCAT GCAGGGACAT 60  
 TCTGCTCCGG TTACGAAAGA GCGAGCTTTG AGTCTGGCTC GGCTGGCTTT GCGACAGGTA 120  
 TCCTTGCGAA TGGGACAAAC AGCAGTATCT GACAAGATTT CCATCGATTA CGTTTATCGG 180  
 CAAGGAGATG CTGAGAGGGG TATCACATCA CAAGAGGAAG GCTCTCCTGC ATATTTTAT 240  
 40 GTAGCTAATC GTGGAATAAA TGAGGGCTAT GCTCTTGTAG CAGCAGATGA CAGAATACCG 300  
 ACAATTTTAG CCTATTACCC CATTGGCCGT TTCGACATGG ACAGTATGCC GGACAATCTT 360  
 CGCATGTGGC TACAAATTTA CGATCAGGAA ATAGGCCCTGA TACTTCCGG AAAAGCTCAG 420  
 CTCATGAAG AGATATTACG TACCGAGGGC GTACCGGCTG AAGTACATGC TCTGATGGAT 480  
 AACGGTCATT TTGGCAACGA TCCCATGCGA TGGAAATCAAG GTTACCCATG GAACAATAAG 540  
 GAACCACTGC TTCTAATGG CAATCATGCC TATACCGGCT GTGTGCTAC TGCTGCAGCA 600  
 45 CAAATCATGC GCTACCATAG CTGGCCGCTT CAAGGTGAAG GCTCTTTCGA TTATCATGCA 660  
 GGTTCATTAG TTGGCAACTG GTCCGGCACA TTTGGTGAAA TGTACGACTG GATCAATATG 720  
 CCGGAAATC CCGACCTTGA TAATCTGACT CAATCTCAAG TGGATGCCTA CGCCCACTG 780  
 ATGCGTGATG TAGTGCATC TGTTTCGATG AGTTTTTATG AAAATGGAAG TGGTACGTAC 840  
 AGCGTTTAG TAGTAGGAGC CTGCGGAAAC AACTTTCGCT ACAAGCGTTC ACTGCAGCTA 900  
 50 CATGTACGGC CCTTATATAC CTCACAGGAG TGGCACGATA TGATCCGCGG GGAAGTTGCC 960  
 TCCGGAAGGC CGGTCTATTA TGCAGGGAAT AACCAGAGCA TAGGACATGC TTTGTTTGC 1020  
 GATGGTTATG CTTCGGATGG TACTTTCCAT TTCAACTGGG GTTGGGGAGG TGTTCACAC 1080  
 GGCTTCTACA AACTAACACT CCTCTCGCCG ACTTTCGTTG GTATCGGAGG TGAGGGAATA 1140  
 GGTTTTACCA TTTATCAAGA GATCATCACC GGTATCGAAC CGGCTAAGAC TCCCGCTGAA 1200  
 55 GCCGTACAG ATGCCTTGCC GATCTTGCCA CTGAAAGACA TAGAAGCCGA GTATAAAGT 1260  
 GAATCCGGAT TGAACGTAGG GTATTCGATA TATAATACAG GTGAAGAGCA ATCAAATCTT 1320  
 GACCTCGGAT ACAGATTGAA CAAGGCTGAC GGAGAAGTCA TAGAGGTGAA AACTTCATCT 1380  
 ATCAATATCT CTTGGTACGG ATACGGAGAG CATCCCGAGA GTTCTCATT GGCACCTAAT 1440  
 CAGTTGTAC CAGGAATCAA CACCATCACC CTACTTTATC GTCGCACAGG CACCGAACAG 1500  
 60 TGGGAGCCGG TACGGCATGC ACAGGGAGGA TATGTCAATA GCATTAAAGT AAATACGACA 1560  
 GACCGGAACA ATGTCTAGT CACGCTAGAT AATAACGAAG GCAAGCTCAG TATCGTCCCC 1620  
 AACAGCTTTG TCGCAGATCT GAATCTTAT GAACATAGTA CGATTACAGT ACAGTTCAAT 1680  
 AGCGACAGCC CTGATGAGAT CCGTACACCC GTAGCCTTTG CTCTATCTAC AGGAGCTACT 1740  
 GCGGACGATG TAATATCTTT GGGCTGGGTA ATGGCTGAAG TTCGGGGCGG TAGCAGCAAC 1800  
 65 TATCCGGTGG TTTGGTCTAA AGACGTTCTC ACTCTCTCGG AAGGCGACTA TACATTGTGG 1860  
 TATAGATTTT CCTCAACAA CCAAAAGGAT GAATGGAAAA AGATCGGAAG CGTGTACGTA 1920  
 AAAACACCGA CAGAGTATAC GCACCCCTTA TTCGAAGTGG GCCATAATCA AACTTCTACC 1980  
 TATACGCTGG ATATGGCACA CAACAGAGTA TTGCCCGACT TTACACTCAA AAATCTCGGA 2040  
 TTGCCTTTCA ATGGTGAGTT GGTGTGTGTT TTCCGCCAAA CACAATCCTC ATCGGGGTCT 2100  
 70 TTATGGGGCA CTCAAGAAAC AGTACATATC AAGCAAGGAG AAAGTTTCGT ATATAAACCT 2160  
 GTTGTGCAAG GCCCTATACC TGATGGATCC TATCGTGCAG CCCTCCATGC ATTGTAAGC 2220  
 GGACAACAAC AGTTGTACCT CAAGGGGAAA AGGAATACA CGGTGAAGAT CGTCAATGGT 2280  
 ACAGCGGTAG AAGCAATAGA ATCGTCAGAA GAGATCAGAG TATTCCCTAA TCCGGCACGC 2340  
 75 GATTATGTGG AAATATCGGC ACCTTGCAAT CCCCAGAGAA CATCTATCAT TCTTTTCGAT 2400  
 CTGTGAGGCA AGATTGTCTAT GAAGAATAGT TTATCAGCGG GGCATGGCAG AATGGATGTC 2460

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AGCCGACTTC CTAATGGGGC CTACATCCTT AAGGTGGATG GATATACGAC GAAAATAAAT 2520  
ATAGTGCAC 2529

## 5 (2) INFORMATION FOR SEQ ID NO:169

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 870 base pairs  
(B) TYPE: nucleic acid  
10 (C) STRANDEDNESS: double  
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

15 (iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:  
20 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:  
(A) NAME/KEY: misc feature  
(B) LOCATION 1...870

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:169

ATGAAAAAGC TATTCTCTC GCTCAGAGT CTTGTAATGG TCTTCGCTGT TGCAAGTTGC 60  
GATATAATCG ACAAGGATCA AACCCTCTTG CCGGCTCCGA CCAATGTGAC ACCCGATAAT 120  
30 CCGGATGACA ATCCTTCGGA GATCGACATT ACGCAGACGC ACACAGAAAA ATATGTTTTG 180  
GCTGAAGAAT TTACCGGCCA AAAATGTCTC AACTGTCCGA AAGGTCATCG CAAACTGGCG 240  
GCTCTCAAGG AGCAATACGG TAAGAGATTG ACTGTTGTCG GTATACATGC CGGCCCTGGA 300  
TCTCTCGTGC CACCTCTTTT CCGTACAGAA GCCGGAGACG CATATTATAG CAAGTTCGCC 360  
AATAATACCC CTCTCCCTGC GCTGATGGTT TCGCGCAAAA AGTTCGGCTC TTCCTACGTT 420  
35 TATGATAAGA GCTACAAAAC GTGGGACGTG CCTATTGCCG AGCAGATGGA GCAAAAGGCG 480  
AAGATCAATA TCTTTGCCGT GCCGAATAC ACCGATACCC AAAAGATCAA GGTGACTGTA 540  
AAGGGTAAAA TACTGGAGGG GAATACACTC CCSAAGTCCA TGGTTCAGGT GTATCTGTTG 600  
GAGGATAAGC TGATCGCTCC GCAGGTGGAT GGCAATACGA CAGTCGAGAA TTACGAGCAC 660  
AATCACGTGT TGCCTGGAGC CGTTAATGGT ATTTGGGGCG AAGAATTTGT GAATCTCAA 720  
40 GATTATTTGT ATACTTACGC CGTTGAACCG CTCTCGGGTA TGTCTTCTGT AGCCGAGAAT 780  
TATTCGATTG TGGCTTTTGT ATACGATGTG CAGACGTTG AAGTGTATGA CGTTGTGCAT 840  
GTAAAGATCA ATCCGCAATC CGATGGCAAA 870

## 45 (2) INFORMATION FOR SEQ ID NO:170

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 669 base pairs  
(B) TYPE: nucleic acid  
50 (C) STRANDEDNESS: double  
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

55 (iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:  
60 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:  
(A) NAME/KEY: misc feature  
(B) LOCATION 1...669

65 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:170

ATGAAGAAAT CAAGTGTAGT AGCCTCAGTT TTGGCCGTGG CTCTCGTGT CGCCGGTTGC 60  
GSACTGAACA ATATGGCAAA AGCGGGCCTT ATCGGCGCCG GAGTAGGAGG TGCCATTGST 120  
70 GCCGGASTAG GTAACGTAGC CGGAAATACG GCTGTCSGTG CCATCGTCGG TACTGCAGTC 180  
GGTGGAGCAG CCGGTGCTCT CATCGGAAAG AAGATGGACA AGCAGAAAAA AGAACTGGAG 240  
GCCGCASTAC CCGATGCTAC GATTGAGACA GTAAATGACG GAGAGGCTAT TCTGGTTACT 300  
TTCGATAGCG GTATCTCTTT TGGGACGAAC TCCAGCACTC TGAGTCCCAA CTCACGCACT 360  
GCGCTGACGA AGTTTGCTGC AAACATGAAC AAAAACCCCG ACACGGATAT TCGTATCGTA 420  
75 GGCCATACGG ACAATACCGG CTCGACAAG ATCAACGATC CTCTGTCTGA GAGACGTGCA 480

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GCCAGCGTAT ATTCTTTCCT GAATTCTCAG GGTGTGAGTA TGTCCGCGAT GGCAGCCGAA 540  
GGGCGTGGGA GCCATGAACC GGTTCGACAG AATAGCACAG TTGCCGGACG TTCGGCCAAC 600  
CGCCGTGTGG AGSTTTATAT CTTGCCGAAT GCCAAGATGA TCGAACAAAGC ACAGCAAGGT 660  
ACGCTGAAG 669

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## (2) INFORMATION FOR SEQ ID NO:171

- 10 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 1011 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: circular
- 15 (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- 20 (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:  
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- 25 (ix) FEATURE:  
(A) NAME/KEY: misc\_feature  
(B) LOCATION 1...1011

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:171

30 ATGTCGAAAA AATCGATCCT TCTGCTTTGC TGTTCGCTGT GCTTCATTTC TGCTACGAAG 60  
GCTGTGACCC CCGTCAGAAA TGTGCGCAAT AGCCAAGTGA ACAGCAAAGC AAAGACCGAA 120  
CGTACAAAGC CCTCGGACTC TGTACGGTAC ATTAGCAACA TGATTGCAGA TCGGCTGGAG 180  
TTCCGCAACA AGATTTCTTC CGAAAAAGAG GTAAGAAAAG CGGAATATGA AAATCGGCTG 240  
GCGATGGAAG CACTCAATTA CCTGCCATA GATTTATATG GTGAAGATTTC TTGGAGCGAG 300  
35 TATGTAAACC CTTTCGTGGG TGCAGGAACC GATGTCGAAA TTCCGAACTC CTATGACATT 360  
GATTGCTCTT CGTTCGTGAT GCCCGTCGAA GATAAGCAGG TCACCTCTCA ATTTGGCTAC 420  
CGTCGCGCTT TCGGACGGAT GCCTATGGT ATPGATCTTT CAGTGAATCG TGGCGATACG 480  
ATACGAGCAG CCTTTGACGG GAAAGTTTGT GTACGCAGCT ATGAAGCGCG TGGCTATGGC 540  
TACTACATAG TCTTGCGCCA TCCGAACGGA CTGGAGACTG TGTACGGACA CATGAGTCGC 600  
40 CAATTGGTAG ACGAGAATCA GATCGTTTCA GCAGGACAAC CGATCGGATT AGGAGGACAG 660  
ACGGGTCGAA GCACCGGTCC TCATCTTAC TTCCGAGACC GCTTCATGGG TATTCCCATC 720  
AATCCGAGTA CCATTATAGA CTTCGATAAC GGAGTGCCGC TCCGAGACAT TTACACATTC 780  
AAACGAGGGA GCAATTCTCG CTATGCAAAA GCCTCTAAGA CTTCTTCTCG CTATGCAAAA 840  
AAAGGGAAGA AAGGCAGACA AGCTTCTTCT CCTATGACCT ATAGAATCAA AAAAGGCGAT 900  
45 ACTTTGGAAG CAATAGCCAA AAGGCACGGC ACTTCTGTTC AGAAACTCTG TGCTACCAAT 960  
GGCATTTGGA AGAGTAAAT TTTGACTCCG GGCAAAGCCT TGAGGATCAA A 1011

## (2) INFORMATION FOR SEQ ID NO:172

- 50 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 453 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
55 (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- 60 (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:  
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- 65 (ix) FEATURE:  
(A) NAME/KEY: misc\_feature  
(B) LOCATION 1...453

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:172

70 ATGGCAAAAA TCAATTCTTA TGCTGAAGGC GTCAGCCTTC CTCGGATCAG AAGACGGATC 60  
GTCGGTAAGT GGATAGCCGA AGTATGCAGC CGATATGGGA AAGCGGTGGG AGAAATCTCC 120  
TATCTTTTCT GTGATGACGA ATATATCCTG AAAGCCCAATC AGGAATTTCT CGATCATGAC 180  
75 TACTACACCG ACATCATCAC CTTCGATTCC TCGGAAGCGG ATACGGTGAA TGGCGACCTG 240



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CTTATCAGTC TCGATACCGT ACGCTCGAAT GCCCGTGCTC TTGATCTTCG ATACGAAGAC 300  
 GAACTGCATC GTGTCAATTAT CCACGGCATA CTGCATCTTT GCGGATTGAA AGACAAGAGC 360  
 AAAAAGGATG AAGCCCAAAAT GCGTGACAGC GAAGAGAAAG CCCTTGTCAT GCTGCGAGAA 420  
 ACCATCGGAT CGGAGCTTTC CCTATTGCAT ACA 453

5

## (2) INFORMATION FOR SEQ ID NO:173

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1173 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...1173
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:173

ATGAAGGTAA AGTACTTAAT GCTCACATTG GTTGGAGCAA TTGCACTGAA CGCAAGTGCA 60  
 CAGGAGAATA CTGTACCGGC AACGGGTCAG TTACCCGCTA AGAATGTTGC TTTTGCTCGC 120  
 AATAAAGCAG GCAGCAATTG GTTTGTAACA CTGCAAGGCG GTGTTGCAGC GCAGTTCCTC 180  
 AATGACAACA ACAACAAAGA CCTCATGGAC CGCTTAGGAG CCATAGGTTT TCTTTCTGTC 240  
 GGAAAGTATC ACAGCCCTTT CTTTGCAACT CGTTTGCAAA TTAACGGAGG TCAAGCCAC 300  
 ACTTTCCTCG GAAAAAATGG CGAACAAAGAA ATCAACACCA ATTTTGGTGC AGCTCACTTC 360  
 GACTTTATGT TTGATGTGGT TAACTACTTT GCACCATATC GCGAAAAATCG TTTCTTCCAT 420  
 TTAATTCCAT GGGTAGGTTG TGGCTACCAA CACAAATTCA TCGGTAGCGA ATGGAGCAAA 480  
 GACAATGTGG AATCACTGAC GCGGAATGTA GGAGTTATGA TGGCTTTCAG ATTAGGAAAG 540  
 CGAGTAGACT TTGTGATCGA AGCACAAGCA GCTCACTCCA ATCTCAATCT AAGTCGCGCA 600  
 TACAATGCCA AGAAAACTCC CGTATTCGAA GATCCCGCAG GACGTTATTA CAATGGATTC 660  
 CAGGGGATGG CTACAGCAGG TCTTAATTTT CGCCTGGGAG CCGTAGGCTT CAATGCCATT 720  
 GAIHCAATGG ACTACGCACT TATCAATGAT CTGAATGGTC AGATTAACCG TTTGCGCAGC 780  
 GAGGTCGAAG AACTCTCAAA ACGTCTGTGTA TCATGCCCCG AATGTCCTGA AGTAACTCCT 840  
 GTTACTAAGA CAGAAAATAT ACTGACGGAA AAAGCTGTAC TGTTCGGTTT CGACAGCCAC 900  
 GTTGTGGACA AAGATCAATT GATCAACCTG TATGACGTAG CTCAGTTTGT AAAAGAAACT 960  
 AACGAGCCGA TTACCGTTGT TGGTTATGCT GATCCTACGG GTAATACTCA ATACAACGAG 1020  
 AAATTGTCTG AGCGTCGGGC TAAAGCCGTT GTTGATGTTT TGACAGGTAA ATATGGTGTG 1080  
 CCTTCCGAAT TAATCTCTGT AGAATGGAAG GGCGACTCTA CGCAACCGTT CAGCAAGAAA 1140  
 GCTTGGAATC GTGTTGTAAT CGTTCGCTCC AAG 1173

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## (2) INFORMATION FOR SEQ ID NO:174

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1155 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...1155
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:174

ATGACATACA GAATTATGAA AGCTAAATCT TTATTATTAG CACTTGCGGG TCTCGCATGC 60

75

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	ACATTCAGTG	CAACAGCCCA	AGAAGCTACT	ACACAGAACA	AAGCAGGGAT	GCACACCGCA	120
	TTCCAACGTG	ATAAGGCCTC	CGATCATTGG	TTCATTGACA	TTGCAGGTGG	AGCAGSTATG	180
	GCTCTCTCGG	GATGGAATAA	TGATGTAGAC	TTTGTAGATC	GTCTAAGTAT	CGTTCCTACT	240
	TTGCGGTATCG	GTAAATGGCA	TGAGCCTTAT	TTGCGGTACTC	GTCTCCAATT	CACAGGATTC	300
5	GACATCTATG	GATTCCCGCA	AGGGAGCAAG	GAGCGTAACC	ACAATTACTT	TGGAAACGCC	360
	CACCTTGACT	TCATGTTCTGA	TCTGACGAAC	TATTTCCGGTG	TATACCGTCC	CAATCGTGTC	420
	TTCCATATCA	TCCCATGGGC	AGGTATAGGA	TTTGGTTATA	AATTCCATAG	CGAAAACGCC	480
	AATGGTGAAA	AAGTAGGAAG	TAAAGATGAT	ATGACCGGAA	CAGTTAATGT	CGGTTTGATG	540
	CTGAAATTC	GCCTATCAAG	AGTCGTAGAC	TTCAATATTG	AAGGACAAGC	TTTTGCCGGA	600
10	AAGATGAACT	TTATCGGGAC	AAAGAGAGGA	AAAGCAGACT	TCCCTGTAAT	GGCTACAGCA	660
	GGTCTAACGT	TCAACCTTGG	CAAGACAGAG	TGGACAGAAA	TTGTTCTTAT	GGACTATGCT	720
	TTGGTCAATG	ACCTGAACAA	CCAAATCAAC	TCACTTCGCG	GTCAAGTGGA	AGAGTTGAGC	780
	CGTCGTCTCTG	TTTCATGCC	TGAATGCCCT	GAGCCTACAC	AGCCTACAGT	TACTCGTGTA	840
15	GTCGTTGACA	ATGTGGTTTA	CTTCCGTATC	AATAGTGCAA	AGATTGATCG	TAATCAAGAA	900
	ATCAATGTTT	ACAATACAGC	TGAATATGCG	AAGACCAACA	ACGCACCGAT	CAAGGTAGTA	960
	GGTTACGCTG	ACGAAAAAAC	CGGTACTGCG	GCCTATAACA	TGAAGCTTTC	AGAGCGTCGT	1020
	GCAAAAGCGG	TAGCCAAGAT	GCTTGAAAAG	TATGGTGTTT	CTGCGGATCG	CATTACAATT	1080
	GAATGGAAGG	GCTCATCAGA	GCAAATCTAT	GAAGAGAACG	CTTGGAATCG	TATTGTAGTA	1140
20	ATGACTGCAG	CGGAA					1155

## (2) INFORMATION FOR SEQ ID NO:175

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 570 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...570
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:175

45	ATGGAATTTT	TCATGTTATT	CATAGCGGCG	GTTTTCGTTA	ATAACGTCGT	GCTGTGCGAG	60
	TTCCCTCGTA	TATGCCCAT	CTTAGGCGTA	TCGAAGAAAG	TAGACACCTC	AATCGGTATG	120
	GGTGCAGCCG	TGACATTCGT	ATTGGCACTG	GCTACCTTGG	TTACCTTCCT	GATTGAGAAG	180
	TTGCTTTTGG	ATCGTTTCGG	ATTGGGCTTT	ATGCAGACCA	TTGCATTTAT	TTTGGTCATT	240
	GCGGCCTTGG	TGCAGATGGT	GGAGATCATA	CTCAAGAAAG	TATCTCCTCC	CCTCTATCAG	300
50	GCACTGGGTG	TATTCTTGCC	CTTGATTACG	ACGAACTGCT	GTGTGCTCGG	TGTGGCTATT	360
	TTGGTTATCC	AGAAGGATTA	TACCTGCTC	CAGAGCTTCG	TCTATGCAAT	ATCCACGGCT	420
	ATCGGTTTCA	CCTTGGCAAT	GGTTACTTTC	GCAGGTATTC	GAGAGCAACT	CGATATGACC	480
	AATCTCCCCA	AAGCTATGAA	GGGAATACCT	TCGGCACTCT	TGGCTGCCCG	TATATTGGCT	540
55	ATGGCTTTCA	TGGGCTTCAG	CGGTATCGCC				570

## (2) INFORMATION FOR SEQ ID NO:176

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 558 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
- (A) NAME/KEY: misc\_feature

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(B) LOCATION 1...558

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:176

5	ATGTTATTCA TAGCGGCGGT TTTCGTTAAT AACGTCGTGC TGTGCGAGTT CCTCGGTATA	60
	TGCCCCATTCT TAGGCGGTATC GAAGAAGGTA GACACCTCAA TCGGTATGGG TGCAGCCGTG	120
	ACATTCTGTAT TGGCACTGGC TACCTTG GTT ACCTTCCTGA TTCAGAAAGTT CGTTTGGAT	180
	CGTTTTCGGAT TGGGCTTTAT GCAGACCATT GCATTTATTT TGGTCATTGC CGCCTTGGTG	240
	CAGATGGTGG AGATCATACT CAAGAAAGTA TCTCCTCCCC TCTATCAGGC ACTGGGTGTA	300
10	TTCTTGCCCT TGATTACGAC GAACTGCTGT GTGCTCGGTG TGGCTATTTT GGTATCCAG	360
	AAGGATTATA CCCTGCTCCA GAGCTTCGTC TATGCAATAT CCACGGCTAT CGGTTTCACC	420
	TTGGCAATGG TTACTTTCGC AGGTATTCGA GAGCAACTCG ATATGACCAA TCTCCCCAAA	480
	GCTATGAAGG GAATACCTTC GGCACCTTG GCTGCCGTA TATTGGCTAT GGCTTTCATG	540
15	GGCTTCAGCG GTATCGCC	558

(2) INFORMATION FOR SEQ ID NO:177

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 2499 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:  
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:  
(A) NAME/KEY: misc\_feature  
(B) LOCATION 1...2499

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:177

40	ATGAACAAC TAAACATTAT CAGCTTCATC ATTGCTTTCC TATTCTTAGG AACGAGCGCA	60
	TCGGCTCAGC AATCGGGCGG ATCCGTTACA GGTACCGTAG TGGACAAAAG CTCAAAAGAA	120
	CCTATCGCAT ACGTACAAGT ATTCTGCAAA GGAACCACTC TCGGAACTTC CACGGATGCA	180
	AACGGAAACT ACTCGATCAA GGGAAATCCCT TCGGGTAATC AAACATATCGT AGCCCGACTC	240
	ATGGGTACT CCACCTGCGA AGAAAAAGTA CATATAGAAA AGGGTGGTTC CCGCCACGTA	300
45	GACCTCTATC TGACCGAAGA GATTCTCTCT CTCGATGGGG TAGTGGTATC TGCCAAATAGA	360
	AACGAGACTT TCCGCGCTCA AGCACCCTCG TTGGTAACGG TACTGTCCGC GGAACTTTTC	420
	CTCAAAACCA ACTCTACCAA CCTGAGTCAG GGACTTAAAT TCCAGCCCGG TCTGCGCGTG	480
	GAGGACAACG GTCAGAACTG CGGTTTCAAC CAAGTTCGTA TCAATGGAGT CGAAGGAGCC	540
	TATTGCAAAA TTCTTATCGA CAGCCATCCC ATCTTCASTT CGCTTGCCGG TGTCTATGGC	600
50	TTGGAGCAGA TGCCCTGCCAA TATGATCGAA CGTGTAGAAG TAATTCGCGG TGGAGGTTTC	660
	GCTCTGTTTC GCTCTAATGC TGTGGGAGGC GTTATCAACG TAATTACGAA AGAACCGCTT	720
	CGCAATTCGG CCGAGATCAG CCATCTACG ATGACCTTCG ACCACGCGAA AGGGTGGGGG	780
	AGCTTCCAAA ATACGACCCA GTTCAACGGT TCTATGCTGA CGGAAGACCG CAAAGCCGGT	840
	GTCATGGTAT TCGGCCAACA CAACTACCGT CCCGGACAGG ATATAGACGG CGACAACCTT	900
55	ACCGAACTAC CCAATCTGCG CAACCGCTCG CTCGGTTTCC GTCATACTA TAAGACCGGT	960
	CTCTACAGCA AAGCAACCCT CGAATATCAC AGCATGCAGG AGTACCGTTC TGGTGGCGAC	1020
	AGACTGGACA ATCCCTCTTT CGAAGCCCGG ATAGCGGAAT ATCTCCAGCA CTATATCAAT	1080
	GGCGGAAGTT TCAAAATTCGA TCAGGGCTTC AGCGGTGGCA AGGATTTCTT CAGTCTGTAT	1140
60	GCTTCAGCAC AAGACGTTCA GCGTCGTAGC TACTACGGGG GTGGCGACTA TACCGAAAAT	1200
	CTGCTGAACG GAGCAGTTCA GAGTGAAGC ACCGAATCGG ACGAATACAA CGATGCTTTC	1260
	ACGGCTCTTA CTCTCTACGG GACTACCAAG GGATTCGATT TGCAAGGAGG AGGTATGTAC	1320
	CGTCATACCT TCGGAGAAAA CTGGGACTTT ACCGGCGGAC TCGAATATAT CTACGGCCAA	1380
	CTCGATGACA GAAGCGGCTA CAGACCGAGC AAAATAGATC AGAATACCTC TACTTTTAGT	1440
	CAGTACGACC AGCTCGAATA TAAGACGGAG AAGTTAAGT CCCTTATCGG AGCACGTATC	1500
65	GACTATGTTT TCCTCAATCA GGATGGCAAA CGCTATATCG ATCCGCTCTT CATTTTCAGT	1560
	CCTAGAGCCA ACGTACGATA CAATCCCAAT AAGAATCTCA GCTTCCGACT CTATACAGC	1620
	GAAGGATTCC GCGCTCCTCA GTATTTGAT GAAGATCTGC ACGTAGAGTT GGCCGGTGGT	1680
	ACTCCTATCA GCCGTGTCCT TTCCCCAAT CTGAAAGAAG AACGTTACG AAGCATCAGT	1740
	GCTTCTTTTC ATTATACCA CAGAGCCGAC GAATGGCAAT TCAATATCAT GGGAGAAGCC	1800
70	TTCTCCACCT TTATCAGCAA TCAGTTCAAA CCATCCGATA AGGTGGAAC CACGAGCGAT	1860
	GGCAAGAAGT GGATCATTCG TACCATCTAC AACGACAAGG ATGGAGTATC GAAGGTATAT	1920
	GGTGTGAATC TGGAGGGAAG AATCGCCTAC AACAAATCGT TCGACCTCCA GCTCGGCGGT	1980
	ACATGGCACA GAAGCCGCTA CGGAAGCATC TATACCGCTG TGGAAGCGGA CAAAACAACG	2040
75	GGACAAGCCG AGATCTCTGT GAAAGACTAT GTACGCACCT CGAATCTGTA CGGCTATTTC	2100
	GTTGTACGG TACGTCTTAC CGAGCACTTC GCCATCAATC TCTCCGGTAC ATTACGGGGC	2160

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5 AAAATGGATG TAGTACACGA AGCCTATGAA GGGGATATTC CCGCAGAACA CATAGCTCCG 2220  
GACGGATCGT TCGACTTTGA AATGAATGGT CAGCAATTCA AAGSTTTGGC CGAAGGTCAT 2280  
GCCAAGCTCG TCAAGACTCC GGCCTTCGCC GATATAGACC TCAAGCTGAG CCACGACTTC 2340  
CACCTTGCTT CCACTATGAC CTTGGAATTG AATGCCGGAA TACAGAACAT ATTCAACAGC 2400  
TATCAGAAAG ACACGGACAA GGGACCGGGT AGAGCTTCTA CTTACGTATA CGGCTCTATG 2460  
CAGCCCAGAA GGATTTTCGT CGGTACAAAG ATCAATTTT 2490

(2) INFORMATION FOR SEQ ID NO:178

10

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 2673 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: circular

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(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

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(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMOHAS GINGIVALIS

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(ix) FEATURE:

- (A) NAME/KEY: misc\_feature  
(B) LOCATION: 1...2673

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:178

ATGTACAAAA AGATTATTGC CGTAGCAGCT CTCTTCTGCG CCAGCATAGG GATCCTGAAA 60  
GGACAGTCCT CCGATCTGAC CCCTCAGGAT ACTATATATA GCCCTGAAAT ATCCTATGCC 120  
AAGCCTATTC ATAAGACCAT AGCATCTATT GAGATCGAGG GAATGAGGTC TTTCGATGAC 180  
35 TTGTCTTTCG GCAATCTTTC AGGCTTGGCT GTAGGTGATG AAGTCCTGAT TCCTGGAGAT 240  
GCCATGTCTG CTGCCGTGAA TAGAATTATG CGTCAGGGCT ACTTCTCAAA TGTGCGAATC 300  
ATCGGTACAGA AGTATTTTAG TGAGAAAGGT TATCGCGATG CCAGCATACG GATAACGCAG 360  
CGCATCAGTA AGGTTACTTT TAGCGGGGTA AAGAAGTCTG AGAGAGAAGA TCTTGAAATG 420  
40 AAAATCGGTC TTCGCGAGGG GATTCAGATG ACCAGAAATA ATGAAGACAA GGTACGGCAA 480  
ATCGGTACAGA AGTATTTTAG TGAGAAAGGT TATCGCGATG CCAGCATACG GATAACGCAG 540  
GAACCGGATC TTTCCAAAGA TGGCTTTGTC AATGTGCTTA TCTCGATTGA GAAGAAAAGC 600  
AAAACCAAGG TGAATGAAAT TTATTTTTCG GGCAACAAGG CCCTTAGCAA TCATAAGCTA 660  
AGAATGCGCA ATGAAGACAC CAATGCCAAA TTCAGTCTTA GAAAGCATAT TCGCTCATCT 720  
TTCTTGAAAC TTTTTAGTAC TCATAAGTTT GTGAAGAGA GCTACCGTGA AGATTGGGTC 780  
45 CGATTGATAG AGAAGTATCA GGAATATGGA TATCGTGATG CTGAAATACT GACCGACAGT 840  
GTGCTGAAGG CTCCTGACGG CAAAAGAGTG GATATTATAT TCAACATCGA AGAGGGGCAG 900  
AAGTATTATA TTAAGGATGT CAACTTTGTG GGCAATTCAC AATATCCATC GGAGTATTTG 960  
GAACGAGTGC TCGGAATAAA ATCCGGAGAT GTGTACAATC AGAGACGATT GGCTAAGCGT 1020  
CTCAATGAAS ATGAAGATGC TGTGGGGAAC CTGTACTATA ACAATGGCTA TATTTTGGCG 1080  
50 TGGGTCGATC CCGTGGAAAC AAATGTAGTG GGGGATTCTG TTTCGCTTGA TATTCGTATA 1140  
GCGGAGGGGA AGCAGGCCAA TATCAATAAG GTGATCATCA AAGGAAATAC TGTGCTGTAC 1200  
GAAGACGCTAG TACGCCGAGA GCTTTACACA AAGCCCGGCC AGCTCTTGA TCGCGAGGAT 1260  
ATCATTAACCT CTATTCGTCT CATCAATCAG CTGGGGCATT TCGATGCCGA AAAATCTATT 1320  
CCCGSTCCGA TTCCCAATCC CGAAACAGGA ACAGTGGATA TAGAGTATGA TTTGGTGCCG 1380  
55 CGTAGCAGTG ACCAATTGGA GCTTCTGTG GGTGGAGTC AGTCCGGACT TCTGTTCCGA 1440  
GGAGCCATTA AGTTCACGAA CTTCTCTGTC GGCAACTTGC TCCATCCCTC GATGTATAAG 1500  
AAAGGGATCA TTCCGCAAGG GATGGGCAA AACTATCAC TGAGTGCTCA GACCAATGGA 1560  
AAGTACTATC AGCAGTATAG TGTACATTT ATGGATCCAT GGTTTGGGGG CAAGCGGCCG 1620  
GATATGTTCA GCTTCAGTGC ATTCTATTCC AAGACTACGG CGATTGACTC CAAGTCTAC 1680  
60 AATAGCAATG CCGGCAACTA CTATAATGCC TACTATAATA GCTACTACAA CAACTATAAT 1740  
AGTTATTACA ACGGTATGTC GAACTATACC GGCGACCTCT ATACTCAGGC CAGCGATCCG 1800  
GATCGTTCGC TTCAGATGTT AGGTACTTCC ATCGGTTACG GTAAGCGTTT GACTTGGCCG 1860  
GACAATTGST TCCAGATTTA TACTTCTCTG AACTACACCT ACTATAGACT CGGAAATTGG 1920  
65 AGCTACAGTA CCTTCCAAAA TTTCCATCAT GGCTCGGCTA ATGATCTCAA CTTGGAGCTG 1980  
CGTCTCTCTC GTACTTCCAT CGATAATCCT ATTTATACCA GAAGCGGATC GGATTTCATG 2040  
GTTTCTGTTG CTGCTACTCT TCCTTATTCT TTGTGGGACA ATCATGACTA TGCCAGCCAG 2100  
AACCTCAGCG GAGGTGATGG TTACAGATT ATCGAGTATC ACAAGTGGA GTTTAGAGGA 2160  
CGAGTTTCTT CTCCATTGCT CAATCCTGCT ACGCATAAAT ATACACCGGT GCTCATGAGT 2220  
CGAGTGGAA GAGCAGTTCT TSGTTCGTAT AATTCCAAAT AGAAATCTCC TTTCCGTACT 2280  
70 TTCTATATGG GAGGTGATGG TATGTCCAGC TATTATGSGT GCTACATGAA TGAGACTATA 2340  
GGTTTGGCGT GTTATAAGAA CGGATCTATT GCCGGTAATA ACTACGACTA TGCATATGCT 2400  
TATATGCGGC TTACGATGGA ACTACGTTTC CGGATTCGT TTGAAAACCT ATTCAATGCG 2460  
TGGCTCTTAG CTTTTCGCGA AGCAGGCAAT CGGTGGCGCA GTATCGACAA TTATAATCCC 2520  
TTTAACCTGA AGCGATCGGC CGGTGTAGGA TTGCGTGTAA CGTTACCGAT GGTCCGAATG 2580  
75 CTCGSTATCG ATTGGGGATA TGGCTTTGAC CGTCCGGACA ATTCTCTAGA GCGAGGAGGA 2640

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AGCAATGTCC ACTTTGTGCT CGGACAGGAG TTC

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## (2) INFORMATION FOR SEQ ID NO:179

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 522 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION: 1...522

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:179

ATGAATGGCG	ATATGAAACG	GTTTTGATT	TTGATCGGCT	TTGCACTGGC	GGTAGCTTTC	60
TCCGGTTTTT	CCCAAAAGTT	CGCTTTGGTA	GATATGGAAT	ATATCCTCAG	GAATATTCCT	120
GACTATGAGA	TGATGAACGA	ACAGCTGGAA	CAGGTGTCCA	AGAAATGGCA	AAATGAAATC	180
GAAGCTCTCG	AAAATGAAGC	CCAATCTATG	TATAAGAAGT	ATCAGAGCGA	TCTCGTATTC	240
TTGTCTGCTG	CACAGAAGAA	AACCCAAGAA	GAGGCTATCG	TAAAGAAAGA	GCAGCAAGCA	300
TCCGAGCTCA	AGCGGAAGTA	TTTCGGCCCG	GAGGGGGAGC	TGTATAAGAA	ACGCTCCGAT	360
CTGATGAAGC	CTATTCAGGA	TGAGATTTGG	AATGCTATCA	AAGAGATTGC	CAAGCGTAAC	420
AACATATCAGA	TGGTGCTTGA	TAGAGGTACG	TCCGGAATTA	TCTTTGCCAG	TCCGTCTATT	480
GACATTAGCG	ACCTTGTA	GAGCAAGATG	GGCTTTAGCA	AG		522

## (2) INFORMATION FOR SEQ ID NO:180

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 510 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION: 1...510

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:180

ATGAAACGCT	TTTTGATTTT	GATCGGCTTT	GCACTGGCGG	TAGCTTTCTC	CGGTTTTTCC	60
CAAAAGTTTC	CTTTGGTAGA	TATGGAATAT	ATCCTCAGGA	ATATTCCTGA	CTATGAGATG	120
ATGAACGAAC	AGCTGGAACA	GGTGTCCAAG	AAATGGCAAA	ATGAAATCGA	AGCTCTCGAA	180
AATGAAGCCC	AATCTATGTA	TAGAAAGTAT	CAGAGCGATC	TCTGATTCTT	GTCTGCTGCA	240
CAGAAGAAAA	CCCAAGAAAG	GGCTATCGTA	AAGAAAGAGC	AGCAAGCATC	CGAGCTCAAG	300
CGGAAGTATT	TGGGCCCGGA	GGGGGAGCTG	TATAAGAAAC	GCTCCGATCT	GATGAAGCCT	360
ATTGAGGATG	AGATTGGGAA	TGCTATCAAA	GAGATTGCCA	AGCGTAACAA	CTATCAGATG	420
GTGCTTGATA	GAGGTACGTC	CGGAATTATC	TTTGCCAGTC	CSTCTATTGA	CATTAGCGAC	480
CTTGTA	GCAAGATGGG	CTTTAGCAAG				510

## (2) INFORMATION FOR SEQ ID NO:181

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 489 base pairs

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(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: circular

5 (ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

10 (vi) ORIGINAL SOURCE:  
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:  
(A) NAME/KEY: misc\_feature  
(B) LOCATION 1...489

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:181

20 ATGAAGAAAT TTTTCTCAT GCTTCTGATG GCTCTTCCTT TGAGCCTCTT GGCACAAAAG 60  
GTGGCAGTGG TAAACACTGA GGAGATCATT TCCAAAATGC CGGAACAAGT AGCTGCTACC 120  
AAACAGCTCA ACGAATTGGC CGAAAAGTAT CGCCTTGATC TCAAGAGTAT GGACGATGAG 180  
TTTGCCAAAA AGACAGAAGA ATTTGTAAAG GAAAAAGACT CTCTACTGGA GAACATCCGC 240  
AATCGTCGTC AGCAGGAACT TCAGGATATT CAAACTCGTT ATCAGCAGTC ATACCAAACG 300  
25 ATGCAGGAGG ATTTGCAAAA GCGCCAACAA CAGCTTTTGG CTCCTATCCA ACAAAGGTG 360  
GCTGATGCCA TCAAGAAAGT GGGTGACGAA GAAACTGTG CCTACATCAT GGAGGCCGGT 420  
ATGATGCTTT ACACCGGAGC TACTGCTATT GACTTGACCG CAAAGGTAAA AGCGAAACTC 480  
GGAATCAAG 489

30 (2) INFORMATION FOR SEQ ID NO:182

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 2481 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: circular

35 (ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

40 (vi) ORIGINAL SOURCE:  
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:  
(A) NAME/KEY: misc\_feature  
(B) LOCATION 1...2481

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:182

55 ATGAAGGAAG CTATTCCTCG AAAGAACAAG TATATAAAGC TCAACGGTAT ATACAGATTG 60  
TCATTCATTG TGCTATGCTG CCTGCTATGC TCTCAGGCAG CTATGGCACA AGGCGTCAGG 120  
GTATCGGGCT ATGTGCTCGA CCGTGGGGAA AAGCCGATCC CGTTGCGCCG AGTCAAAGTG 180  
CGTGGTACGG GGACAGGCGC AACGACGAAT CTGAAAGGAT ACTACGAGTT TCGGATGAAG 240  
GCCACGACGG ACAGCATCAC GATCGAGTTC AGCTCCATGG GGTACCAAGG GGTAAAGTCG 300  
AGCTTTCCGT CTCTGACCAA GGACACTCGG CTGAATGTTT GTTGGCAGA GGCCGAGATG 360  
60 GAGCTTTTGA GCGTGACGGT ACAGGCCACA AAACGCAGAC TCAACACGAT GGAGCGCGTC 420  
AATACCCGAG ACCTTCGTGT CAATGCAGGG CCTACGGGAG GGGTGGAATC GCTCATCAAT 480  
ACCTACGCAG GAGTAACGCA GAACAATGAA CTAAGCTCGC AATACTCGGT TCGCGGAGGA 540  
AGCTACGATG AGAATATGGT CTATGTAAAC GGAGTGSAGG TTTATCGCCC GCTGCTGGTT 600  
CGCTCTGCAC AGCAGGAAGG TCTGAGCTTC GTCAATCCGG ATCTGACACA ATCCGTACAG 660  
65 TTCTCCGCGG GAGGGTTTAC GGCGACTAT GGCGACAAGA TGTCCTCGGT ACTGGATATT 720  
CGTACAAGC AACCGCAGGA GAAGGAAGGA GCGGTACTCC TCGGGATGCT ACAATCGAAT 780  
GCCTACTATG GCAGCAGTGC CGGAGCCTTC AGCCAAATCA CGGTGTACG CTACAAGAGT 840  
GCCAAATCGC TCTTGGGCAC TACGGACACG AAAGCCGAAT ACGATCCGAT CTATGCGGAC 900  
GGACAGACAT TCATGACGTA CCGTTTCAGC CCCAAGCTGT CGGTAGTTT CCTCGGCAAT 960  
70 ATTTCGCAAA CTCGCTACAA GTTTGTCCCT CAGACCCGTG AGACGAGCTT CGGTACACTG 1020  
AGCGATGCCA AAAAGTTGAA GATCTTTTTC GACGGTCAGG AACAAGATCG TTTCCTGACC 1080  
TACTTCGGTG CCTTCAGCAT GAACTTCGTG CCGGACGACA AACAGCGGCA TACGGTTACG 1140  
CTTTCGGGCT TCACAGTAA CGAACGGGAG ACCTACGATA TTCAGGGAGA ATACTTTCTG 1200  
AACGATGTGC AGCTGGGGG GAGCGGAAGT GCTTCGATGG CTTCGGGGCTC AGAGAACTCC 1260  
75 AACGGCTTGG GCATCGGGCG CAATCACGAG CATGCGCGCA ACAGGCTGAG CTACCGCGTG 1320

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5 CTGAACATGG GTTACAGAGG GGAGATGAAG CTGAACGAGA AGCATCGCCT GCAAGCCGGC 1380  
 GTATCGGCAC AGATGGAGAA AATAGCCGAC CATATCAGCG AATGGGAACG GAGGGATTCC 1440  
 GTAGGATACA ACCTACCTCA CTCGGAGACC GTATTGCTGA TGTACAATAA CCTATATGCC 1500  
 GATACGCAGA TGAGGGGAAC GCGCTTGTCG GCATTGCTAC AGGATCGATT CAACCTCAGC 1560  
 ATGGGAGGAG GTACATTTTC TCTCATTCGG GGTATCAGAG CTTCTGTGGT GAGCTTCAAC 1620  
 AAGGAGTTGC TCGTCAGCCC ACGTATCAGC GTGGGTATT CTCCGAAAG CAACCCGGCT 1680  
 TTGGTACTGC GTGCAGCCGC CGGACTTTAT TATCAGGCAC CGTTTTACAA AGAGCTAAGG 1740  
 CAGACGCATA AGGATGCCGA AGGCAATAAC GTGGTTGTCC TCAACGAGAA GATCCGCTCT 1800  
 CAGGGAGCTT TTCACATTCT CGCAGGAGCA GACTATACCT TCGAAATGGG GGGGCGAAAA 1860  
 10 TACAAGTTTA CGGCAGAGGC TTAACAAG AGCCTGTTCA ACATCAACCC GTATATAATA 1920  
 GAGAACSTGA AGATCCGCTA TCTGGGCGAA AACATCGGTT CGGGTTATGC TCGGGGTATC 1980  
 GATCTCAAGC TCTTCGGCGA ACTGGTACCC GGAGTGGATT CGTGGCTGAC GGCTTCCATT 2040  
 ATAAAGCCCC GTCAGAAACT GGATGGCTAC GGTTCCTTAC CACTGATGAA CGCACCCACT 2100  
 TACAATTTCT CCTTCTTCTT TCAGGAGTAC GTGCCGGGCA ATAAACGCAT CACAGCCACC 2160  
 15 CTGCGGGCTG CACTAAGCGG AGGATTGCCC GAGCTCAATC CGAGCAAAGG GCTTAGCTCG 2220  
 CCGGCCTTTA CCGCACCGGC CTATAAGCST GTCGATCTGG GGGTAATGTA CAAATGGCTC 2280  
 GACCCGGATG ACTCCTTTGC CGGCCGAAGC AAATGGCTAA TGGGAGTAAA AGGGGCTCTC 2340  
 ATAGGGGCTG ACCTCTTCAA TCTGTTCGAC ATGACCAACG TCAATTTCTA CTACTGGGTG 2400  
 20 TCGGATGCCT ACCAACAGCA ATACGCCGTA CCGAACTACC TGACACGCCG CCAATTCAAC 2460  
 CTGCGTCTCC TCGTCGAATT C 2481

## (2) INFORMATION FOR SEQ ID NO:183

- 25 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 2016 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 30 (D) TOPOLOGY: circular  
 (ii) MOLECULE TYPE: DNA (genomic)  
 (iii) HYPOTHETICAL: NO  
 35 (iv) ANTI-SENSE: NO  
 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS  
 40 (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...2016  
 45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:183

ATGTACAGCG GACATCATAA AATCCATTAT CCTTTTCTTA TCCTGTTGGT ATGCCTTGCT 60  
 TTTGCTGCCT GCAAGAGCGT GAAGTTGAAA GATGCGGAGA AGGCACATGA TCGCCAAGAG 120  
 TATACCAAGG CTGCCGATAT GTACAATACA TTATACAGGC GTACCCGACG AAAGCAGGTG 180  
 50 GAGATGAAAG CTTATACGGC TTTCCGATCC GGTGAAAAC TCGTGCCGC CGSCAGACAA 240  
 GCCAAAGCTT TGGTGGGCTA TCTGAATGCC AGACGCTACG GGTATCCGGA TTCTGTGGTA 300  
 CTGCTCCGTT TGGCACAGAC TTATCAGCAA GGAGGTAACT ATAAGGAAGC CGAGGTACTC 360  
 TTCGTGGGAT ATCTGGAAGC TTATCCGAAA AGTTATTTTG CAGCTATCGG TTTGGAGGGG 420  
 TGTCTCTTTG CCGGCCAGCA AAAGGAATAT CCTACACGTT ACCGGATACG GCGAGCTGCC 480  
 GAGTGGAAAT CGGCACGGGG CCACTTCGGC CCGGCCTATG CACCCGATGC TTCGGCTCTC 540  
 55 TATTTACATG CGAGCAGAAG CAAAGACGAC GGTTTGGATA ATAGCAGCAT AACGGGACTG 600  
 AAACCCAACG ACATTTATAT CATCAAACGA GATGCACAAG GACGATGGGG ACGTCCCGAT 660  
 AGCGTGTCGG GAGGAATCAA CACTCCATGG GATGAAGGCG TGCCAACGAT CACGCCCGAT 720  
 GGTAATACCA TATATTATAC GTTGGCGCAG CAAGGAGCGG ATTACGACCG TACGGTACAG 780  
 ATCTATTCGG CCGCTCGGAG CGGAGAAGGC GGTGGAGCA ACGGTTCCGT CGTGGACATT 840  
 60 ATGCGCGATT CGTCCGTAT GGCTGCTCAT CCTCTATGT CCGCATCCGG CGATTACCTG 900  
 TATTTCTTCA GCAATATAGG CGGTAGCTAT GCGGCAAGG ATATTTATCG TGTCAAGGTG 960  
 TCGGATCGTT CTATATGGTT ACCGGAGAAT TTGGGGCCTG ATATCAATAC GCCGGGGGAC 1020  
 GAAATGTTTC CCTTCATAGA TGGGGATAGT ACCCTTTTCT TCGCTTCGGA CGGACACGCC 1080  
 GGTCCTGGGAG GACTGGATAT TTTCAAAGCC ACGCTGSACT CTACCGGCCA ATGGCATGTA 1140  
 65 GTCAATATGG GACAACCGGT CAATTCCTCT GCCGATGATT TCGGCTTGGC TGTGGAGCCT 1200  
 AAAGGCAAAA ACAAGAAGA AGCTTTGCCG GACAACGGAG TCAAAGGTGT ATTTTGTTC 1260  
 AACCGAGGCG ATGCACGGG ATGGCCGCAC CTCTTCCATT TCGAACTGCC GGCTATCTAC 1320  
 ACCGAGATTC AAGGTTATGT GATGGACAGA GAAGAAAATC CCATAGCCGG AGCCACTGTC 1380  
 AGGATCGTAG GCGAACGGGG CCCCGTAGGA CAGGGATTCT TGAATACTCG TGACGATGGC 1440  
 70 TCTTATAAGA TGACGTGCA GGGCGATACT CGCTATSTAA TGCTTGGCGG AGCATCGGGT 1500  
 TATTTGAATC AGTACGTAGA ACTCAAGACC GATACCGCCA AGCAGAGTGA GACCTACTAT 1560  
 TTGGACTTTT TCCTTGATC GCGTGAGAAA GCGAGGGCT TGCAAAATAT TTTCTATGAT 1620  
 TTCGATAAAG CTACTCTTCG CCCCAGAAAG ATGAAGAGCT TGGACGAAT GATTCGTATC 1680  
 CTCACGGACA ATCCGGATAT TCGATCGGAA TTGGGTTTCC ATGCCGACAG GAAAGGCCCC 1740  
 75 GATGCTTACA ACCTCGGACT ATCTGACCGC AGAGCCAAAT CCGTGGTGGG TTACCTCAGG 1800

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5 AGTCGTGGCA TAGCGGCCGA CAGGCTTACG TGGAAAGGCT ACGGTAAGTC TGTCCCCAAG 1860  
 ACGGTGACAG CCAAAATTCG CGAACGGCAC GATTTCTCGA AGGAAGGCGA TGTGCTCACC 1920  
 GAGGAATTTCG TAGCACCTTT GACCGAGGAG CAGCAGTCAG TCTGCGACCA ACTGAACCGT 1980  
 CGTACCGAGT TCCGTGTGAT CGAAGAAGAG TTGCGT 2016

## (2) INFORMATION FOR SEQ ID NO:184

- 10 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 2124 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular
- 15 (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- 20 (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- 25 (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION: 1...2124
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:184

30 ATGAAAAAGT TTTTCTTCGC GCTACTATCG ATTGGTATTT CAGCGCAGGC TTTTGCCAAG 60  
 ACGGACAACG TCCCGACAGA TTCGCTACGA GTACACAATC TTCAGACCGT CACGGTCTAT 120  
 TCTACACGCA CGGCCGTACC TCTGAAAAAG ATACCGGCCA AGATGGAACAT CATCTCATCG 180  
 CGCAACATCA AGCAGTCCGG CTTTAACAAC ATGACCGACA TCCTCAAGAC GCAAAGTTCCG 240  
 CTCGATGTCA TACAATACCC GGGCTTTAGT TCGAACATCG GTATCCGCGG TTTCAAGCCC 300  
 35 TCCGGCAAGT ATGTAACCGT ATTGGTAAAC GGCATCCCTG CGGGAACGGA CAATATCTCT 360  
 ACGTCAACA CGAGCAACAT CGAACAAATC GAGATCCTCA AAGGCCCGTT CTCTTCCATC 420  
 TACGGCACCA ATGCCATGGG CGGTGTGGTG AACATCATCA CCCACAAATC CAAGGACAAG 480  
 ATCCATGGCA ACGTTTCTCT CTTCGGCGGT AGCTACCAGA CCATGGCCGG ATCATTCAAC 540  
 TTGGGTGGCC GCTTCGAGGA TATTTTCTCA TTCGATCTTA GTCTGGGCTT GGACAAGCAG 600  
 40 AACAAAGGACT ATAAGACCGG ATCAAAACAAT TTCTTATCCC TGAGCAAATC GGAAGAAGCT 660  
 ATAGTAGATG TAAATGCTAC CAAAAACAAG AAAATGAAGG GGAGCGACTA TACTGTAGCA 720  
 ACGGGACGTC TGCGTTTCGG TATCGACTTC ACGCCCGAAT GGTGCTGAA TCTGTATCAA 780  
 AACGTATTTC TCGGAGATGC GATCCCGTA GGAGGATCTA TATGGGGCGT TTACGGAGAA 840  
 TCCAAAAAAA ATCTGAATCG TTCTTCGACC TCTTTCGAGC TGCTCGGCAA ACATGGCTGC 900  
 45 CACACGCTTC AATTCCTCCC CTACTTCAAC ATAGAGAAAT CGGAGAATA TAACAATGCC 960  
 GATCCCACCG GTTTCATCAA CTACAAAGC GACTACTACA CCTATGGTGC CCTACTCCAG 1020  
 GACAAGATTI CCTTTGGAGG ACAAATATC GTACTCGGTG TCGACAGCCG AAACATGACG 1080  
 ATGGAGTCAG AAGATTTCGA GCAGGCAGGA GTGAATACAA AGCCATACAA CCCCAGATAT 1140  
 GGCACGAACA ATATCGSTTT GTTCGGACAG GCCAATTTCT ACCTGCTGAA CGATGCTCTA 1200  
 50 TCGATATCTG CCGGTGCACG TGCCGACTTC ATGTCTTTG ACCTGAAAGC GAACGAGTAT 1260  
 CTCAACAATG AAGCCAAACA GGAACCTCAT AAGTAATCA ATCCGAATGT CGGAATCAAA 1320  
 TATGAGTTTG TGAAGGCCCT TACAGCTCAT GGTACATTG GTAGTGCATT CAGTGCTCCC 1380  
 GATGCTTTCC AAAAAGCAGG CCAATACGTA GGCCCGTTG GCACGACCAT AGGCAATCCT 1440  
 55 GACCTGAAAC CCGAAAAGTC CATGACCTGG GACTTCGGTA TCGGATACAG CAATGCACGC 1500  
 TCGGGGATCC AAGCCGACGT AACCTTAACC TATTTCCACA CCGACCACAA AGATCTGATC 1560  
 TTGTCCAGCC CTGACTATGC TAATAATATC ACCACATACA TCAATGCCGA CAAGGCTCGT 1620  
 ATGAGCGGTA TCGAGGCCCT TTTGTCTTAT GACTTCGGCA GCCTCTTTGC CAACAAGTTC 1680  
 TCTCTCCGCG CATTTGCGAA TGCCACGATC ATGCTCAATT CCGAGATGAA GAAAAGCCAG 1740  
 60 ACGGATGCC CTGGAGCGA AATGTACTAC GTTCGCAAGC AGAACATCAC CTTGGGTATC 1800  
 GAATATCGTG GCAAAGAAGG ACTTGAAGTG ATGCTCAACG GTCGCTTCAT GGGACGCAGG 1860  
 ATCGAGCAAA ACTGGTATGC TTTACTACCC GAAGTTCCGCC CCGAACTCCA GCAACTGCTT 1920  
 GCAGCAGAAG AGCCTGAATT GGCTGCTCAG GGACTGCTCC GTCATCCGCA AGCAATGGTG 1980  
 TTCAATGCCT CTGCTTACTA CCACATGAAC AAGTATCTCA CCTTCGGTGT GAACCTGAAC 2040  
 65 AACATCTTGG ATGAGCTTTA TACGGAGAAA GACGGCTACC ACATGCCCGG ACGTAACATC 2100  
 ATGGGTAAGG TTATGGTCAA CTTC 2124

## (2) INFORMATION FOR SEQ ID NO:185

- 70 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1386 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 75 (D) TOPOLOGY: circular



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(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

5 (iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:  
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

10 (ix) FEATURE:  
(A) NAME/KEY: misc\_feature  
(B) LOCATION 1...1386

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:185

ATGAACAGGT	TTTCAATCA	TTGGCCCTGC	ATCCTCGTGG	GSTTTGTA	CTGGTTTGTA	60
TGGGCGAGTC	GGACTGTGGC	ACAAAACGCC	TCCGAAACGA	CGGTATCGTA	CGATACGGAT	120
ACGCGCGTAC	TCTCCGAAGC	CGATGTGCTT	CGGATCGCTC	TTAGTGAGAA	TGCCACAGTG	180
AAAGTGGCCG	ATATGGATGT	GCGCAAACAG	GAATATGCAC	GTAGGGCAGC	ACGTGCCGAT	240
CTCTTCCCGA	AASTAGACCT	CAATGGCGTT	TACAGCCATA	CGCTAAAGAA	GCAGGTCTTA	300
TATATAGATA	TGCCCCGGTT	CAGCAGTAGC	GAAGGTATCG	AAATGGGGCG	TACACACAAT	360
ACGCAAGGAG	GGGTGAACGT	CTCCATGCCA	TTGGTGTCCG	CACAGCTTTG	GAAAAGCATT	420
GCCATGACCG	GAGAACAGCT	CGATCTGGCT	CTGGAGAAAG	CTCGCAGCTC	CCGAATCGAT	480
TTGGTGGCAG	AGGTGAAGAA	GGCTTACCTC	AGTGTATTGT	TGSCCGAGGA	CTCTTATGGC	540
GTATTCAAGC	GCAGCTATGA	CAATGCTCTG	GCCAATTATA	AGAACATATC	CGACAAGTTC	600
GATCGTGGAC	TTGTGGCCGA	GTATGATAAG	ATTCGAGCCA	ATGTACAGGT	ACGCAACATC	660
GAGCCTAACC	TCTTGCAAGC	GCAGAACTCC	GTAGCCCTTG	CTCTCTGGCA	GCTCAAGGTC	720
CTGATGAGCA	TGGAAGTGGA	AACTCCGATC	AGACTCTCCG	GTTCAATTGT	CGACTATAAA	780
GAACAAGTCT	ATACCGGCTA	TTTTGCCGCC	GATACGCTTA	TTTCCAACAA	CTCTCCCTG	840
CGTCAGCTCG	ATATACAGCG	TGCTCTGGCT	GTCAGTGCAG	ACAAGCTGAA	CAAGTACAGC	900
TTTCTGCTTA	CACCTCAATCT	GGGAGGGCAG	TACACCTATT	CGCTCAACAG	CAACGACATC	960
AAATTCTGGG	GGGAGGGACA	ACGCTGGACG	CCTTTCTCCA	CCATATCGCT	CAGCCTGTAC	1020
ATTCTTATAT	TCAATGGAGG	CAAACTGCTG	TACAACGTGA	AGCAAAGTGC	TTTATCGATC	1080
CGTCAGATCG	ATCTGCAACG	ACGCCACATA	GAGCAATCCA	TCCGAATGGG	AATCAAGAAC	1140
CAAAATGACC	GTCGCGTAC	CTGTATGCAG	AGATTTGTGG	CCTCGGAAGA	GGCTGTCCGA	1200
AGTGCAAGAA	AGGGCTATCA	GATAGCAGAG	AAACGCTATC	AGACAGGGCA	AGGCACTCTC	1260
GTGAGGCTCA	ACGATGCCGA	TGTGGCTCTT	TTGCAGGCTC	GACTCAATTA	TAATCAGGCC	1320
ATATTGACT	TTATGACCGC	AAAGGCCGAA	TTGGACAAGA	TGAACGGCAT	GGGGATTCCC	1380
GAACAA						1386

40 (2) INFORMATION FOR SEQ ID NO:186

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 1476 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: circular

45 (ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

50 (vi) ORIGINAL SOURCE:  
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:  
(A) NAME/KEY: misc\_feature  
(B) LOCATION 1...1476

55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:186

ATGTGGGGGG	ACAGCCATGG	AGTGGCGCCG	AACCAAGTGC	GCCGAACGCT	GGTGAAGGTA	60
GCCTTAAGTG	AATCCCTTCC	TCCGGGTGCA	AAACASATTC	GTATCGGATT	CTCTCTTCCG	120
AAAGAAACGG	AGGAAAAAGT	CACCGCCCTA	TATCTCCTTG	TGAGTGATTC	TTTAGCGGGT	180
CGCGACTTGC	CGGACTACAA	AGGGCGAGTC	TCTTACGATA	GCTTCCCGAT	CTCAAAGGAA	240
GATCGTACCA	CAGCCCTTTC	TGCGGATTCT	GTAGSCGGAC	GCCGCTTCTT	TTATTTGGCT	300
GCGGATATAG	GGCCTGTTGC	TTCTTTTTC	CGATCCGATA	CGCTGACTGC	CCGTGTGGAA	360
GAGGTGGCTG	TGATGGCCG	CCCTTTGCCG	TTGAAAGAGC	TGTGCGCTGC	CTCCGCTCGT	420
CTGTATAGGG	GGTATGAGGC	CCTCTTTGTA	CCCGGTGATG	GCGGATCGCG	GAATATCGT	480
ATCCCGGCCA	TTTTGAAAAA	GGCTAATGGA	ACACTCATAG	CGATGGCCGA	CAGACGAAAA	540
TATAATCAGA	CGGATCTGCC	GGAGGATATA	GATATAGTCA	TGCGGCGCAG	TACGGACGGA	600
GGGAAATCGT	GGAGCGATCC	CAGGATTATC	GTACAGGGAG	AGGGGCGCAA	TCATGGCTTT	660

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	GGCGATGTAG	CCCTGGTGCA	AACCCAAGCA	GGAAAGCTCC	TGATGATCTT	TGTCGGTGGA	720
	GTAGGCCTGT	GGCAGTCTAC	CCCCGATCGT	CCTCAGCGCA	CTTATATATC	GGAAAGTCGG	780
	GACGAAGGAC	TGACTTGGTC	GCCTCCTCGG	GATATAACCC	ATTTCATCTT	CGGCAAGGAT	840
	TGTGCGGATC	CGGGACGCAG	TCGCTGGTTG	GCCTCCTTTT	GTGCTTCGGG	ACAAGGGCTT	900
5	GTGCTGCCAT	CCGGTCGTAT	CACGTTTGTG	GCTGCCATCC	GCGAATCAGG	GCAGGAGTAC	960
	GTCCTGAACA	ACTATGTCCT	CTATAGCGAC	GATGAGGGCG	ATACATGGCA	GCTTTCCGAC	1020
	TGTGCATACC	GCCGTGGCGA	TGAGGCAAG	CTTTCATTGA	TGCCCGATGG	CAGGGTACTG	1080
	ATGAGCATAC	GCAATCAGGG	ACGGCAGGAG	AGCCGACAGC	GTTTCTTCGC	TCTCTCCTCC	1140
	GACGATGGCC	TTACTTGGGA	GAGAGCCAAG	CAGTTCGAGG	GCATCCATGA	CCCCGGCTGT	1200
10	AATGGAGCTA	TGCTTCAAGT	GAAAAGGAAC	GGAAGGGATC	AAGTGCTGCA	CTCCCTGCCT	1260
	CTCGGCCCGG	ATGGGCGTCG	CGATGGAGCT	GTCTATCTCT	TGATCATGT	CTCCGGCCGC	1320
	TGGTCCGCTC	CCGTGTGTGT	CAATTCAGGA	TCGAGTGCCT	ACTCGGATAT	GA CTCTGCTG	1380
	GCGGATGGAA	CGATCGGTTA	TTTCGTCGAA	GAGGGCGATG	AGATCTCATT	GGTTTTTCATT	1440
15	CGGTTCTGTC	TTGACGATCT	CTTCGATGTC	CGGCAA			1476

## (2) INFORMATION FOR SEQ ID NO:187

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 735 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...735
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:187
- |    |             |            |            |            |            |             |     |
|----|-------------|------------|------------|------------|------------|-------------|-----|
| 40 | ATGAAAAAAG  | AAAAACTTTG | GATTGCGATC | GTGCGCGGTT | TGGCTTTCGT | ATTGGGCCTT  | 60  |
|    | TATGCTCTTG  | GCCGCACTGT | CGCTCAGCTA | CGCCGCTCTC | AGCCTTCGGT | GA CTGTGACC | 120 |
|    | GGTATGGCCG  | AGCGTAATTT | CAATCCGAT  | CTGATCGTTT | GGACTGCTTC | GTACCAGCTC  | 180 |
|    | CAGATGATGG  | ATCTCGAATC | GGCTACAAG  | GCTTTGAAGG | AAAAACAGAT | ATTGGTAGCA  | 240 |
|    | GA CTATTTGA | AAAACAAGCA | GCTGCCCGAT | TGCTCTTATA | TCTTCTCAAG | CGTAGCCATC  | 300 |
| 45 | TCTAAAGAAT  | ACAACTACTA | TTACGATCCT | CGGCAGGAAC | AAAACGTCAG | GACCTTTGCC  | 360 |
|    | GGGTATCTGC  | TCAGCCAGAC | AGTTACGGTG | ACCTCACAGG | ACATCGAACA | TGTGGAGAAA  | 420 |
|    | ATATCTCGCG  | ATATAACGGA | GCTGATCAAT | CAGGGGGTAG | AGATTACCTC | CGACCGTCCG  | 480 |
|    | GCCTATTACT  | ACACCAAGCT | CAATGATCTG | AAGGTGGAGA | TGCTGCGCAA | TGCTCCGAA   | 540 |
|    | GACGCTTTCA  | ATCTGCTTC  | GGTCATTGCG | GAGGGGAGCG | GTTCCTCCGT | GGGTAAGATG  | 600 |
| 50 | CTATCTTCTT  | CGATGGGCGT | GTTCCAGATA | GTGGGGCTCA | ACTCGAACGA | AGATTATAGC  | 660 |
|    | TGGGGAGGTT  | CGTTCAATAC | GTCTTCCAAG | ATGAAGACGG | CAAGCATAAC | GGTTAAGGCT  | 720 |
|    | TCTTTCGCTT  | TGAAG      |            |            |            |             | 735 |

## 55 (2) INFORMATION FOR SEQ ID NO:188

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 828 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...828

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## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:188

5 ATGAAAAA CAATTGCAAT TATCGCCTCA GCCCTCTTGG CTTTAGGAGC CGTCGGCTGT 60  
 AAGAAAAATG CTGACACTAC CGCTGTCAGT GAAAAGGATA GCATAGCCTT GTCCATGGGT 120  
 ATTTTGTACG GACAGGATTT TGCCAATCAG TTCGAAATGT CCCGCTTGCA AGGCCAGCCG 180  
 ATTGATTCGG TAGCTTTCTT GGACGGTTTC AAATATGGTA TCGATACGAC GCGCTTCTCG 240  
 TACAATCTGG GAGCCATCTA TGCTTCCAAT ATAGCTCGTC AGCTGGCTCA TGATCCATC 300  
 GATATCGACA AGTTCTATGC AGCCATGCGT GCGGCTCTTC TTAAAGACAC CGTATCTATC 360  
 10 GCCATGAAGC TATGAGATGC ACAGGCTTTC ATGCAACGAA TCCAAGCCAA AAAGCAGCGA 420  
 GAAAACAATA TGAAGCAGTT TGGCCAGAAC ATCGAAAAGG GTAATGAATA CATCGATACC 480  
 TTTAAAAAAG AAGATGGTGT AACTGTTACG ACAACTGGTC TGGCATACAA GACTCTTCAG 540  
 GAAGGTACGG GAGCTACTCC CTCTTTGGCC GATACTGTAC GTGTCAAGTA TGTGGGTACT 600  
 CTGCTCGATG GTAAAGAGTT CGACAAAAC GAAGAAGSAA TCGAATTTGC CGTTACCGGT 660  
 GTGATTAAAG GCTGGACGGA GATGCTCCAA CTCATGAAGG TCGGTCAGAA AGTTCGCGTG 720  
 15 TGAATCCAC ACCGCTGGC TTATGGGGAG ACCGGCAACT ATACCATCGA ACCGTTCTCT 780  
 ACCCTGACGT TCGAGATGGA ACTTATCGGG ATCAAGCCCG GGAAAAAG 828

## (2) INFORMATION FOR SEQ ID NO:189

20

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2325 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular

25

## (ii) MOLECULE TYPE: DNA (genomic)

30

## (iii) HYPOTHETICAL: NO

## (iv) ANTI-SENSE: NO

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

35

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...2325

40

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:189

ATGAAAGTAT TACGGCAAGT ATTCCCTCCCC ATCCTTTTGG TCCTACTGAC AGGTGCCTGC 60  
 TCCACCACAA AGAATCTGCC GGAAGGCCGAA CAGCTGTATA TCGGAATGGG CAAGACACAG 120  
 45 ATACTCCGGC AGGACAAGAG CCACGCCGGC CAACAGGCTC TGACCGAAGT GGAGASTACA 180  
 CTGAAAGTTA CACCCAATGG AGCTATTTTC GGCAGTGCAA GTGCCTCCTT ACCCAAGATA 240  
 TATGGCTATA CAACAGCTTC GTGGGGGATT CCACTGTGAT TTCGAAATGG 300  
 ATATTCGACA AGTTTGCAGC CAAGCCGGTT TTCATCAGTC AGGTCAAATC CGATAGCCGG 360  
 GCTAAGGTGG CGACGAACAT CCTCCGCGAA CACGGGTACT TCGATGCTAA AGTAAAAAGC 420  
 AGTGTGACAC CTCGAAAAA GGACTCGCTC AAAGCCAAAA TCCTCTATAC GGTGGATATG 480  
 50 GCCTCTCCTT ATCATTACGA CAGCATCAAT CCCTTACCGA TCAGCACTTT CCCCAGACAGC 540  
 ATTCTGGCTT ACAGGCAGAC TCCGTCTTTG ATCAGGAAGG GAGACCAGTT CAATTTGGCA 600  
 AAGCTGCACG AAGAGCGTCA GACCATCAGT GCCCTGCTGA GAGACAATGG TTACTACTAC 660  
 TTCCGCCAC AGGATATTAT CTACGAAGCC GATACCTCC TCGTAAGAGG TGCCGTATGC 720  
 CTGCGAGCCA AGTCTCGGA AGATACTCCA CCCCAGGCC TCGCGCCGTG GAGGATAGGG 780  
 55 AAACGGACAG CAGTCTTGCT CGGAATGAAC GGAGAAAGCC CGACAGACTC GCTCGAAGTG 840  
 GAGGATATGA AAGTCTTTA CTATCGTAAA ATGCCGGTTC GCCCCAAGAT TTTGGCCAAA 900  
 CGCTTTCGTT TCTTCTCCGG CAATCTGTAT CGGCAGAAAG ACAGATGAGC GACACGCAAA 960  
 TCCTTGGCTC GTTGGGAGC CTCTCCGTT ATCGATCTCA ATTTTGGCA ACGCGATTCC 1020  
 60 ATTTCCGGCC TTTTGGATGT GCGACTGCTA ACCACCCTCG ACAAACCTTG GGATGCATCA 1080  
 TTAGAGACCT TGTTCACGAG CAAAAGCAAT GACTTCATCG GTCCCGGACT GAATTTTGCT 1140  
 CTTGCTCGGC GCAATGTATT CGGCGGAGGA GAAATCTTT CTGGAATAT CGSTGGATCG 1200  
 TATGAGTGGG AGACCGGCAA TCGTCCCGAA AATAGCAGCA ATCGGCTGAT CGATATAAAT 1260  
 TCGTACAACA TGAATACGGC CGTGAACCTC TCGTTTCCCT CGATTGTATT TCCCGGTCG 1320  
 CTGGATAAAT ACTATTACTA CCCCAGACT ACGACTTTTC AGGCTTCTGC CACCGCGCTG 1380  
 65 AACAGGGCAC ACTACTTTAG CATGTACTCT TTCGGCTTT CGACCACTA CGAATTTGAG 1440  
 CCTTCCAAGG AACACCGGCA TGCTATTTTC CGCTCAAGC TCAACTACAA CCTCCTGGGG 1500  
 CATCAGACAG AAACCTTTCA GGCCATTACG GCGAACATC CGCCCTGCT GCTCAGCCTT 1560  
 CAGAGTCAGT TCCTTGCTCA AATGGGGTAT ATCTATACT TCAACAAATC CGTTTCAGAG 1620  
 AAAAGTCTCT ATCATCTTTG GATGCAATTC GGAATATCCG AGGCAGGCAA TCTCCTGAAT 1680  
 70 CTGATCTATC TGCGAGCCGG CAAGAAGTAC AGCGACACCA AGAATTTCTG CGGCGTCCCC 1740  
 TTCTCTCAGT TCATCAAAGC CACGGGAGAA CTCGCTATT CCTATACCAT AGACCGCAAT 1800  
 CAGTCACTGG CAACCCGTTT CGGGACAGGC GTGATATATA GCTATGGCAA TATGCGAGTG 1860  
 GCACCCCTATA GCGAGCAGTT CTATGTAGGC GGTGCCAATA GTATCAGAGC TTTCACCGTC 1920  
 CGTAGCATCG GCGCCGAGC GTTCAATCCG GATTCCGACA ATCAGTATTC CTATTTGGAT 1980  
 75 CAGGTGGGCG AATTCAAAC CGAAGCCAAC GTGGAATATA GAGGCAAGCT TTTGCGGGAT 2040

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5 CTCCACGCAG CCGTTTTCTT CGATGCGGGC AACGTTTGSC TCTTGAGGGA GGATTCTTCC 2100  
CGTCCGGGGC GTGCTCTGTC CGAAGTGGGA TCGGTGAGCA ATTTCTTGAA TAGCATCGCT 2160  
CTCGGCACCG GTGTCGSCCT TCGCTACGAT CTGGCATTTC TCGTGGTTCG TGTCGATGTC 2220  
GGCTTCGGTC TCCACCTTCC TTACAATACG GGTAAGAAAG GTTACTACAA TATCCCACGC 2280  
TTTAAGGATG CCATCGGTTT CCATTTGGCT GTCGGCTATC CCTTC 2325

## (2) INFORMATION FOR SEQ ID NO:190

- 10 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 2322 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: circular
- 15 (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- 20 (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:  
(A) ORGANISM: PORPHYROMONAS GINGIVALIS
- 25 (ix) FEATURE:  
(A) NAME/KEY: misc\_feature  
(B) LOCATION: 1...2322
- 30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:190

ATGTCTCTGC ATTCCGTTTC GTATCTAATC GGCATTGCCG GCTGCTTGCT CCTCATGCTT 60  
GCTTCTCTCT GCTCGGTTCAC CCGTTATGTG CCGGACGGTA GCAGACTATT AGACAGGGTA 120  
ACGATCGCAA GCGAAACGGG CAGTATCGCT CTGCCGGAAG ATATTCGGGA CTATACCCCTC 180  
CAGCAACCCA ATTACAGACT GTTCGGGATG ACTCGCTGGC TACTGCGCGT CTATAGCAGC 240  
35 TCGAATCCGA ACAGCAACAG CTGGTGGAAAC CGTTCGCTCC GGAAAATGGG CGAACCGCCT 300  
GTCCTCATCG ATTCTGTCTT CACCGATCGT ACTGCCAACC GTCTGGCAAA GCGGATGGCC 360  
GGCGATGGCT TTCTCGATGC TACTGCTCGT GCCGTGGTAG ACACCGGCTT GTACAAGAAA 420  
GCTCGCATTA CTTATCTGAT TCAGCCCGGA AGCCGTTATT ATATACGCAA TATGGCTTTG 480  
GATGTGAAGA ATCCACTCCT TCCTCCCGTT GCGCTTGGCA ATTCGCTTCC TTCGGCATAC 540  
40 AAGGTCCGGA TCAGCGAGGG TTCTCCCTTG TCGCCCATCG TACTCGATGA AGAGAGAAAG 600  
GCGATAGCTC GTCATATGCG CAACAACGGC TTCTGGAAAT TCTCCGCCGA GGATGTTTAT 660  
TATGAAGCAG ATACTACCGT TTCAGGAGGA TCGGGTACGA AATCTGCCGA TCTGAAATTA 720  
GTGGTCAATG GCATCGGGCG TTATCCATAT CGGATCGGCA GGGTATTCTT TCATGCCGAT 780  
TATGATCCTC TCGAATCGGA CTTACAGATT CAGGAGCTGC CACGTATCGA TTCGATTTCG 840  
45 CGTGGCGATT ACAGTGTCTA CTATGGGAGT AGGGGACGTT ATATCCGGGC ATCGGCTCTC 900  
ACGCGGTCCG TGTCCGTTAC ACCGGGAGCT TTTTCTGCG AGGATGATGT GGAACGCTCT 960  
TATATCAAGC TGAATGCGCT CCCTATCGTT CGGAACGTGA ATATCCGATT TGTGGAGCAC 1020  
AATGGTAAGG ATGAGATTGC TCTGGCGGAT AGCTCTCGCC TTGTGGACTG CTATATTCTT 1080  
ACCGTTCCGG CCAAGAGCAA ATCGTTGAA GCGGAAGTCC TCGGCACCAA TTCCGCTGGA 1140  
50 GACTTCGGGG CGGCTTTGTC TCTCGSTTTC ACCGATCGCA ATTTGTTTCG TGGGGCGGAG 1200  
ATGTTCAATA TCAAACTCAA GGGTGTCTAC GAAGCCATTG GCAAGGGTTC GCACAGCTTC 1260  
ATGGAATATG GGTGGAAAG CTCGCTCCGT TCCTCTCGTC TCCTCTTCC ATTCAATTCT 1320  
GACGAAACGC GCCGGCGGCT ACGGGCATCC ACGGAATGGA AGATCGGGTA TAATTACCAG 1380  
ACACGTCGGG AGTTTGATCG GGTGATTCTC TCCGCTCAAC TCAATTATTC ATGGCAGACC 1440  
55 TACCTGCACA ATCGTCTGCG TCATACGATC CGCCTGCTGG ATGTGATTA TCTCCATCTC 1500  
CCGTACATCG ATCCCGACTT CGCCCAATCC CTTCGGCTTA CGACTGCACT GTATAACTAC 1560  
ACGGAGCAGT TTATCCTCGG CTCGGCATAT ATACTGAACT ATACCACGGC TTCGTCCATG 1620  
GAGCGTACCG TATCCAATCC TTTTACGGCA CGGTTCASTA TCCAGACAGC CGGCAACCTG 1680  
CTGCAAGCCA TTCTTTATCT GACCGATTCT CCGAAAGACG AACACGGGTT GTATAAAATG 1740  
60 TTCGCTCTGC ACTATGCTCA GTTCGTCAAG CTCGATCTCG ATCTGGCTAA AACCGTTCTT 1800  
CTCGAAAAGS ACAATACTTT GGCATCTCAT CTGGGTTTCG GACTGGCTTT CCTTATGGC 1860  
AATGCTCGCC ATATACCTTT TGAGTTACGT TACTTTGCCG GAGGATCGAA CAGCGTTCGC 1920  
GGCTGGAGTG TCCGTACCTT CCGCCCGGGG AGTATGAAGA TGACTCCGGA CAAGACCTTC 1980  
75 TTGATCAGA TGGGTGATAT TCGTCTGGAT CTGAATGTCG AATACAGGAC AAAGCTGTTT 2040  
TGGAAGTTTC GCGCAGCAGC TTTGTGCGAT GCCGGCAATG TCTGGACGAT AAAGGAGTAT 2100  
GAGAACTCAG AGGACGGTCT CTTTCGTTTC GATCGCTTCT ACAAGGAAAT AGCTTTGGCC 2160  
TACGCTCTGG GGCTTCGTCT CGACTTCGAT TATTTCTCTG TCGGGCTGGA TGCCGGACTG 2220  
AAAGCCTAGC ATCCTCAGCA GACAGGGCGT TACAAATGGG CTATCACACG CCCAAACCTT 2280  
70 TCTTCCAATT TCGCTTGGA CATTGCASTA GGCTATCCGT TC 2322

## (2) INFORMATION FOR SEQ ID NO:191

- 75 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 2601 base pairs

129/ 490

(B) TYPE: nucleic acid  
(C) STRAINEDNESS: double  
(D) TOPOLOGY: circular

5 (ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

10

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

15

(A) NAME/KEY: misc\_feature

(B) LOCATION 1...2601

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:191

20 ATGAGAAAAA GAATTCTACA ACTTTTCCTG ACCGCATTGC TGCTGGCATT AGGCTCCTCT 60  
CTCGCCATAG CGCAAAACAGT GGTGACCGGT AAGGTGATCG ATTACAGAAC GTCCGAACCG 120  
CTCATCGGTG TATCCGTAAAG CACCGGTGAG GGAGCATCCC TCCGCGGTGT AACCCCGAT 180  
ATGGATGGTG GCTTCCGATT CGAAGTACCG GCCAAATCTG TCTTGACTTT CCGTTGCGTA 240  
GGTTATGCTA CCGTAACTCG CTCTATAGGC AGAGGTTCTC AAGAAGACCT CGGTACGATT 300  
25 CTCTCGATC CCCAGGCCAT CGGCTTGGAT GAGATTGAGG TAATAGCCTC TGTGGTGCCC 360  
AAAGACCGTA TGACGCCGGT ACCCGTTTCC AATATCCGTG TGGCTGATAT TCAGGCAGCA 420  
TCGTTGAATG TCGAATTTCC CGAACTGGTT AAATCCACTC CCTCTACCTA TACGACAAAA 480  
GGAAGCGGAG GTTTCGGTGA TGGTCGTACC AATGTGCGTG GATTCGACAC TTACAACCTC 540  
GGTGTACTCA TCAACGGAGT TCCTGTCAAT GGTATGGAAG ACGGGAAGT ATATTGGAGC 600  
30 AATTGAGTGT GTCTGATGAA TCAAGCCAGT ACCATTGAGA TTCAGCGCGG ACTCGGAGCC 660  
TCCAAGCTCG GTATCAGCTC GGTAGGTGGT ACGATGAACA TTATCACGAA GACTACGGAC 720  
GCCAACACCG GAGGTTCGGC TTATGTGGT ATGGGTAATG ATGGATTGCA CAAAGAATCG 780  
TTCTCCATTT CTACGGGTAT GAACGACGGT TGGGCTATCA CCATTGCGAG CTCCCATATG 840  
ACGGGTCTGG GTTATGTGAA GGGGCTGAAG GGACGTGCAT TCTCTTACTT CTTCAACGTT 900  
35 TCGAAGAAAT TCAATGAACG TCATACCTTC TCTCTTACCG GATTCGGTGC ACCACAATGG 960  
CACAAACCAAC GTTCTTCCAA ATATTCTGTA GCGGACTATG ACAAATACGG CATCGTCCAC 1020  
AATCAATCCT TCGGCTATCT GCGAGGCGAA CTGACTCCTA CGGCTTATGC TTACAATACG 1080  
TACCACAAGC CCCAGTTCTC GCTGAACCACT TTCTGGAAGA TGGATGAAAA TACCTCTCTT 1140  
TATACCGCAN CCTACGCATC TTTGGCTACC GGTGGAGGTC GTGCGCGTTA TGGAAAGAAC 1200  
40 AGTAAGTGGG TATTGATCAA CTACAACACC GGACAACCCCT ATGAACAAAC AAAGGTGACT 1260  
CCCGATGGAC TTATCGACTA CGATGCCGTA CTGGCTGCCA ATGCTGCGGC GAGCAATGGC 1320  
TCGGAAGCAA TTTTGGCCCT TGGCTCCAAC TCTCACAGT GGTTCGGTCT ACTCTCTTCA 1380  
TTCAAGSAGA AACTTAATAG TTCGCTGACT TTGACAGCCG GATACGATGG GCGTTACTAC 1440  
CGTGGCGACC ACTATGACAA GATCACCGAT CTGCTCGGCG GTAGCTACTA CATAGAGGAT 1500  
45 CCCAAGACAA AGCTCGCATA CCATGCGGAA GGTGAGCAAC TGAAAGTGGG TGACATTGTA 1560  
AATCGGGACT ACACAGGCGA AATCATGTGG CACGGCCTCT TCGCACAGAT GGAGCATTCG 1620  
TCCGAATGGA TCGATGCATT CGTATCAGGA TCTATCAACT ACGAACTATA CCGCAATCAC 1680  
AACTATGGCG GTAGCAAGTC CACCGGCTAC CTGCCCCGGG TATCGCCGTG GAAAAGCTTC 1740  
CTTCCGTGGA GTGGCAAGGC AGGTCTGAGC TACAAGTTGG CACAGGGACA CAATGTATTC 1800  
50 GCCAATGGCG GTTTCCTTAC ACGTGCACCA CTCTTTGGCA ATATCTATGC TGCGGGGGCT 1860  
ATCATTTCCA ATGACAAAGC CAATATGGAA AAGGTGCTTA CAGGAGAGST CGGCTATGGA 1920  
TTCACGAATC ACAAAAACTT CGAGTTCAAT ATCAACGGAT ACTATACGAA GTGGATGGAT 1980  
CGCGTGACCT CGAAGAGAAT CGGAAACGAG TATGTTTATC TCAATGGCGT TGATGCTGTT 2040  
CACTGTGGGG TAGAGGCTGA GGTGAGCTAT CGTCCTATTC GTGAGATCGA CCTTCGCGGT 2100  
55 ATGTTCTCTC TCGGTGACTG GACTTGGCAA AACAATGTAA GTTACACTTC TTACGACGAA 2160  
GCCGGCAATG AGACAGGGCA GGAATAAACC TATATCAAGG GTCTTCACGT CGGAGATGCA 2220  
GCACAGATGA CGGCTGCTGT ATCGGCAGAC ATAGAGCTGT TCAAGGGTTT CCATGTCATA 2280  
GGTAAGTACA ACTTCCTTGG CAAGAACTAT GCAGGATTC ACCCCGCAAC CGGTAATGCA 2340  
CAGCAGTACG AAGCGGATGG CAAAGAAATC GTGGAATCAT GGAAGTTGCC CGATGTAGGT 2400  
60 CTGTTTCGATC TGTCTGCATC CTACAATTTT AAGCTTGGTT CACTCAGCAC CACATCTCAT 2460  
TTCAACATGG ACAACGTAGC CGACAAGCGA TATGTGAGCG ATGCCGACGA CAATATCATC 2520  
GSTAAGAAAC ACGATGAGGC TTCGGCTCTC GTATGTTACG GTTTCGCGCG CACTTGGTCT 2580  
ACCGGTATTC GTGTAAACTT C 2601

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(2) INFORMATION FOR SEQ ID NO:192

(i) SEQUENCE CHARACTERISTICS:

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(A) LENGTH: 1293 base pairs  
(B) TYPE: nucleic acid  
(C) STRAINEDNESS: double  
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

75

130/490

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

5 (vi) ORIGINAL SOURCE:  
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:  
(A) NAME/KEY: misc\_feature  
10 (B) LOCATION 1...1293

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:192

15	ATGAAGTTTT CAATCCGCCT TTTCTCTGCT ATCATCTTTC TCCTCTCTGC ATTTATCCTG	60
	CCTGCTCTCG GACAAAAATC CAAGCAGGTA CAGCGACTTG AGAAGCAACG TAAGGAGGCC	120
	CTCAAAGCCA TCGAAAAAAC CGATCGCGAA CTACGAAATA CCAAGAAAGA CAAGCAAGAC	180
	AAACAAAAGC ATCTCAACCT CCTGAACAAG CAGGTTGCTC AACGCAAGCA GATGGTACAA	240
	CTCTTGGACA ATGAGGTCAA AGAGTTGCAA TCCGACATTG ATTCCATGAC GGGTGTATGT	300
	CATCAGCTCT CTGTAGAAGA GAAAGCCCGA TCCGATGAAT ATGCCCAAGC TCTACAGTCT	360
20	ATGCAAAAGC GGAACGCTC GTTGGATCGC ATCCTTTTCA TTTTCATCGGC CAAGAGCTTT	420
	GACGAAGGCA TCGGACGGAT GCGTTTCTTG GAACAATACG CTCTCTGCATA CAAGCTGGCA	480
	TCTGTCCGGC TGGCGATAC ACGTAGCAAG TTGGAGACTG AACGTGCGAC TGTAGAAGAC	540
	GCCAAAAAGG AGAAAGGACA TCTCTTAGTC ATCAGAGAAG AGGAAAAAAA GAAACTCGAA	600
	GGACAGCAAG CCGAGCAACG TCGGCAGGTG CAGGCTTGGG GAGCCAAACA AAAAGACTTG	660
25	GAAGCGCAGC TGGAAAAGCA GAAAAAGCAA GCGGAAGCTC TGAACAGAAA GATCGAGAAA	720
	CAGATTGCCA AGGAAATAGA AGCTGCCGAA CGTCGTGCTC GAGAAGAACG TGAACGGTTG	780
	GCACGCGAAG CCAAAGCCAA GGTAAAGCCG GTTCTCTGCG AACCGGAACG GAAGGCGGAG	840
	ACCAAAGGCG GCTATGCTAT GGATGCCCTT GAGCGTGCTC TCTCGGGCAG CTTTGACACG	900
	AACAAAGGTC GCTGCCCCGG CCCCGTTGCG GGCAGATACC GAATCGTAAG CGACTTTGGC	960
30	GTGCATCAGC ACAGTGAGCT GAAAAAGTA CAAGTTAATA ATGGAGGTAT CGACATCGCT	1020
	GTAGCAACAG GATCCGATGC TACCAGCGTA TTGGATGGTG TAGTGTCCAG TGTATTGCTG	1080
	ATACCCGTTT ATAATTCGGC CGTAATGGTT CGTCACGGTA ACTATATCAC GGGTTTATGG	1140
	AATCTGAGCA AAGTGTATGT AAATTCGGCG ACTCGTGTTA AAACGGGTCA GGCTCTTGGT	1200
	CGTGCCTATA CGGATCCTTC CAACAACCA ACCATTATTC ACTTCGAAAT CTGGAAGAA	1260
35	CGCAGCAAAC AAAACCCAAG ACTATGGTTA CGA	1293

(2) INFORMATION FOR SEQ ID NO:193

40 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 999 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: circular

45 (ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

50 (iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:  
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

55 (ix) FEATURE:  
(A) NAME/KEY: misc\_feature  
(B) LOCATION 1...999

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:193

60	ATGAAAAAGT ATTTGTTATA TGCCCTCGTTG CTAACGAGTG TTTTGCTCTT TTCCTGTTCA	60
	AAGAACAATC CTAACGAGCC GGTGGAAGAC AGATCCATCG AAATTTCTAT AAGGGTAGAT	120
	GATTTCACCA AAAGGGGTGA GGCAGTACGC TATGAAAGGA ATCAAGGAAG TGCTGCCGAA	180
	AGGCTCATTA CCAATCTTTA CCTCTTGTG TTCGATCAGT CAGGGGCGAA TCCGCGGAAA	240
65	TACTATATTA CCGGTAACAC TTTACCGGA GGGACCTGGC TTCCTGACGA TATGAAGGTG	300
	AAGTTGGATA TGACACAATC CGAGGCCGGA GAGCGCAAAG TATATGTCGT AGCCAAATGTT	360
	GATAATGCGG TTTAAACGGC TCTTGATGCT GTCGCTAACG AAAGCGATTT GCAGACTGTA	420
	AAGAGGACGA TCGCAATGCC GTGGTCGACC GATATAGCCT CTCCTTTCTT GATGTCGGGA	480
	AACAGACAC ACGACTTCTT GGCCAAATCGT CTTTGGGACA ATGTGCCCTT TGTGCGTGCC	540
70	ATTGCCAAGG TGGAGCTGAA TATCTCGCTG AGTGAGAAAT TTCAGATTGT GCCGATAATT	600
	GTCAATGGTA GTTTGAGTGA GTTCAAGTTC AGATACGTAA ACTTCGACAA GGAGACCTAC	660
	GTAGTGAAGC CAACGACCAA GCCGGACAAT CTCATTAGTT CTGCTAATGG TGTTTGGCCT	720
	CAGATTACAG ATTGGACTGT ATGGGGTGCT TCCTTAAATA CTTCTCCTGC TCCGGATGCG	780
	GGCAGAGGTT ATACATTGGA TGCAAATGGC AAGGTAACGG CACTACGGAT TGTACCTAT	840
75	CTGAATGAGC GCGATAGCAA AGGGGCTACG GTAGAGGTCT CATTGCCTCG TGTGGATGAT	900

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GGCACCCCTTC CTCCTCCGGA ATTCGGTCCG GAGCTTTATC GTTTGCCTTT GCCGGACAAG 960  
ATCCTGCGCA ATCATTGGTA CAAGTATGAA GTCGAGATT 999

## 5 (2) INFORMATION FOR SEQ ID NO:194

(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 945 base pairs  
10      (B) TYPE: nucleic acid  
        (C) STRANDEDNESS: double  
        (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

15 (iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

20 (vi) ORIGINAL SOURCE:  
    (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:  
    (A) NAME/KEY: misc\_feature  
    (B) LOCATION 1...945

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:194

ATGATCAGAA CGATACTTTC ACGATATGTA TCCTCGAACT TTTGGAGTCG GGGAGCTACC 60  
30 TTTTTTTTCA CGATTTTCCC GGCTTCATC CTCGCCGCTA CTGCTTTGCC GGCTTGTGGA 120  
GGGGGTACTG CTTCAGGCTC CGATCGTACG CTGGCTGTGA CCATCGAGCC ACAGAAATAC 180  
TTCATCGAST CCATTGCGGA TAAGTCGGTG CAGGTGCTGG CATTGGTACC GGCCGGCAGC 240  
AATCCGGAGG AATACGACCC TTGCCTACC GTGATGAAGC GTTTGTCCGA AGCAGATGCC 300  
TACTTCTATA TAGGAGGACT GGGGTTCGAG CAAAGAAATC TCGCTGCCAT TCGGGACAAT 360  
AACCTAAGC TCCCTCTTTT CGAAATGGGC AAAGCCTTGG CGGATGCCGG AAGTGCAGAT 420  
35 CTCCACGGCT CCTGCACAGA TCATTCTCAT ACAGACCTGC ATGCCCATGA TCCGCACTAT 480  
TGGAGCAGTG TGGTAGGGGC AAAGGCACTC AGTCGTGCTG CATACGACGC GCTTGTGGAG 540  
CTTTATCCGA ACGAGAAAGA CAAATGGGAC AAAGGGCACG ACCGTCTCAA CGGACGTATC 600  
GACAGCGTGA AGAGACTCGT CGATACCATG TTTGCCAATG GCAAAGCAGA CAAAGCCTTC 660  
GTATATATAC ACCCATCGCT CAGCTTTTTT GCCCAAGAGT TCGGCCTGCG GCAGATCGTC 720  
40 ATAGAGGAAG ATGGGAAAGA GCCTACGGCT GCCCACTTC GTCGTGTGAT CGATCAGGCA 780  
CGTGCCGATG GTGTCAGAAAT CGTATTTATC CAACCCGAAT TTGAAACGCG TCAGGCGGAG 840  
GACATCGCAC GCGAGATCGG TGCTCGTCCG GTAAGGATCA ATCCTCTGCG CAGCTCGTGG 900  
GAGGAGGAAA TTTTACATAT TGCTCGCGCT TTGGCTCATG AACGG 945

## 45 (2) INFORMATION FOR SEQ ID NO:195

(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 2544 base pairs  
50      (B) TYPE: nucleic acid  
        (C) STRANDEDNESS: double  
        (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

55 (iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

60 (vi) ORIGINAL SOURCE:  
    (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:  
    (A) NAME/KEY: misc\_feature  
    (B) LOCATION 1...2544

65 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:195

ATGATCGGAA AAAAAATCTT TTTTATCCTG CTGGCGCTCA TTGCGTTCAG TGGGCTGAAC 60  
70 GCAGCGACAG AACTTGAGTT CAAGTACCG ACCGATGCCA ATATCATCGG TCACGTCAAA 120  
GACAGCAAGA CGGGTGAACA CCTTGTCGGT ATCACTATTG CTATCAAAGG CACTACCTTT 180  
GGTACATCTA CAGATGCAAC CGGGCACTAC TATCTTCGTA ACTTGCGTCC GGGTGAGATC 240  
ACTTTGATTA TGGGTGGCAT GGGCTATAAG AGCCAGGAGC GCGTAGTCCG CGTAGAAAAG 300  
GACAAGACTA TCGAGGTGAA TTTGGAAGCA GAAGAGGATG CCATCAATCT GGACGAAGTC 360  
75 GTGATTTCCG CCAACCGCGA ACTGACGCTT CGCCGTCTTG CTCCTACTCT GTTAAATGTA 420

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5	TTGAACGAAA AAGTCTTCTC GCAAGTCAAT GCTTCTAACC TGGCTCAAGG CTTGTCATTC	480
	CAGCCGGGAG TTGCTGTAGA GAACAACTGT CAGAAGTGTG GTTCAATCA AGTTCGTATC	540
	AATGGACTGG ATGGTCGTTA TGCACAGATC CTCATCGACA GCCGTCCCAT CATGAGTGCC	600
	CTTGCCGGTG TTTACGGTCT GGAGCAGATC CCTGCCAATA TGATCGAACG TGTGGAGGTA	660
	GTACGTGGTG GAGGATCGGC CTGTACGGT TCTTCTGCTA TTGCCGGAGT GGTGAATATC	720
	ATCACCAAGG AACCTTCTCA CAATTCTTTC ACATTCAATG AATCTCTGAG CTTTACCGGT	780
	TTCAGCAAGC TGGATAACAA CACGAACCTC AATGCCTCCA TCGTCAGCGA TGACAACCGT	840
	GCCGCTGCCA TGGTATTCGG GCAGGCTCGT TACCGCAACC ATTGGGATGC TAACAATGAC	900
	GGTTATTCGG AATTGGGTAA AATAGATGCC CGCTCGCTGG GAGCGCATTC TTATTTGCGC	960
10	TTGAGCGACT ACAGCAAATT GACGGGAGAG TTTCACACGA TCAGTGAATT CCGCCGTGGT	1020
	GGCGATCGTA TCGATTTGCC TCCTCACGTA GTGGGTGTAG CTGAACAAAC TGACCATAGC	1080
	GTATTTAGCG GAAACTTGAA ATACGATCTC TTCTCTTCCA ACTATAAACA CCACTTCCAG	1140
	GCTTATACTT CCGGACAGAT CGTAAATCGC AAGAGCTATT ACGGAGGTAT CGGAGAGATT	1200
	GACGTCAATG GCGACCCCGG TGGTACGGAA GGCTACCCCTA TCCCTCAAGA TCAATACGGC	1260
15	AATAATTATG TCGTGACCAA AGGCAAGACA TATATGGGGG GTATCCAGTA CAGCTACGAC	1320
	TTGGACAAAT GCCTCCTCAT GCCTTCGCAA CTTTTGTTCG GAGCCGAATA TACGCGTGAT	1380
	GAACCTCAATG ACGTGATGCC CATCCTTTCA TGGCAGACCG GCGAGGATGC CAATGGGAAT	1440
	ACCATTCCTC TCTATCCCGA ATTGGATCAG AATATCAACA ACTACAGCCT ATTCGGTCAG	1500
20	AACGAATGGA AAAATGACAG ATGGAGCATC TTCTTTGGCG CTCGCTTGA CAAGCATAGC	1560
	GAAGTCAAGG ATATGATTCT GAGTCCTCGT ACCACACTGC GTTTCACAGT GAATCCGGAC	1620
	ATCAACCTGC GCGCTACATA TGCAAAAGGG TTCCGCGCAC CGCAGGTATT CGATGAAGAC	1680
	TTGCACGTAG GGGTTGTAGG CGGTGAGGCA CAGAAAGTAT TCAACGATCC GAACCTCAAG	1740
	CCTGAATTTT CTCATGCATT CAGTTTGAGT GCCGATATGT ATCATCGTTT CCGTAACGTC	1800
25	CAGACCAACT TCCTTGTTGGA AGGCTTCTAT ACTCGTTTGC TGGATGTATT CACCAACGAG	1860
	GAGCAGCCTG ATCAGCACGA TGGCATCAAA CGCTACACGC GTATCAACGG TAGCGGAGCC	1920
	AAAGTATTGG GTCTCAATCT GGAAGGTAAG GTCGCATACA AGTCCTTCCA GCTCCAAGCC	1980
	GSTCTTACCC TGGCCAGCAA CAAATACGAC GAAGCACAGG AGTGGGGTCT GAATACGGTG	2040
	AAAGACACCA ACGGAGCTTT TGTACCGAG GCCAATGCAA ATGGACAACA GGAATACAAG	2100
30	AACGAATCCA TGACGATAC GCAGATCACC CGTACCCCCA GCGTATACGG TTATTTTACT	2160
	TTGGCCTACA ATCCTGCTCA CTCATGGAAC ATAGCCCTTA CGGGAGCATA TACCGGTCAG	2220
	ATGTATGTAC CCCACGCTAT CGAATATGGT GTGAAGTCTG CCGAACTGGA TATTATGCAG	2280
	AACATCCTG AGATTACCGA CGAAACCGGA AAGGCTCCCC GTATTGATGA GCTGAAGAAG	2340
	ACACCTGCAT TCTTCGATTT GGGCTTGAAG GTGGGTATG ACTTCCACGT ATTCCAGGCT	2400
35	ACTGAGGTTT AACTCTATGT AGGTATGAAC AATATCTTCA ACTCTTTCCA GAAGGACTTC	2460
	GATCGTGSAG CTGCACGTGA CAGCGGATAT ATCTATGGTC CTACGCAGCC GCGTACAGGC	2520
	TACATGGGCT TGSTAGTGAA GTTC	2544

## (2) INFORMATION FOR SEQ ID NO:196

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 606 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

## (ii) MOLECULE TYPE: DNA (genomic)

## (iii) HYPOTHETICAL: NO

## (iv) ANTI-SENSE: NO

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...606

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:196

65	ATGACAGTAA AGCGCGCAGT GCGAATAGCA CTTCTCACGC TGATAGGCAT TCTTTTTTCC	60
	TCACCTTCTC TTGTTCCGGC GCAAAGTCTT TTCAGCACCG AACATGTCTT GCAACTATAC	120
	AACAAGATAC TCTATGGAGA GTCGGCGGGC GATACCGTCC CAGAGAAAAC GGCAGGTGAG	180
	TCGGCATTTT CTTTTATAGA CAAACTCATC AATCTCGGCC GCACTTTCTT CGGCAACCA	240
	TATCGCTATC GGGTCCCTTC CCCATGGCCG ATGGACTGCT CGGGCTATGT GTCTTACCTC	300
	TACTCCAAAT TCGACATCAA ACTCCCACGT GGTGCGGCAG CACAGAGCCA ATATACGAAT	360
	CCTATCGAGC GCGAGGATGT TCGTCCGGGC GACCTCCTTT TTTTCAAGG CCGCAATGCA	420
70	CGCAGCAACC GTATCGGGCA TGTAGCTTTG GTCGTATCTG TCGATGAAGA TGATATTACC	480
	ATGATGCACA GCGCAATTG GCGAGGGATC GTGATCGAAA AACTCAATCG CAGTGCATAC	540
	TTCTCCGTC GCTTGGTGAG CTATGGCAGG GTACCCGGAG CCAAGAGAGT GATCCCACGA	600
	AAAAAT	606

## (2) INFORMATION FOR SEQ ID NO:197



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- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 1365 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:  
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:  
(A) NAME/KEY: misc\_feature  
(B) LOCATION 1...1365
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:197

ATGAAACGGA CAATCCTCCT GACGGCACTG ACCGTCCTAT CTTCGCTCTC CTTGCTTCGT 60  
GCACAAAATG AATCCGAAGC ATCAACCAAT CCGATGTCAG GCCTCTCCCT GGAAGACTGT 120  
ATCCGGATAG CCAAGGAGCG CAACCTGAAT CTGCGCAGAC AGGAGATCGA ACAAGAAAAC 180  
CGAATCATTG GTCTCGATGC AGCAGGACAC AGTTTCCTGC CCTCGGTCAA TGCAGGCATC 240  
GGACACAACCT ATAGCTTCGG ACGTTCGAAA GACAAAACGG GAGTAACCGT AGATCGCTCC 300  
TCGATGAATA CCAATCTCAG CATCGGAGCT TCGGTGGAAG TATTCAGCGG CACACGTCGT 360  
CTGCACGACC TCAAGCAGCA AAAGTACAAC GTGGAGGATG GTATAGCCCG ACTTCAAAAA 420  
GCGCGTGAAG ACCTCAGCCT GCAAAATCGCG GCTCTCTATA TCAATTGCT CTTCCGTCAG 480  
GAAATGACTC GTACGGCAGA AACACAGTTG GCACTGATTC GCGAGCAACG CAATCGCACG 540  
GCCGAAATGG TTCGCGTAGG TAAATGGGCA GAGGGTAAGC TCCTCGACAT AAATGCCAG 600  
ATGGCCCAAG ACGAACAACCT TCTCGTACAA TATCGTTCCG AGGAGGAGCT GGCTCGTCTG 660  
GACTTGGGGC AAGCCCTCGA ACTGGAGCAC CCGAAAAGCA TTGCAGTCAA GGCTCCCGAC 720  
ACAGACGCTC TCGTAGCAGA AAGGTTGGGA TCTCTCCTTG CTCCCGAAGA GATCTATCGC 780  
ACGGCTCTCG GCTTGAAACC GGCAGTGCAT TCGAGCGAGC TGCAAAATAGC TTCGGCACGC 840  
GAAGGTCTGG CCTCGGCTCG TCGGGCATAC TTCCCGACGC TCAGCCTCTC TGCCGGATAC 900  
AGCAACGGTT ACTTCCGCGA CCTCGGCAAG GAGTATGCCG CCATCAACCC CTCCTTCTCC 960  
GAACAGTGGG AGAACAACGG CAGCTACAGT ATCGGACTCT CTTTGAATAT CCCCATCTTC 1020  
TCTGCCATGC AAACGCAAGA TCGGTTTCGG AGCAGTCGCC TGCAAAATACG CTCAGCGAG 1080  
CTTCGACTCG TCGAAGAGAA AAAAGCCCTC TATAAAGAGA TCAGGCAAGC ATACAGCAAT 1140  
GCCGTGGCAG CCGATAAGGC CATCGCAGCA GCCGAAAACA GCAAGGCCGC TACGCTCAAG 1200  
GCATACGAAT ACGCTCGCGA CAGCTTCGAG GCAGGGCGCT TGTCTGCCTA CGAATATGCC 1260  
GAGGCAAAAA CAAAATACGC CCTCAGCCAA GTGGAAGAAC TTCGTGCCAA GTATGACTTC 1320  
ATATACAAAG CCAAAGTTT GGATTTCTAT CAGGGCAAG ACTTC 1365

- (2) INFORMATION FOR SEQ ID NO:198
- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 1332 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:  
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:  
(A) NAME/KEY: misc\_feature  
(B) LOCATION 1...1332
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:198

ATGCGTTTCC AACATTATCT CATCTGTACG GCTGCCGTAG CCGCTTTGGC TCGGAATCCC 60  
CTTACGGGCC AATCGAATAT GACCCTCGAA GAGTGCATAG ACTATGCACG CCGGCACAGT 120  
TCGGCCGTGG CGCTGTCCGC TCGGGAATG GAGCAGTCCA AGGCCGATTA CCTTCAGGCC 180  
TCGGCAATT TTCTGCCCCG TGTATCGGCC GGAACCGGTG CTTGTTGGAA TTTCGGACGC 240  
GGATTGGATG CCGAGACGAA TACCTACACC GACATCAACA GCTTCAACAA TTCGTACAGC 300

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	ATACATGCCA	CGATGACCCT	TTTCGACGGT	TTGCAGAGTG	TCTATCGACT	GCGGATGGCG	360
	CATGCACGCC	GGGAGGCTTC	GCGCCTCTCC	GTTCGCGAGC	AGCAGGAGCT	GGCAGCTCTC	420
	GGCACCACGG	AGGCCTACTA	CGACCTCGTC	TATGCGCGCC	AAATGCAAGA	GCTGGCCATG	480
5	CAGAAGTACG	AGGAGAGCAG	CCGCCTCCAC	CGGCAGACGG	CTCGAATGGA	AGAGCTGGGG	540
	ATGAAGAGTC	GTCCCGATGT	CCTCGAGATG	CAGTCCGCGA	TGGCCGGTGA	CCGTTTGGCC	600
	CTGACTCAAG	CGGACAATCA	GTGCATCATC	GCTCTGATCC	GGCTCAAAGA	AAAAATGAAC	660
	TTCCCCATCG	ATGACGAACT	CGTCGTAGAC	GATATGCCGG	CTGACAGTCT	CTCCGCCGAC	720
	ATGGCCGAAT	CGGACAGCTC	GGCCGGCGTC	TTCCGCCGTG	CTGCCCATCA	TCATCCCGTC	780
	CTCCCTCCGTG	CCAAACTCGA	CGAGCAGGCT	GCCACCGACC	GTTTGCGAGC	CGCGCGAGGT	840
10	GCATTCTCTG	CGAGTGTGTC	GGTATCCGGA	GGATGGAACA	CGGGATTCTC	ACGCTTTTTC	900
	AATGGATCGG	ACTATACGCC	CTTCAGCGAG	CAGTTTCGGA	ACCGTCGGGG	GGAATACGTC	960
	AGTCTGAATC	TGAGTATCCC	CATCTTTTCG	GGATTGAGCC	TTGTGAGCCA	TCTGCGTCAG	1020
	GCGCGTGCCG	AACGCAGGGC	GGCAATCGTC	CGACGGGGCG	AAGCGGAGCG	CAGGCTCTAC	1080
	AGCGAGATCG	CCCAAGCCAT	GGCCGACCGG	GATGCCGCTC	TGGCTTCTTA	CCGCCAGGCG	1140
15	AAGGAGCATA	CGGACGCCAT	GCAAAACCGT	TACGAAGCCG	TCTTGCAAGC	TTATGAGGAG	1200
	GGGCTGAATA	CGGCCATCGA	CCTGACCACT	CAGGCCAATC	GGCTCCTGGA	TGCCCGTGTG	1260
	CAGCGACTGA	GAGCGGCCAT	GACCTACCGG	CTCAAAATGCA	AACTCATAGC	CTATTACGGC	1320
	TGCCTTTCGG	AC					1332
20	(2) INFORMATION FOR SEQ ID NO:199						
	(i) SEQUENCE CHARACTERISTICS:						
25	(A) LENGTH: 2820 base pairs						
	(B) TYPE: nucleic acid						
	(C) STRANDEDNESS: double						
	(D) TOPOLOGY: circular						
30	(ii) MOLECULE TYPE: DNA (genomic)						
	(iii) HYPOTHETICAL: NO						
	(iv) ANTI-SENSE: NO						
35	(vi) ORIGINAL SOURCE:						
	(A) ORGANISM: PORYPHYROMONAS GINGIVALIS						
	(ix) FEATURE:						
40	(A) NAME/KEY: misc_feature						
	(B) LOCATION 1...2820						
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:199						
45	ATGAACAAAT	TTTACAAATC	ACTTTTGCAG	TCAGGACTGG	CTGCCCTTCGT	GTCGATGGCA	60
	ACTGCACTGA	CCGCTTCTGC	ACAGATTTCG	TTCGGAGGGG	AACCCCTTGAG	TTTCTCTTCA	120
	AGATCCGCGG	GAACGCATTC	ATTCGACGAT	GCAATGACTA	TCCGCCTTAC	TCCGGATTTC	180
	AATCCGGAAG	ACCTGATCGC	ACAGAGCCGT	TGGCAATCGC	AAAGAGATGG	CCGGCCCCGC	240
	CGGATAGGAC	AAGTAATACC	GGTGGATGTG	GACTTTGCAT	CCAAGGCTTC	GCACATCTCT	300
50	TCCATCGGAG	ACGTAGATGT	ATATCGCCTG	CAATTCAAGT	TGGAAGGAGC	CAAAGCCATT	360
	ACGCTTTTAT	ACGATGCATT	CAATATTCCG	GAGGGCGGAC	GCCTCTATAT	CTATACCCCC	420
	GACCATGAAA	TTGTGTTGGG	AGCATATACG	AACGCCACTC	ATCGCCGCAA	CGGAGCTTTT	480
	GCCACAGAGC	CGGTACCGGG	GASTGAGCTT	ATTATGGATT	ATGAAGTGTC	TCGCGGAGGG	540
	ACTTTGCCTG	ACATCAAGAT	CTCCGGTGGC	GGTTATATAT	TCGACAAAGT	CGGCGGACGC	600
55	CCCGTAACGG	ATAACCATTA	CGGGATCGGT	GAGGACGATT	CCGATTCGGA	TTGCCGAGATC	660
	AACATCAATT	GTCTTGAAGG	TGCAGACTGG	CAGGCAGAGA	AGAACGGTGT	GGTGCAAATG	720
	ATCATGGTAA	AAGGACAGTA	TATCTCAATG	TGCTCAGGCA	ACCTGCTCAA	TAATACGAAA	780
	GGAGACTTTA	CTCCGCTGAT	CATTTCTGCC	GGACACTGTG	CTTCCATAAC	AACCAATTTT	840
	GGTGTAACGC	AATCCGAGTT	GGATAAGTGG	ATCTTCACTT	TCCACTATGA	AAAAAGAGGA	900
60	TGCAGCAATG	GTACATTGGC	CATCTTCCGT	GGCAACAGTA	TCATCGGAGC	TTCCATGAAG	960
	GCTTTCCCTC	CGATCAAAGG	TAAATCCGAT	GGTCTCTTGC	TGCAACTCAA	CGATGAAGTC	1020
	CCTCTGCGCT	ATCGTGTCTA	TTACAATGGA	TGGGACAGTA	CGCCCGATAT	TCCCTCGAGC	1080
	GGTGCCGGTA	TTCATCATCC	GGCCGGGAGT	GCCATGAAGA	TTTCCATCCT	AAAGAAGACT	1140
	CCGGCTCTGA	ATACATGAT	CTCCTCCAGT	GGTTCGGGAG	GGACTGACGA	TCACTTCTAT	1200
65	TTCAATAACG	ATCAAGGTGG	TACGGAAGGA	GGATCGTCCG	GTTCTTCTCT	CTTCAATCAG	1260
	AATAAGCAGC	TGGTCGGCAC	ACTGACCGGA	GGTGCCGCGA	ATTGTGGCGG	GACGGAGTTC	1320
	TACGGCAGAC	TGAACAGTCA	TTGGAACGAG	TATGCATCCG	ATGGCAATAC	GAGCCGCATG	1380
	GACATCTATC	TGGATCCCCA	AAACAATGGC	CAGACGACCA	TCCTCAACGG	AACGTATCGT	1440
	GACGGTTATA	AGCCTTTGCC	CTCTGTGCCC	CGGCTATTGT	TGCAGTCTAC	AGGCGATCAG	1500
70	GTGCAATTGA	ATTGGACGGC	TGTTCTCGCC	GATCAATATC	CATCATCTTA	TCAGGTCGAA	1560
	TACCAATAT	TCCGAAATGG	AAAGGAAATA	GCTACGACAA	AGGAGTTGTC	CTATTCCGGAT	1620
	GCCATCGACG	AAAGTATTAT	CGGTAGCGGT	ATCATTCGAT	ACGAAGTAAG	CGACGCTTTC	1680
	ATTTATCCCT	CGCCGTTGGA	TGGAGTGGAA	TCTTATAAGG	ATACGGACAA	GACTTCTGCC	1740
	GACCTTGCCA	TAGGAGACAT	TCAGACCAAG	CTGAAGCCGG	ACGTAACACC	TCTCCCCGGA	1800
75	GGAGGAGTAT	CAITTAAGCTG	GAAAGTTCCT	TTCTTAAGCC	AGTTGGTTTC	CCGATTCGGA	1860
	GAAAGCCCCA	ATCCTGTGTT	CAAAACCTTT	GAAGTGCCCT	ATGTTTCTGC	CGCAGCCGCA	1920

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	CAAAACCCCA	ATCCTCCCGT	TGGCGTAGTC	ATTGCAGACA	AGTTTATGGC	CGGTACATAT	1980
	CCCGAAAAGG	CTGCTATCGC	TGCCGTTTAT	GTAATGCCAT	CCGCTCCGGA	CTCTACTTTC	2040
	CACCTCTTCC	TCAAGAGCAA	CACAAACAGA	AGATTGCAGA	AGGTGACAAAC	TCCCTCCGAT	2100
	TGGCAGGCCG	GAACATGGTT	GAGGATCAAT	TTGGATAAGC	CGTTCCCGGT	GAATAATGAC	2160
5	CATATGCTTT	TTGCCGGTAT	CAGAATGCCT	AATAAGTACA	AGCTCAATCG	TGCTATCCGT	2220
	TATGTAAGAA	ATCCGGATAA	CCTTTTCTCC	ATTACCGGTA	AGAAGATTTC	ATATAACAAC	2280
	GGAGTCTCTT	TCGAAGGCTA	CGGAATACCC	TCGCTCTTGG	GCTATATGGC	TATCAAATAT	2340
	CTGGTGGTAA	ATACCGATGC	TCCGAAGATC	GATATGTTCG	TTGTACAGGA	GCCTTATGCT	2400
	AAGGGAACGA	ATGTGGCTCC	ATTCCCCGAA	TTGGTCGGCA	TATATGTCTA	TAAGAACGGA	2460
10	ACATTTATCG	GCACACAGGA	TCCATCCGTC	ACAACTTAT	CGGTTTCAGA	CGGAACAGAG	2520
	AGCGATGAAT	ACGAAATAAA	ACTGGTATAT	AAGGGATCGG	GCATTTTCGAA	TGGCGTTGCT	2580
	CAGATTGAGA	ATAACATGTC	TGTCGTTGCA	TATCCGCTCG	TTGTAACAGA	TCGTTTCAGC	2640
	ATTAAGAACG	CTCATATGGT	TCACGCTGCC	GCCCTCTACT	CATTGGATGG	CAAGCAGGTT	2700
	CGTTCTTGGA	ACAACCTCCG	CAATGGCGTG	ACATTCAGTG	TTCAAGGACT	TACGGCCGGT	2760
15	ACTTATATGC	TCGTTATGCA	GACGGCAAAC	GGCCCTGTGA	GCCAAAAGAT	CGTGAAGCAG	2820

## (2) INFORMATION FOR SEQ ID NO:200

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 2010 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION: 1...2010
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:200

40	ATGAAATATC	TTATCAGACT	CTTCTTATCA	TTGATGTTAC	TCTCTCTCTG	GACGGGCTGT	60
	ACACACGAGG	AGCTCTCTAT	TTGCGATGGC	GAGAATACGC	TTGTTTTTACG	CGTAGAGACC	120
	GGTAAAGCCC	CAAAATGCTCG	TGCCACAGAA	CCCGGTCAGG	GCATATACAA	TGAGAATAAA	180
	GTAGGCTCCA	TTTCTGTGCT	CTTCTATTTA	GAGGGACAAC	TTCGTTGGCA	GGTGAAGTCT	240
45	ACAGACTATC	AAATCCATGA	AGGGGCTTAT	ATCATTCCGG	TCAAAGAGCA	AATGCGACCA	300
	CTATTCAATG	GCAACAACAA	CTTCAGCATC	TATGTAGTGG	CCAATCTCGA	TTTCAATGCT	360
	CCGGCCACAG	AAGCTGCGCT	TTCTCAATTT	GTGGTAGAGA	AATCTATTGA	AGTCTCTTCT	420
	ACGACAGCCC	CTGCCGATTT	CGTAATGCTT	GCTCATGGCA	ATAAGCAGAT	CAATATGGCT	480
	ACGACAGAAG	GGAAACTGTT	GGGGGATTAT	AAACTCAAAC	GAGTGGCAGC	AAAGATTGCG	540
50	ATGATAAAAC	CCACCATCAA	TGTGCAAGGA	TATGAAGTGG	TCGGAAATAT	ACAGGCAAAG	600
	TTTCGCAATT	CCGTAAACGAA	GGGGTTCCCT	ACCACAGAAG	CTCAAGAGAT	CCCAGCTGCT	660
	GCATCCATATA	AGACATCGGA	ATATCTTGAT	ATTGCAGAST	CGGCACCTGC	CAATTCTATC	720
	CATTTCTATT	CTTACTATAA	CAAATGGACA	CTCTCCACAC	CGGAGAAGCG	ACCGGAATTC	780
	TTTCATCATGG	TCAAATTCAA	AAAGACAGGA	CAGCCGGACA	ACACAGCCAA	ACCGTACTAC	840
55	TACAGAGTGC	CCCTCGAATC	TCAGGACAAT	CAGGTCAAGA	GCAATGTCCT	CTATAATCTG	900
	AATGTGAAAA	TCGAAATCTT	GGGTTCTTTA	CAAGAGCCGG	AAGCTGTTTC	TGTAAACGGC	960
	ACACTCGCAA	TAGAAGAATG	GATTCTCCAT	CAGGATGCAT	TCAATCTGCC	TGCCACCAAT	1020
	TACTTGATAG	TGGAACAGCA	CGAAATCTTC	ATGAATAACG	TGAACACATA	CTCGGTGAAA	1080
	TATCAAACCTT	CGCAGAAACC	AATCAGCATT	AGCATACAGT	CAGTTACCTT	TAGCTACGTC	1140
60	TCTTCTGATG	GCACTCAGCA	CAATGATCTT	GTAGCAAGTA	GTAGCGACCA	GTATCCTACG	1200
	ATTACAAGCG	ATAATACAAG	CATCATAATC	ACTTCCAAGA	TACCGTTAA	TAACGTACCA	1260
	AAGAAGATCG	TTTTTGAGGT	AATAATGGG	GTAGCCGTT	TGAAAGAGAC	TGTCACAGTA	1320
	CTCCAATATC	CTGCACAATT	TATTGTCAAT	ACACTTGGCA	CAGCATCGGC	ATGGAGACCA	1380
65	GACGGATCTT	TGGCTCCGGG	GCTTAACAAT	AAAGCGATT	ACCATGTCGT	AGTACTGGTT	1440
	CCACCCGAGA	ATTTATTTGA	AGATGGGACA	CAGACAATCA	TCGGTTATCC	CCCCACTGAA	1500
	ACAATTTCTT	TTTATAAGAA	AGAGAACAAT	ACCTATCCGA	TAGTATGGTC	TGACACAAAT	1560
	ACGACAAAAC	AGGACCTTGA	GACATCAAGA	ATGATTTCAC	CTTCCTTTGA	GTAGCCCTCC	1620
	CAACTTGGGG	CTACTCTCCC	GATGCCCTAT	CTCGAGTATT	GGCCAGGGAC	ATCATATCTC	1680
	CTTGACTATT	CGGGAAACTA	TAATAATAAG	AGATACGCCT	TGTTTAATTG	CGCTTTTTTAC	1740
70	TGGGAGAAAA	GAAAAGTTAA	TAACGAAGAA	ATTAATTCG	ATGACTGGCG	TTTGCCGACA	1800
	GAAGCTGAGA	TCAAAATTGAT	AGATAAGCTG	CAACATAATG	AGCAGAGTGC	TGTCCAAGCT	1860
	ATCATGACAG	GGAATTATTA	TTGGGATAGT	TACTCTGCAA	ATGGGTCTTA	TAAATGCAA	1920
	GGAGGAGGGG	GCCAAGGAAA	TTCCTCCAAA	GCCTATGTTT	GTTGCGTGCG	GGATGTGAAA	1980
75	AAGCCGATTC	GTGACAAGAA	GTCAGGTAAG				2010

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## (2) INFORMATION FOR SEQ ID NO:201

- (i) SEQUENCE CHARACTERISTICS:  
5 (A) LENGTH: 3846 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: circular
- 10 (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- 15 (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:  
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- 20 (ix) FEATURE:  
(A) NAME/KEY: misc feature  
(B) LOCATION 1...3846
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:201

25 ATGCGAAAAA TTTTGAGCTT TTTGATGATG TGCTCTCTGC ATTTAGGTCT ACAATCTCAG 60  
ACTTGGCATG GAGATCCGGA CTCAGTGGCA GCCCTACCTT CTATCGGTAT TCAAGAGTCA 120  
AGTTGTACCC GAATCACGTT CGAGGTTGTT TTCCCGGGAT TTTATAGTGT GGAAAAACGA 180  
GAAGGCAACC AAGTCTTTCA GCGCATTTCC ATGCCGGGTT GTGGCTCGTT TGGGAATCTG 240  
GGCGAAGCTG AATTGCTGT TTTGAAAAAG ATGATAGCCG TTCCGGGAAT TTCAACAGCT 300  
AACGTTGCTG TAAAAATCAA AGAGACGGAG ACATTCGACA ATTATAATAT CTATCCTAAT 360  
CCTACCTATG TCGTAGAGGA GTTGCCGTGAG GGGGGGACTT ATCTGGTAGA GGCTTTCGGG 420  
ATAAACAAATG ACTATTATAG CCAAAATGTA AGCCTCCCTT CTACTCACTA TGTCTATTCT 480  
CAAGACGGGT ATTTTCGCTC ACAAAGATTT ATCGAAGTTA CCCTGTATCC TTTTCGATAC 540  
AACCCCTGTC GACAAGAAAT TCTATTGCA AAAAAAATCG AGGTTACAAT AACTTTCGAT 600  
35 AATCCTCAGC CACCTTTACA AAAAAACACC GGCATATTTA ACAAAGTAGC CTCCTCTGCA 660  
TTTATTAAAT ATGAAGCTGA TGGCAATCG GCGATAGAAA ATGATATGGT GTTCAGTCTG 720  
GGTACAACAA CGTACATAAG CGGAAATGTT GCCAGCAACC TCCCTCAGAA CTGTGACTAC 780  
TTGGTTATTT ACGATGATAT GTTCAACGTA AATCAACAAC CACACGACGA AATCAAACGG 840  
CTGTGCGAAC ATAGAGCCTT CTACAACGGC TTTGATGTAG CTGCTGTAAG TATAAAGGAC 900  
40 GTATTGAATA GCTTCCCATC AAATGCCACC TCATACATCA ACGAACTAA ACTGAAAAAT 960  
TTCATTCGCT CAGTTTACAA CCAAAGCAAT GCGAAGAGGA CTTTAGATGG CAAACTGGGA 1020  
TACGTGCTAC TGATCGGAAA ACCATTGAGC AAATATTTGG CTGACACTGA TAATACAAAA 1080  
GTCCCAACCT GTTTTATTTA TAATGCTCTC TTAATTCCAA GTCATCCAAC TTTTGGTTCT 1140  
ATATGCGCCT CCGACTATTT TTTTAGTTGT GTTTCGCCCC TTGATACTGT CGGCGATTGT 1200  
45 TTTATCGGTC GATTTAGCGT CACCAATGCT CATGAATTGC ACAATCTGAT TGAAAAGACT 1260  
ATCAACAAAG AAATCTCATA TAATCCTATT GCACACAAAA ATATTCTTTA CGCAGAAGGG 1320  
AAAGGCTCGC ATGCTCCAAT CTTACGTTTA TTCTTAAAG AAATCGCCTC TGGTTACACA 1380  
GTCAACTCTA TCTTAAATC TAATCAGGTC TCTGCAATAG ACTCGATATT TGACTGCTTG 1440  
AATAATGTTA CCGATCATTT TATTTTAACC ACTCATGGAA TGCCGACTGT TTGGGGGATA 1500  
50 GGGCAGGGAC TCGACGTCAA TACTCTAACA GCCCGATTGA ACAATACATC TTCGCAGGGA 1560  
TTATGTACGA GTCTATCATG TAGTTCGGCT GTAGCAGATT CAACTATTAG ATCGCTTGGA 1620  
GAAGTCCTGA CCACATACGC ACCTAACAAAG GGATTCTCGG CTTTCTTAGG AGGAAGCAGA 1680  
GCCACCCAAT ATGCCGTTTA TTTAGAAGGC CCCTGTCTCT CGTCAGAATT TTATGAATAT 1740  
TTACCTTATT CTTTATATCA CAATCTCTCG ACTGTGTTTG GCGAAATGTT GCTATCATCC 1800  
55 ATTATCAATA CTAATTCTGT TGATACGTAT TCGAAATTCA ACTTCAATTT GCTTGGCGAC 1860  
CCTGCACTAA ACATTATGGC TCATGGCATG GAGGTTAGTA ATTGTATTAC ACTACCAAAC 1920  
AACACCATTA TAAGCAGTCC GATAACAATA AAAAAATGGT GCTGCCTAAA AATACCGGAA 1980  
AAAGGAGTTT TGCATTTTAC TAATAATGGC TCCATACAAG TCATGTCCGG AGGAACCTGT 2040  
60 GAAATAGGCA ATCAGGCTAA AATATCGGGA GAGACCGGTG CTAACCCAC CTTTATTACC 2100  
GTTTACGCGC ATGGTCTTGC GATTAACAAG CAGGTAGAGA TAGACAATAT AGACCGACTT 2160  
AAGTGTGTTT CTACGCATTC GGTCTATGCC AAATTTCATT TTGACAGTGT GAAATCAAC 2220  
AGTGCCCGCG TGTATACAAC GAAGTGTATT GTGGAGATAA GCAATTGCGA ATTTACCAAT 2280  
CGAAGTGACA TTATTTCAAA GAATTGTGAC CTAAGCGTTG AAAACAGTAT GTTTAGCAGT 2340  
TCGGGGATAA CGGTATTCAA GCCTATGGCT ACAAGTCCA TCACCGGATT ATCTACAAAA 2400  
65 GCAAAGATTA CCGACAATAC TTTTTTTGCG ACAGGAAACT TCGCCTACCA TATCACAAAC 2460  
ACGCCAGGCT TAACAGCAAC CTCCAATGCT GCCATCAAGT TAGACAATAT TCCGTAGTAT 2520  
TACATTTCCG GTAATAAAAT AGTCAATTGC GATGAGGCTC TTGTACTAAA TAATAGTGGC 2580  
AACAGAACGA ACAGACTCCA CAATATCACA CGGAATGTGA TAAAAAATG TAGGATTGGG 2640  
AGCAGCGCTT ATAATTCTTA TGGTATTATC AACCAGAAATA AGATCAGTAA CAATCATATA 2700  
70 GGAGTACGTC TCCTCAACAA CAGTTGTTT TATTTGATG ATGCTCCTGT AATCAATGAA 2760  
GAAGATAAGC AGACGTTTAT TTCTAATAGG ACTTGGCAGC TCTATTATC AAACGGTACA 2820  
TTCCCTCTCA ACTTCCATTA CAACAGCTTG CAGGGGGGAG ATACAGATAC ATGGATTTAC 2880  
AACGACAGCT ATACGAATCG CTATATTGAC GTTTCAAATA ATCACTGGGG CAACAATGAT 2940  
TTGTTTGTAT CGAATCAGGT TTTCAATACG CCAGACTTGT TCATTGAGT ACCTTTTGTG 3000  
75 GATGGATTGC CAAATGGGAG ATCGGGCAAT AGCTCTGCTG AAGCAGTAGA ATTCCAAACA 3060

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5 GCATTGGACT GTATTGGCAA TAGCGATTAT CTTTCGGCAA AAGTGGCTCT CAAGATGATG 3120  
 GTTGAACCT ACCCGGAATC CGACTTTGCA ATAGCTGCTT TGAAGGAATT GTTCAGGATA 3180  
 GAGAAAATGT CAGGCAACGA TTACGAAGGC TTGAAAAGATT ATTTGAGATC CAATCCAACC 3240  
 ATCATCTCTT CCCAGAAGTT GTTCCCGACA GCTGATTTCC TGTCTGCGCG ATGCGATATT 3300  
 GTGTGTGAAA ACTATCAGTC TGCCATCGAT TGGTACGAAA ATCGCTTGAA TAGTGAAATC 3360  
 TCCTATCAGG ACASTGTTT TGCAGTCATT GACCTTGGTG ACATTTATTG GAATATGCAG 3420  
 TTAGACTCAC TCAGAGGGAC TGGTATAGAT TTGAACATAC TTTCCTGTGA ACAAAGGAAA 3480  
 TCGCTCGAAA GCCATCAAAA TGTAATAAAT TATTTGTTGT CAACTCTTCC CGAATCAACA 3540  
 GGTACTCTCC TGCTCCATT AGAATGCAAC AAATCAAGCC TTGATAAATC CAAGATAATC 3600  
 10 TCTATTTGCG CCAATCCGGC GAAAGCTGTT GTAACAATA TCTACTATAC CGATAACCTT 3660  
 TCCTGTTCTG TAATAAAAT ATATGGAATA AATGGAGCCT CGGCTGATAT AACCGGGTTG 3720  
 CCCAAACATC TATCCGAAGG TTATTACAGC ATACAGTTCA ATACATCCAA CTTTGATCCC 3780  
 GGTTTCTACC TGGTAACGCT AAATGTTGAT CAGAAAATTA TAGATACGGA AAAATTACGA 3840  
 ATCAAA 3846

## (2) INFORMATION FOR SEQ ID NO:202

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 3822 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...3822
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:202

40 ATGATGTGCT CTCTGCATTT AGGTCTACAA TCTCAGACTT GGCATGGAGA TCCGGACTCA 60  
 GTGGCAGCCC TACCTTCTAT CGGTATTCAA GAGTCAAGTT GTACCCGAAT CACGTTGAG 120  
 GTTGTGTTTCC CCGGATTTTA TAGTGTGGAA AAACGAGAAG GCAACCAAGT CTTTCAGCGC 180  
 ATTTCCATGC CGGGTTGTGG CTCGTTTGGG AATCTGGGCG AAGCTGAATT GCCTGTTTGG 240  
 AAAAAAGATGA TAGCCGTTCC GGAATTTTCA ACAGCTAAGC TTGCTGTAAA AATCAAAGAG 300  
 45 ACGGAGACAT TCACAAATTA TAATATCTAT CCTAATCCTA CCTATGTCGT AGAGGAGTTG 360  
 CCTGAGGGGG GGACTTATCT GGTAGAGGCT TTGCGGATAA ACAATGACTA TTATAGCCAA 420  
 AATGTAAGCC TCCCTTCTAC TCACTATGTC TATTCTCAAG ACGGGTATTT TCGCTCACA 480  
 AGATTTATGA AGATTACCTT GTATCCTTTT CGATACAACC CTGTCCGACA AGAAATCTTA 540  
 TTTGCAAAA AATCGAGST TACAATAACT TTCGATAATC CTCAGCCACC TTACAAAAA 600  
 50 AACACCGGCA TATTTAACAA AGTAGCCTCC TCTGCATTTA TTAATTATGA AGCTGATGGC 660  
 AAATCGGCGA TAGAAAATGA TATGGTGTTC AGTCGTGGTA CAACAACGTA CATAAGCGGA 720  
 AATGTTGCCA GCAACCTCCC TCAGAACTGT GACTACTTGG TTATTTACGA TGATATGTTT 780  
 AACGTAATC ACAACCCACA CGACGAAATC AAACGGCTGT GCGAACATAG AGCCTTCTAC 840  
 AACGGCTTTG ATGTAGCTGC TGTAAGTATA AAGGACGTAT TGAATAGCTT CCCATCAAAT 900  
 55 GCCACCTCAT ACATCAACGA AACTAACTG AAAAATTTCA TTCGCTCAGT TTACAACCAA 960  
 AGCAATGCGA AGAGGACTTT AGATGGCAA CTGGGATACG TGCTACTGAT CGGAAAACCA 1020  
 TTGAGCAAAT ATTTGGCTGA CACTGATAAT ACAAAGTCC CAACCTCTTT TATTCATAAT 1080  
 GTCTCCTTAA TTCCAAGTCA TCCAACCTTT GGTTCATAT GCGCCTCCGA CTATTTTTTT 1140  
 AGTTGTGTTT CGCCCTTGA TACTGTGCGC GATTGTTTA TCGGTGATTT TAGCGTCACC 1200  
 60 AATGCTCATG AATTGCACAA TCTGATTGAA AAGACTATCA ACAAAGAAAT CTATATAAT 1260  
 CCTATTGCAC ACAAAAATAT TCTTTACGCA GAAGGGAAAG GCTGCGATGC TCCAATCTTA 1320  
 CTAAACGCCC GATTGAACAA TACATCTTGC CAGGGATTAT GTACGAGTCT ATCATGTAAT 1380  
 CAGGTCTCTG CAATAGACTC GATATTTGAC TGCTTGAATA ATGGTTCCCA TCATTTTAT 1440  
 TTTAACACTC ATGGAATGCC GACTGTTTGG GGGATAGGGC AGGGACTCGA CGTCAATACT 1500  
 65 CTAACAGCCC GATTGAACAA TACATCTTGC CAGGGATTAT GTACGAGTCT ATCATGTAAT 1560  
 TCGCTGTAG CAGATTC AAC TATTAGATCG CTTGGAGAAG TCCTGACCAC ATACGCACCT 1620  
 AACAAAGGAT TCTCGGCTTT CTAGGAGGA AGCAGAGCCA CCCAATATGC CGTTTATTTA 1680  
 GAAGGCCCTT GTCTCCGTC AGAATTTTAT GAATATTTAT CTTATTCTTT ATATCACAAT 1740  
 CTCTCGACTG TTGTTGGCGA AATGTTGCTA TCATCCATTA TCAATACTAA TTCTGTTGAT 1800  
 70 ACGTATTGGA AATTCAACTT CAATTTGCTT GGGGACCCTG CACTAAACAT TATGGCTCAT 1860  
 GGCATGGAGG TTAGTAATTG TATTACACTA CCAACAACCA CATTATTAAG CAGTCCGATA 1920  
 ACAATAAAAA ATGGTGGCTG CCTAAAAATA CCGGAAAAAG GAGTTTGTGA TTTTACTAAT 1980  
 AATGGCTCCA TACAAGTCAT GTCCGGAGGA ACTCTGGAAT TAGGCAATCA GGCTAAAAATA 2040  
 TCCGGAGAGA CCGGTGCTAA CCCACCTTT ATTACCGTTT ACGGCGATGG TCTTGCGATT 2100  
 75 AACAAAGCAGG TAGAGATAGA CAATATAGAC CGACTTAACT TGTTTTCTAC GCATTGGGTG 2160

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5	ATGCCCAAT	TTCATTTTGA	CAGTGTGAAA	TTCAACAGTG	CCCCGCTGTA	TACAACGAAC	2220
	TGTATTGTGG	AGATAAGCAA	TTGCCGAATT	ACCAATCGAA	GTGACATTAT	TTCAAAGAAT	2280
	TGTGACCTAA	GCGTTGAAAA	CAGTATGTTT	AGCAGTTCGG	GGATAACGGT	ATTCAAGCCT	2340
	ATGGCTACAA	GCTCCATCAC	CGGATTATCT	ACAAAAGCAA	AGATTACCGA	CAATACTTTT	2400
	TTTGGGACAG	GAAACTTCGC	CTACCATATC	ACAAACACGC	CAGGCTTAAC	AGCAACCTCC	2460
	AATGCTGCCA	TCAAGTTAGA	CAATATTCTT	GAGTATTACA	TTTCCGGTAA	TAAAAATAGT	2520
	AATTGCGATG	AGGCTCTTGT	ACTAAATAAT	AGTGGCAACA	GAACGAACAG	ACTCCACAAT	2580
	ATCACACGSA	ATGTGATAAA	AAACTGTAGG	ATTGGGAGCA	CGCTTTTATA	TTCCTATGGT	2640
	ATTTACAACC	GAAATAAGAT	CAGTAACAAT	CATATAGGAG	TACGTCTCCT	CAACAACAGT	2700
10	TGTTTTTATT	TCGATAATGC	TCCTGTAATC	AATGAAGAAG	ATAAGCAGAC	GTTTATTCTT	2760
	AATAGGACTT	GGCAGCTCTA	TTCATCAAAC	GGTACATTCC	CTCTCAACTT	CCATTACAAC	2820
	AGCTTGCAGG	GGGGAGATAC	AGATACATGG	ATTTACAACG	ACACGTATAC	GAATCGCTAT	2880
	ATTGACGTTT	CAAATAATCA	CTGGGGCAAC	AATGATTGTG	TTGATCCGAA	TCAGGTTTTC	2940
	AATACGCCAG	ACTTGTTCAT	TTGGATACCT	TTTTGGGATG	GATTGCCAAA	TGGGAGATCG	3000
15	GGCAATAGCT	CTGCTGAAGC	AGTAGAATTC	CAAACAGCAT	TGGAGTGTAT	TGGCAATAGC	3060
	GATTATCTTT	CGGCAAAAAGT	GGCTCTCAAG	ATGATGGTTG	AAACCTACCC	GGAAATCCGAC	3120
	TTTGGCAATAG	CTGCTTTGAA	GGAATTGTTC	AGGATAGAGA	AAATGTCAGG	CAACGATTAC	3180
	GAAGGCTTGA	AAGATTATTT	CAGATCCAAT	CCAACCATCA	TCTCTTCCCA	GAACCTGTTT	3240
20	CCGACAGCTG	ATTTCTGTGC	TGCGCGATGC	GATATTGTGT	GTGAAAACCTA	TCAGTCTGCC	3300
	ATCGATTGGT	ACGAAAATCG	CTTGAATAGT	GAAATCTCCT	ATCAGGACAG	TGTTTTTGCA	3360
	GTCATTGACC	TTGGTGACAT	TTATTGGAAT	ATGCASTTAG	ACTCACTCAG	AGGGACTGGT	3420
	ATAGATTTTG	ACATACTTTC	CTGTGAACAA	AGGAAATCGC	TGAAAAGCCA	TCAAAATGTA	3480
	AAAAATTATT	TGTTGTCAAC	TCTTCCCGAA	TCAACAGGTA	CTCTCCTGCC	TCCATTAGAA	3540
	TGCACAAAT	CAAGCCTTGA	TAAATCCAAG	ATAATCTCTA	TTTCGCCCAA	TCCGGCGAAA	3600
25	GCTGTGTGTA	CAATAATCTA	CTATACCGAT	AACCTTCTCT	GTTCTGTAAT	AAAAATATAT	3660
	GGAATAAATG	GAGCCTCGGC	TGATATAACC	GGGTTGCCCA	AACATCTATC	CGAAGGTTAT	3720
	TACAGCATAC	AGTTCAATAC	ATCCAACTTT	GATCCCGGTT	TCTACCTGGT	AACGCTAAAT	3780
	GTTGATCAGA	AAATTATAGA	TACGGAAAAA	TTACGAATCA	AA		3822

30

(2) INFORMATION FOR SEQ ID NO:203

35

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 2775 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular

40

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

45

(v) ORIGINAL SOURCE:  
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

50

(vi) FEATURE:  
 (A) NAME/KEY: misc feature  
 (B) LOCATION 1...2775

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:203

55	ATGGCTATCA	TGATGAAAAG	TATTGTTTTT	AGAGCATTTT	TAACGATTTT	GCTCTCGTGG	60
	GCAGCGATCA	CGAATCCGAC	TGCTCAAGAG	ATCTCAGGCA	TGAATGCATC	CTGTCTGGCT	120
	GCTCCGGCTC	AACCGGATAC	TATCTTATAT	GAAAGTTTGG	AGAATGGACC	TGTTCCCAAT	180
	GGCTGGCTTG	AGATAGATGC	TGATGCTGAT	GGTGCCACTT	GGGGAAGCCC	ATCAGGCTCT	240
	TTCTCTGTAC	CTTACGGACA	CAATGGCCTT	TGCACCTACT	CCCATATACG	TTCCGGTATC	300
60	TCAACAGCGG	GCAACTATCT	GATTACACCC	AATATAGAAG	GAGCCAAACG	GGTCAAGTAC	360
	TGGGTATGCA	ATCAGTATAG	TACCAATCCG	GAACATTACG	CAGTAATGGT	ATCGACAACG	420
	GGGACTGCCA	TTGAAGACTT	TGTTTTGTTG	TTTGATGATT	CCATAACAGG	GAAACCGACT	480
	CCTCTTGTAT	GGCGTAGACG	AATCGTGGAC	TTACCGGAAG	GGACCAATAA	TATTGCATGG	540
	CGACATTACA	AAGTCACCGA	CTCACACACA	GAATTCTTGA	AATTGGATGA	TGTCATGTG	600
	TATAGTTCGA	TGGAAGGGCC	CGAACCTGCT	ACCGACTTCA	CAGTAATCAA	TATTGGTCAG	660
65	AATGTGGGAC	GATTGACTTG	GAACTATCCG	GAGGATTATC	AACCGGAAGG	AAAGGGGAAT	720
	GAAGAGTTGC	AGCTTAGCGG	CTACAACATC	TATGCGAACG	GTACACTACT	GGCACAATAA	780
	AAAGATSTCT	CCATACCTGA	GTATGTGGAC	AGCACTTACT	CTTTGCGAGA	CAATCCCTTG	840
	CAAGTGGAGT	ACTGCGTTAC	AGCCGTTTAC	GATGAAAGCA	TAGAATCTTC	GACCGTATGT	900
	GGCAGCGCTC	ATTACGCCAC	GGATGCCATC	CTTTATGAAA	ATTTTGAGAA	TGGACCTGTT	960
70	CCCAATGTTT	GGCTTGTGAT	AGACGCTGAT	GGAGATGGAT	TTAGCTGGGG	ACACTATTTG	1020
	AATGCATACG	ACGCTTTTCC	CGGCCATAAT	GGAGGCCATT	GCTCCTTGTC	GGCTTCTTAT	1080
	GTTCCGGGTA	TAGGCCCGGT	GACTCCCGAC	AACTATCTGA	TTACCCCCAA	GGTTGAAGGA	1140
	GCCAAACGTG	TCAAGTACTG	GGTAAGCAGC	CAGGATGCCA	ATTGGGCAGC	GGAACATTAC	1200
	GCGGTGATGG	CTTCGACAAC	GGGGACTGCT	GTCGGAGATT	TCGTCAATAT	GTTTGAAGAA	1260
75	ACCATGACAG	CGAAGCCGAC	CGGCGCATGG	TATGAAAGAA	CCATCAACTT	ACCTGAAGGG	1320

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ACTAAATACA TCGCATGGCG GCATTACAAC TGTACCGATA TATATTCTT GAAGTTGGAC 1380  
 GATATCACTG TATTCGGGAC TCCTGCATCA GAGCCCGAAC CTGTTACCGA TTTCGTTGTC 1440  
 TCGCTTATTG AAAACAACAA GGGACGATTA AAGTGGGAAT ATCTTAACGG CTACGAACCC 1500  
 GATAAGACTG ATGATAAAGA CCCATTGCAG CTTGCCGGCT ACAATATCTA TGCAAACGGC 1560  
 5 TCGCTCCTTG TTCACATACA AGACCCGACT GTTTTGGAGT ATATCGATGA GACTTATTCT 1620  
 TCACGAGACG ATCAGGTGGA AGTGGGAATAT TGTGTCAC TGCGTTTATA CGACAATATC 1680  
 GASTCCCAAT CGSTTTGCGA TAAGCTGATT TATGATTCTC AATCGGACAT TATCTTATAT 1740  
 GAAGGCTTTG AGGCCGGAAG TATTCCTGAA GGCTGGTTGT TGATTGATGC TGATGGCGAC 1800  
 AATGTTAATT GGGACTATTA TCCTTGGACT ATGTATGGAC ATGACAGTGA GAAGTGTATT 1860  
 10 GCATCCCTT CGTACTTACC GATGATTGGC GTTTTAACTC CGGATAACTA TTTGGTTACA 1920  
 CCCAGACTCG AAGGAGCCAA GCTTGTCAAG TATTGGGTAA GTGCGCAAGA TGCTGTTTAT 1980  
 TCGGCTGAGC ATTATGCTGT GATGGTTTCT ACTACGGGAA CTGCTGTGA AGATTTTGTG 2040  
 CTCTTGTTTC AAGAGACAAT GACCGCTAAG GCTAACGGTG CATGGTATGA GCGAACTATT 2100  
 ACATTGCTCT CAGGAACAAA ATATATTGCC TGGCGGCATT ATGATTGCAC CGATATGTTT 2160  
 15 TCCTTGCTCT TGGATGACAT TACGGTTTAT CGTCTACTG AGACTGTTCC CGAGCCTGTT 2220  
 ACTGATTTCT TGTCTCGCT TATTGAGAAT AACAAGGGTC GCCTGAAATG GAATTATCCT 2280  
 AACGGCTACG AACCCGATAA GACTGATGAT AAAAAACCAT TGCAGCTTAC CGGCTACAA 2340  
 ATCTATGCAA ATGGCTCGCT CCTTGTTCAC ATACAAGACC CGACTGTTT GGAGTATATC 2400  
 GATGAGACTT ATTCTTCACG AGACGGTCAG GTGGAAATGG AATATTGTGT CACTGCCGTT 2460  
 20 TATAACGACA ATATCGAGTC CCAATCGGTT TGCAGTAAGC TGAACATATA TATCACATCC 2520  
 TTGGATAATA TTCAATCTGA TACAAGCTTG AAAATATATC CTAATCCGGC ATCSTATGTG 2580  
 GTAAGGATAG AGGGATTGAG TCGGAGCAAG TCGACAATCG AGTTGTATAA TGCGCTGGGA 2640  
 ATTTGCATAT TAAGGGAAGA GACTCATTCA GAGAAACCG AAATCGATGT TTCACGCTCT 2700  
 AATGACGGAG TCTACTTGAT TAAAGTAGTC GGTGGAAATA AAACAACAAC CGAAAAGGTA 2760  
 25 GAGATAAAGA GGCCG 2775

(2) INFORMATION FOR SEQ ID NO:204

- 30 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 2766 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular  
 35 (ii) MOLECULE TYPE: DNA (genomic)  
 (iii) HYPOTHETICAL: NO  
 40 (iv) ANTI-SENSE: NO  
 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS  
 45 (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...2766  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:204

50 ATGATGAAAA GTATTGTTTT TAGAGCATT CTAACGATT TGCCTCTGTC GGCAGCGATC 60  
 ACGAATCCGA CTGCTCAAGA GATCTCAGGC ATGAATGCAT CCTGTCTGGC TGCTCCGGCT 120  
 CAACCGGATA CTATCTTATA TGAAAGTTTT GAGAATGGAC CTGTTCCCAA TGGCTGGCTT 180  
 55 GAGATAGATG CTGATGCTGA TGGTGCCACT TGGGGAAGCC CATCAGGCTC TTTCTCTGTA 240  
 CCTTACGGAC ACAATGGCCT TTGCACCTAC TCCCATATAC GTTCCGGTAT CTCAACAGCG 300  
 GGCAACTATC TGATTACACC CAATATAGAA GGAGCCAAAC GGGTCAAGTA CTGGGTATGC 360  
 AATCAGTATA GTACCAATCC GGAACATTAC GCAGTAATGG TATCGACAAC GGGGACTGCC 420  
 ATTGAAGACT TTGTTTGTGTT GTTTGATGAT TCCATAACAG GGAAACCGAC TCCTCTGTA 480  
 60 TGGCGTAGAC GAATCGTGGG CTTACCGGAA GGGACCAAAT ATATTGCATG GCGACATTAC 540  
 AAAGTCACCG ACTCACACAC AGAATCTTTC AAATTGGATG ATGCTACTGT GTATAGGTCTG 600  
 ATCGAAGGGC CCGAACCTGC TACCGACTTC ACAGTAATCA ATATTGTTCA GAATGTGGGA 660  
 CGATTGACTT GGAATATCC GGAGGATTAT CAACCGGAAG GAAAGGGGAA TGAAGAGTTG 720  
 CAGCTTAGCG GCTACAACAT CTATGCGAAC GGTACACTAC TGGCACAAT AAAAGATGTC 780  
 65 TCCATACTGG AGTATGTGGA CAGCACTTAC TCTTTGCGAG ACAATCCCTT GCAAGTGGAG 840  
 TACTGCGTTA CAGCGGTTTA CGATGAAAGC ATAGAATCTT CGACCGTATG TGGCACGCTG 900  
 CATTACGCCA CGGATGCCAT CCTTTATGAA AATTTTGAGA ATGGACCTGT TCCCAATGGT 960  
 TGGCTTGTGA TAGACGCTGA TGGAGATGGA TTTAGCTGGG GACACTATTT GAATGCATAC 1020  
 GACGCTTTTC CCGGCCATAA TGGAGGCCAT TGCTCCTTGT CGGCTTCTTA TGTCCGGGT 1080  
 ATAGGCCCGG TGACTCCCGA CAACTATCTG ATTACCCCCA AGGTGGAAGG AGCCAAACGT 1140  
 70 GTCAAGTACT GGTAAAGCAC GCAGGATGCC AATTGGGCAG CGGAACATTA CGCGGTGATG 1200  
 GCTTCGACAA CGGGGACTGC TGTGCGAGAT TTGCTCATAT TGTTCGAAGA AACCATGACA 1260  
 GCGAAGCCGA CCGCGCATG GTATGAAAGA ACCATCAACT TACCTGAAGG GACTAAATAC 1320  
 ATCGCATGSC GGCATTACAA CTGTACCGAT ATATATTTCT TGAAGTTGGA CGATATCACT 1380  
 GTATTGCGGA CTCCTGCATC AGAGCCCGAA CCTGTTACCG ATTTGCTTGT CTCGCTTATT 1440  
 75 GAAACAACA AGGGACGATT AAAGTGAAT TATCCTAACG GCTACGAACC CGATAAGACT 1500

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5 GATGATAAAG ACCCATTGCA GCTTGCCGGC TACAATATCT ATGCAAACGG CTCGCTCCTT 1560  
GTTTCACATAC AAGACCCGAC TGTTTTGGAG TATATCGATG AGACTTATTC TTCACGAGAC 1620  
GATCAGGTGG AAGTGAATA TTGTGTCACT GCCGTTTATA ACGACAATAT CGAGTCCCAA 1680  
TCGGTTTTCG ATAAAGCTGAT TTATGATTCT CAATCGGACA TTATCTTATA TGAAGGCTTT 1740  
GAGGCCGGAA GTATTCCTGA AGGCTGGTTG TTGATTGATG CTGATGGCGA CAATGTAAAT 1800  
TGGGACTATT ATCCTTGGAC TATGTATGGA CATGACASTG AGAAGTGTAT TGCATCCCCCT 1860  
TCGTACTTAC CGATGATTGG CGTTTTAACT CCGGATAACT ATTTGGTTAC ACCCAGACTC 1920  
GAAGGAGCCA AGCTTGTCAA GTATTGGGTA AGTGCGCAAG ATGCTGTTTA TTCGGCTGAG 1980  
CATTATGCTG TGATGGTTTC TACTACGGGA ACTGCTGTTG AAGATTTTGT CCTCTTGTTT 2040  
10 GAAGAGACAA TGACCGCTAA GGCTAACGGT GCATGGTATG AGCGAATAAT TACATTGCCT 2100  
GCAGGAACAA AATATATTGC CTGGCGGCAT TATGATTGCA CCGATATGTT TTTCTTGCTC 2160  
TTGGATGACA TTACGGTTTA TCGTCTTACT GAGACTGTTT CCGAGCCTGT TACTGATTTC 2220  
TTTGTCTCGC TTATTGAGAA TAACAAGGGT CGCTGAAAT GGAATTATCC TAACGGCTAC 2280  
GAACCCGATA AGACTGATGA TAAAAAACCA TTGCAGCTTA CCGGTACAA CATCTATGCA 2340  
15 AATGGCTCGC TCCTTGTTCA CATAACAAGC CCGACTGTTT TGGAGTATAT CGATGAGACT 2400  
TATTCTTAC GAGACGGTCA GGTGGAATG GAATATTGTG TCACTGCCGT TTATAACGCA 2460  
AATATCGAGT CCAATCGGT TTGCGATAAG CTGAACATA CTATCACATC CTTGGATAAT 2520  
ATTCAATCTG ATACAAGCTT GAAAATATAT CCTAATCCGG CATCGTATGT GGTAAAGGATA 2580  
GAGGGATTGA GTCCGAGCAA GTCCGACATC GAGTTGTATA ATGCGCTGGG AATTGCGATA 2640  
20 TTAAGGGGAA AGACTCATTC AGAGAAAACG GAAATCGATG TTTACGCTCT CAATGACGGA 2700  
GTCTACTTGA TTAAAGTAGT CGGTGGAAAT AAAACAACAA CCGAAAAGGT AGAGATAAAG 2760  
AGGCCG

25 (2) INFORMATION FOR SEQ ID NO:205

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 2763 base pairs  
(B) TYPE: nucleic acid  
30 (C) STRANDEDNESS: double  
(D) TOPOLOGY: circular  
(ii) MOLECULE TYPE: DNA (genomic)  
35 (iii) HYPOTHETICAL: NO  
(iv) ANTI-SENSE: NO  
(vi) ORIGINAL SOURCE:  
40 (A) ORGANISM: PORPHYROMONAS GINGIVALIS  
(ix) FEATURE:  
(A) NAME/KEY: misc feature  
(B) LOCATION 1...2763  
45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:205

ATGAAAAGTA TTGTTTTAG AGCATTCTA ACGATTTTGC TCTCGTGGGC AGCGATCAGG 60  
AATCCGACTG CTCAGAGAT CTCAGGCATG AATGCATCCT GTCTGGCTGC TCCGGCTCAA 120  
50 CCGGATACTA TCTTATATGA AAGTTTGGAG AATGGACCTG TTCCAATGG CTGGCTTGAG 180  
ATAGATGCTG ATGCTGATGG TGCCACTTGG GGAAGCCCAT CAGGCTCTTT CTCTGTACCT 240  
TACGGACACA ATGGCCCTTG CACCTACTCC CATATACGTT CCGGTATCTC AACAGCGGGC 300  
AACTATCTGA TTACACCCAA TATAGAAGGA GCCAAACGGG TCAAGTACTG GGTATGCAAT 360  
CAGTATAGTA CCAATCCGGA ACATTACGCA GTAATGGTAT CGACAACGGG GACTGCCATT 420  
55 GAAGACTTTG TTTTGTGTT TSATGATTCC ATAACAGGGA AACCGACTCC TCTTGTATGG 480  
CGTAGACGAA TCGTGGACTT ACCGGAAGGG ACCAAATATA TTGCATGGCG ACATTACAAA 540  
GTCACCGACT CACACACAGA ATTCTTGAAA TTGGATGATG TCACTGTGTA TAGGTCGATC 600  
GAAGGGCCCG AACCTGCTAC CGACTTCACA GTAATCAATA TTGGTCAGAA TGTGGGACGA 660  
TTGACTTGGG ACTATCCGGA GGATTATCAA CCGGAAGGAA AGGGGAATGA AGAGTTGCAG 720  
60 CTAGCGGCT ACAACATCTA TGCGAACGGT ACCTACTGCG CACAAATAAA AGATGTCTCC 780  
ATACTGGAGT ATGTGGACAG CACTTACTCT TTGCGAGACA ATCCCTTGCA AGTGGAGTAC 840  
TGCGTTACAG CCGTTTACGA TGAAAGCATA GAATCTTCSA CCGTATGTGG CACGCTGCAT 900  
TACGCCACGG ATGCCATCCT TTATGAAAAA TTTGAGAATG GACCTGTTCC CAATGGTTGG 960  
CTTGTGATAG ACGCTGATGG AGATGGATTT AGCTGGGGAC ACTATTTGAA TGCATACGAC 1020  
65 GCTTTTCCCG GCCATAATGG AGGCCATTGC TCCTTGTGCG CTTCCTTATGT TCCGGGTATA 1080  
GGCCCCGTGA CTCCCGACAA CTATCTGATT ACCCCCAAGG TTGAAGGAGC CAAACGTGTC 1140  
AAGTACTTGG TAAGCAGCA GATGATGCAAT TGGGAGCGG AACATTACGC GGTGATGGCT 1200  
TCGACAACGG GGAAGTGTGT CGGAGATTTC GTCATATTGT TCGAAGAAAC CATGACAGGG 1260  
AAGCCGACCG GCGCATGGTA TGAAAGAACC ATCAACTTAC CTGAAGGGAC TAAATACATC 1320  
70 GCATGGCGGC ATTACAACTG TACCGATATA TATTTCTTGA AGTTGGAAGA TACTACTGTA 1380  
TTCCGGGACTC CTGCATCAGA GCGCGAACCT GTTACCGATT TCGTGTGCTC GCTTATTGAA 1440  
AACAACAGG GACGATTAAA GTGGAATTAT CCTAAGCGCT ACGAAGCCGA TAAGACTGAT 1500  
GATAAAGACC CATTGCAGCT TGCCGGCTAC AATATCTATG CAAACGGCTC GCTCCTTGT 1560  
CACATACAAG ACCCGACTGT TTTGGAGTAT ATCGATGAGA CTTATTCTTC ACGAGACGAT 1620  
75 CAGGTGGAAG TGGAATATTG TGTCACTGCC GTTTATAACG ACAAATATCGA GTCCCAATCG 1680



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5	GTTTGGCATA	AGCTGATTTA	TGATTCTCAA	TCGGACATTA	TCTTATATGA	AGGCTTTGAG	1740
	GCCGGAAGTA	TTCTGGAAGG	CTGGTTGTTG	ATTGATGCTG	ATGGCGACAA	TGTTAATTGG	1800
	GACTATTATC	CTTGGACTAT	GTATGGACAT	GACAGTGAGA	AGTGTATTGC	ATCCCTTCG	1860
	TACTTACCGA	TGATTGGCGT	TTTAACTCCG	GATAACTATT	TGGTTACACC	CAGACTCGAA	1920
	GGAGCCAAGC	TTGTCAAGTA	TTGGGTAAAT	GCGCAAGATG	CTGTTTATTC	GGCTGAGCAT	1980
	TATGCTGTGA	TGGTTTCTAC	TACGGGAACT	GCTGTTGAAG	ATTTTGTCTT	CTTGTTCGAA	2040
	GAGACAATGA	CCGCTAAGGC	TAACGGTGCA	TGGTATGAGC	GAACATTAC	ATTGCCTGCA	2100
	GGAAACAAAT	ATATTGCCTG	GCGGCATTAT	GATTGCACCG	ATATGTTTTT	CTTGCTCTTG	2160
	GATGACATTA	CGGTTTATCG	TTCTACTGAG	ACTGTTCCCG	AGCCTGTTAC	TGATTTCGTT	2220
10	GTCTCGCTTA	TTGAGAATAA	CAAGGGTCGC	CTGAAATGGA	ATTATCCTAA	CGGCTACGAA	2280
	CCCGATAAGA	CTGATGATAA	AAAACCATTG	CAGCTTACCG	GCTACAACAT	CTATGCAAAT	2340
	GGCTCGCTCC	TTGTTTACAT	ACAAGACCCG	ACTGTTTTGG	AGTATATCGA	TGAGACTTAT	2400
	TCCTCACGAG	ACGGTCAGGT	GGAAATGGAA	TATTGTGTCA	CTGCCGTTTA	TAACGACAAAT	2460
	ATCGAGTCCC	AATCGGTTTG	CGATAAGCTG	AACTATACTA	TCACATCCTT	GGATAATATT	2520
15	CAATCTGATA	CAAGCTTGAA	AATATATCCT	AATCGGCGAT	CGTATGTGGT	AAGGATAGAG	2580
	GGATTGAGTC	GGAGCAAGTC	GACAATCGAG	TTGTATAATG	CGCTGGGAAT	TTGCATATTA	2640
	AGGGAAGAGA	CTCATTTCAG	GAAAACGGAA	ATCGATGTTT	CACGTCTCAA	TGACGGAGTC	2700
	TACTTGATTA	AAGTAGTCGG	TGGAAATAAA	ACAACAACCG	AAAAGGTAGA	GATAAAGAGG	2760
20	CCG						2763

## (2) INFORMATION FOR SEQ ID NO:206

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1779 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...1779
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:206

45	ATGAACAGCA	TCATGAAATA	TCAATTATAT	ACGGCCGTCA	TAATGGCTCT	CTCTGTATCA	60
	TCCGTTTGGG	GTCAAACCCC	ACGAAATACA	GAAACCAAAC	GCCCCGACAC	GCTGCGCAGG	120
	GAGCTTACTA	TCCGTTAATGA	CCAGACTGTG	GAGATGGAGC	ATGCGGATCC	GCTTCCGGCT	180
	GCATACAAGG	CCATCGAACC	TCGATTAAAA	CCTTTCCGTC	CGGAATATAA	CAAGCGTACA	240
	TTCCGATTGG	TCCCTGAAGT	TTCTCTTTCA	GGCAGGAACA	ATCTTCCGAA	TATCCTGCCG	300
50	ACGGAAGGTG	ATATGAAGCA	CCGGGGGTAC	CTGAATATCG	GTATCGGCCA	TACGCTAAAC	360
	CAGCGAATGG	ATGCCGGCTA	TCGTCTGATA	GATGCAGAGC	AGGAGAGACT	GAATCTTTTC	420
	CTCTCCTATC	GTGGGATGAA	ATCGGCTTTC	AATACGGGTG	ACTTCGACGG	CGACAGAAAG	480
	GATAGACGAA	TGATGGCAGG	AGTGGACTAC	GAGCAGCGCA	GGCCTTCTTT	TGTGCTTGCT	540
	ACCGGCTTGT	ATTATTCGAA	CCATTATTTT	AATAACTACG	GACGGGGAGC	TACCAACCAAT	600
55	GTGGGCAGCA	TCCCTCAGCT	ATCGACACCT	GTTACTCCTC	AGATGGACAA	CGGGACCCAC	660
	AACGTCCTGT	TATACTTGGG	TGCAAAAAAT	GATGTGATCG	ATGCCAGGAT	CGACTATCGT	720
	TTCTTCCGTT	CTATTCCCTA	TCTGGGTACC	GATCCGATGA	AGGCTCTCAC	AGAACATACG	780
	CCTGAAGTGA	ACGTGACGAT	GAGTAATGAG	TTGTCCGATG	ATATTAAGCT	CGGTGTCGAA	840
	GTTCGTACGG	GAGGATTGTT	TTTTGCCAAA	AACAGCGAAA	TGATTCAAAC	GGGCGTTCTG	900
60	TCCGAAACCG	ACCGCAACCT	GTATTATGTG	GAGGGCGCGC	CCACAATCGG	ATTTGTCGSA	960
	GACTCGGACA	ATATGCAATG	GAACATACAG	GCCGGAGTAG	GGATTCTTTC	CCATTTCGGA	1020
	GCCAAAGGGA	GGTTGTTTTT	CTGGCCTAAA	CTGGATGCTT	CGCTTAGTAT	CTTCCCTTCA	1080
	TGGCGTGTGT	ATGCGAAAGC	CTTCGGCGGT	GTGATTGCGA	ATGGTCTCGC	CGATGTTATG	1140
	CAAGAGSAGA	TGCCCTACCT	GATGCCCAAT	ACGATTGTAC	TCCCTTCGCG	CAATGCTTTG	1200
65	ACCGCCCAAT	TAGGGGTGAA	GGGGAATATA	GCCGATGTGG	TACGTATGSA	GGTTTATGGC	1260
	GACTTCTCCA	AGCTGACAGG	TGTGCCCTTC	TATACTCCGA	CTCTACCCCT	ATATAATCCA	1320
	TCCGACTTGT	ATCAGTATAA	TGTGAGTTTC	TTGCCGATAT	ATGCCGACGG	CAGCCGCTGG	1380
	CGCGCAGGTG	GTAGCTGGA	ATACTCTTAT	CGCGATATGC	TCCGCTTTCT	GGTAGACGCA	1440
	TCCTATGGCA	AGTGGAAATTT	GGATGGAGGA	CTTGTCGCTT	CCATGCAACG	CGATCTTATA	1500
70	TTGAAGSAGS	AAGTAGGTGT	TCATCCCATT	GCCCCATTGG	ATGTCAGACT	CCGGTATACA	1560
	CAGCTGAACG	GACGGTATCG	GTATTCTTTC	GGCTCGGCTG	GCTCGGAAGC	CTTGGGTATC	1620
	GGTAAATGAC	ATCTTCTTAG	TGCGGATGTT	TCATACAAAC	TGAAAAAGAA	CTTGAGCCTT	1680
	TATCTCAAAA	TCGATAATAT	GCTGGCGGAA	ACGACAGAAC	TTATCGGTGA	TTATCCTATG	1740
75	CAGCCGTTCC	ATTGTTTCGC	CGGTTTTAGC	TGGACTTTC			1779

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## (2) INFORMATION FOR SEQ ID NO:207

- (i) SEQUENCE CHARACTERISTICS:  
5 (A) LENGTH: 1767 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (v) ORIGINAL SOURCE:  
15 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:  
20 (A) NAME/KEY: misc\_feature  
(B) LOCATION 1...1767

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:207

25 ATGAATATC AATTATATAC GSCCGTCATA ATGGCTCTCT CTGTATCATC CGTTTGCGGT 60  
CAAAACCCAC GAAATACAGA AACCAAACGC CCGACACGC TGCACAGGA GCTTACTATC 120  
GTAAATGACC AGACTGTGGA GATGGAGCAT GCGGATCCGC TTCGCGCTGC ATACAAGGCC 180  
ATCGAACCTC GATTAAACCC TTTCGGTCCG GAATATAACA AGCGTACATT CGGATTTGTC 240  
CCTGAAGTTT CCTCTTCAGG CAGGAACAAT CTTCGGAATA TCCTGCCGAC GGAAGSTCAT 300  
ATGAAGCACC GGGGGTACCT GAATATCGGT ATCGGCCATA CGCTAAACCA GCGAATGGAT 360  
GCGGGCTATC GTCTGATAGA TGCAGAGCAG GAGAGACTGA ATCTTTTCCT CTCCTATCGT 420  
GGGATGAAAT CGGCTTTCAA TACCGGTGAC TTCGACGGCG ACAGAAAGGA TAGACGAATG 480  
ATGGCAGGAG TGGACTACGA GCAGCGCAGG CCTTCCTTTG TGCTTGCTAC CGGCTTGAT 540  
TATTCGAACC ATTATTTCAA TAACTACGGA CGGGGAGCTA CCACCAATGT GGGCAGCATC 600  
35 CCTCAGCTAT CGACACCTGT TACTCCTCAG ATGGACAACG GGACCCACAA CGTCCGTGTA 660  
TACTTGGGTG CAAAAAATGA TGTGATCGAT GCCAGGATCG ACTATCGTTT CTTCGGTTCT 720  
ATTCCCTATC TGGGTACCGA TCCGATGAAG GCTCTCACAG AACATACGCC TGAAGTGAAC 780  
GTGACGATGA GTAATGAGTT GTCCGATGAT ATTAAGCTCG GTGTCGAAGT TCGTACGGGA 840  
GGATTGTTTT TTGCCAAAAA CAGCGAAATG ATTCAAACGG GCGTTCTGTC CGAAACCGAC 900  
40 CGCAACCTGT ATTATGTGGA GGGCGCGCCC ACAATCGGAT TTGTCGGAGA CTCGACAAAT 960  
ATGCAATGGA ACATACAGGC CGGAGTAGGG ATTTCTTCCC ATTTGCGAGC CAAAGGGAGG 1020  
TTGTTTTTCT GGCCTAAACT GGATGCTTCG CTTAGTATCT TCCCTTCATG GCGTGTGTAT 1080  
GCGAAAGCCT TCGGCGGTGT GATTGAAAT GGTCTCGCGG ATGTTATGCA AGAGGAGATG 1140  
CCTACCTGA TGCCCAATAC GATTGTACTC CCTTCGCGCA ATGCTTTGAC CGCCCAATTA 1200  
45 GGGGTGAAGG GGAATATAGC CGATGTGGTA CGTATGGAGG TTTATGGCGA CTCTCCAAG 1260  
CTGACAGGTG TGCCTTTCTA TACTCGACT CTACCTTTAT ATAATCCATC CCACTTGAT 1320  
CAGTATAATG TGAGTTTCTT GCCGATATAT GCCGACGGCA GCGCTGGCG CGCAGSTGGT 1380  
AAGCTGGAAT ACTCTTATCG CGATATGCTC CGCTTTCTGG TAGACGCATC CTATGGCAAG 1440  
TGGAATTTGG ATGGAGGACT TGTGCGCTCC ATGCAGCCCG ATCTTATATT GAAGGCAGAA 1500  
50 GTAGETTTTC ATCCCATGTC CCCATTGGAT GTCGAGCTCC GGTATACACA GCTGAACGGA 1560  
CGGTATCGGT ATTCTTTCCG CTCGGCTGSC TCGGAAGCCT TGGGTATCGG TAATGTACAT 1620  
CTTCTTAGTG CGGATGTTTC ATACAAGCTG AAAAAGAACT TGAGCCTTTA TCTCAAAATC 1680  
GATAATATGC TGGCGGAAAC GACAGAGCTT ATCGGTATT ATCCTATGCA GCGTTCCAT 1740  
55 TGTTCGCGCG GTTTTAGCTG GACTTTC 1767

## (2) INFORMATION FOR SEQ ID NO:208

- (i) SEQUENCE CHARACTERISTICS:  
60 (A) LENGTH: 1038 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (v) ORIGINAL SOURCE:  
70 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:  
75 (A) NAME/KEY: misc\_feature

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(B) LOCATION 1...1038

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:208

5 ATGATGGAAA AATGTATCTT TGCTCACTAT CCACATAACC TTGTGTTTAT GATTGCAAG 60  
CATTTTCGGTA TCATTTTGGG ATTTCTTTCT CTTGTGTTTT CGGCAGGTGC TCAACAAGAG 120  
AAGCAGGTGT TTCATTTTCT GAACCTTCCG GCTACTGCAC AGGCTTTGGC TGCCGGAGGC 180  
AAAGCTATCA CCATCGTAGA CGACAATCCC GGAAGTGGCT TTGAGAATCC GGCTCTGCTC 240  
GGATATGAAT CCGGTGGCCG CGCCTTTCTT TCCTATTAT ATTATATGAG TGGTTCGCAT 300  
10 ATGGGCAATG CCGTGTATGC CTCGTCCGTC GGAGAGCGTG GCATGTGGGG TGTGGCATG 360  
CGTTTCTCTA ACTACGGGTC TATGCAAGGA TACGATCAGA ATGCGATTGC CACCGGCTCT 420  
TTTAGTGCTT CGSATATAGC TGTACAAGGA TTTTACAGCC ATGAACTGAG CAACCACTTC 480  
CGCGGTGGAG TCAGCCTAAA AGCATTTGAT TCTTCTATCG AGACGTATAG TTCTTTGGC 540  
CTTGCTGTGG ATGTCGGTAT CAGTTATTAC GACGATGACA AAGGATATTG CGCTCCGCT 600  
15 CTGTTCAAGA ACSTAGGGGC GCAACTGAAA GGCTATAATG AAGAACGGGA ACCGCTCGAT 660  
TGGGATTTCC AGCTCGGCTT TTCCCGCAGT TTTATCAATG CTCCGTTTCG CTTGCACATC 720  
ACGTTGTTCA ATCTGAATCC GCACTATTTT AAGCGTCTTG TACCAGCGCA TCTGTCCAAG 780  
ATGCAAAAGT TCCTCCGACA CTTCTCGATA GGAGCAGAAT TTACTCCTTC CGAGAGGTTT 840  
TGGGTCCGGC TGGGATATAC GCCACAGATT GCACAGGAT TCGAGGTGGA AGGCGGCAAC 900  
20 AAATGGGAG GTCTTTCGGC CGGCGTCGGT TTCACTTCAG GTGTAGTACG TGTAGGCGTA 960  
TCTGCTGCCA CCTATCATCC TGCAGCTCTT TCGTTCATGT GTTCGGTAGG TATCGSTTTG 1020  
GACGATAAGA GCATCTTC 1038

25 (2) INFORMATION FOR SEQ ID NO:209

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1035 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc\_feature

(B) LOCATION 1...1035

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:209

ATGGAAAAAT GTATCTTTCG TCACTATCCA CATAACCTTG TGTTTCATGAT TCGCAAGCAT 60  
TTCGSTATCA TTTTGGGATT TCTTTCTCTT GTGTTTTCGG CAGGTGCTCA ACAAGAGAAG 120  
CAGGTGTTTC ATTTTCTGAA CCTTCCGGCT ACTGCACAGG CTTTGGCTGC CGGAGGCAAA 180  
GCTATCACC A TCGTAGACGA CAATCCCAGG CTGGCTTTTG AGAATCCGGC TCTGCTCGGA 240  
TATGAATCCG GTGGCCGCGC CTTTCTTTCC TATTATATAT ATATGAGTGG TTCGCATATG 300  
GGCAATGCCT GTTATGCCTC GTCCGTCCGA GAGCGTGGCA TGTGGGGTGT TGGCATGCST 360  
TTCCTGAAC T ACGGTCTAT GCAAGGATAC GATCAGAATG CGATTGCCAC CGGCTCTTTT 420  
55 AGTGCTTCGG ATATAGCTGT ACAAGGATTT TACAGCCATG AACTGAGCAA CCACTTCCGC 480  
GGTGGAGTCA GCCTAAAAGC ATTGTATTCT TCTATCGAGA CGTATAGTTC CTTTGGCCTT 540  
GGTGTGGATG TCGGTATCAG TTATTACGAC GATGACAAAG GATATCCGC TTCCGCTCTG 600  
TTCAAGAACG TAGGGGCGCA ACTGAAAGGC TATAATGAAG AACGGGAACC GCTCGATTGG 660  
GATTTCCAGC TCGGCTTTTC CCGCAGTTTT ATCAATGCTC CGTTTCGCTT GCACATCACG 720  
60 TTGTTCAATC TGAATCCGCA CTATTCAAG CGTCTGTGAC CACGCGATCT GTCCAAGATG 780  
CAAAAGTTCC TCCGACACTT CTCGATAGGA GCAGAAATTA CTCCTTCCGA GAGGTTTTGG 840  
GTCGGGCTGG GATATACGCC ACAGATTGCA CAGGATTTCC AGGTGGAAGG CGGCAACAAA 900  
TGGGGAGGTC TTTCCGCCGG CGTCGGTTTC ACTTCAGSTG TACTACGTGT AGGCGTATCT 960  
65 GCTGCCACCT ATCATCCTGC AGCTCTTTTC TTATGTGTGT CGGTAGGTAT CCGTTTGGAC 1020  
GATAAGAGCA TCTTC 1035

(2) INFORMATION FOR SEQ ID NO:210

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 990 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

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(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

5 (iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:  
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

10 (ix) FEATURE:  
(A) NAME/KEY: misc\_feature  
(B) LOCATION 1...990

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:210

ATGATTCGCA	AGCATTCGG	TATCATTTT	GGATTCTTT	CTCTGTGTT	TTCCGCGAGGT	60
GCTCAACAAG	AGAAGCAGGT	GTTTCATTTT	CTGAACCTTC	CGGCTACTGC	ACAGGCTTTG	120
GCTGCCGAG	GCAAAGCTAT	CACCATCGTA	GACGACAATC	CCGGACTGGC	TTTGTAGAAT	180
CCGGCTCTGC	TCGGATATGA	ATCCGGTGGC	CGCGCTTTTC	TTTCTATTT	ATATTATATG	240
AGTGGTTCGC	ATATGGGCAA	TGCCTGTTAT	GCCTCCTCCG	TCGGAGAGCG	TGGCATGTGG	300
GGTGTTCGCA	TGCGTTTCCT	GAACCTACGGG	TCTATGCAAG	GATACGATCA	GAATGCGATT	360
GCCACCGGCT	CTTTTAGTGC	TTCGGATATA	GCTGTACAAG	GATTTTACAG	CCATGAACTG	420
AGCAACCACT	TCCGCGGTGG	AGTCAGCCTA	AAAGCATTGT	ATTCTTCTAT	CGAGACGSTAT	480
AGTTCTCTTG	GCCTTGGTGT	GGATGTCGGT	ATCAGTTATT	ACGACGATGA	CAAAGGATAT	540
TCGCGTTCCG	CTCTGTTCAA	GAACGTAGGG	GCGCAACTGA	AAGGCTATAA	TGAAGAACGG	600
GAACCGCTCG	ATTGGGATTT	CCAGCTCGGC	TTTTCCCGCA	GTTTTATCAA	TGCTCCGTTT	660
CGCTTGCACT	TCACGTTGTT	CAATCTGAAT	CCGCACTATT	TCAAGCGTCT	TGTACCACGC	720
GATCTGTCCA	AGATGCAAAA	GTTCTCCGA	CACCTCTCGA	TAGGAGCAGA	ATTTACTCCT	780
TCCGAGAGGT	TTTGGGTCGG	GCTGGGATAT	ACGCCACAGA	TTGCACAGGA	TTTCGAGGTG	840
GAAGGCGGCA	ACAAATGGGG	AGGTCTTTCC	GCCGCGCTCG	GTTTCACTTC	AGGTGTAGTA	900
CGTGTAGGCG	TATCTGCTGC	CACCTATCAT	CCTGCAGCTC	TTTCGTTTAT	GTGTTCCGTA	960
GGTATCCGTT	TGSACGATAA	GAGCATCTTC				990

35 (2) INFORMATION FOR SEQ ID NO:211

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 972 base pairs  
(B) TYPE: nucleic acid  
40 (C) STRANDEDNESS: double  
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

45 (iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:  
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

50 (ix) FEATURE:  
(A) NAME/KEY: misc\_feature  
(B) LOCATION 1...972

55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:211

ATGTGCCTCG	AACCCATAAT	TGCTCCGATT	TCATCCGAGT	TGCTCGAGCA	GGAGCTGACT	60
GCCGATCGTT	TTCTGCGGAT	GACAAACAAA	GCCGCAATG	AGATCTATGT	TTTTACGGCC	120
GAAGAAGCTC	CGCATTCGAT	GAAAGAAGTA	GGCCGACTGC	GAGAAGAAGC	CTTTCGGCAT	180
TATGGCGGAG	GTAATGGCAA	GGCGATCGAT	ATAGACGAGT	TCGACACCAT	GCCCGGGAGC	240
TACAAACAGC	TGATCGTATG	GGATCCGCAA	AACAAGGCTA	TACTCGGAGG	CTACCGCTTT	300
ATCTATGGGC	GGGACGTTGC	TTTCGATACC	GATGGCAAGC	CTTTGCTGGC	AACGGCAGAG	360
ATGTTTCGCT	TCAGTGATGC	TTTTTTGCAC	GATTATCTCC	CCTACACAGT	CGAATTGGGA	420
CGTTTCGTTG	TGTCGCTCCA	GTACCAATCG	ACACGGATGG	GCACAAAGGC	CATTTTTGTG	480
CTGGACAATC	TTTGGGACGG	TATCGGAGCA	CTCACTGTAG	TCAATCCAGA	GGCACTCTAT	540
TTCTATGGCA	AGGTGACCAT	GTACAAAGAC	TATGATCGGC	GAGCTCGCAA	TCTGATCCTG	600
TATTTTCTTC	GCAAGCACTT	CTCCGATCCG	GAAGGCTTGG	TCAAGCCTAT	TCATCCCTTA	660
CCGATAGAGA	TCAATGCGGA	GGACGAAGCC	TTGTTCTCCT	CATCCGACTT	TGACACCAAT	720
TACAAGACTC	TCAATATAGA	AGTGGCGAAG	CTGGGTATCA	ATATCCCTCC	TCTCGTGAGT	780
GCATATATAG	CTTTGTCTCC	GGAGATGCGT	GTTTTCCGCA	CTGCAGTGAA	TGAGTCTTTC	840
GGAGAGGTGG	AGGAAACCGG	CATATTCATT	GCTGTGGGTA	AGATCCTGGA	AGAGAAAAAA	900
CAACGGCACA	TAGAGAGCTT	CATCCTCAGC	CGGAACGAAA	AAAAAGGTCT	CGACAGTAGC	960
AATGGCCGAT	CA					972

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(2) INFORMATION FOR SEQ ID NO:212

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 1641 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:  
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:  
(A) NAME/KEY: misc feature  
(B) LOCATION 1...1641

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:212

25	ATGAAAACCA TTGTAAGATA CAGCCGCCCT CCGGTCGCTC TCTTCTTTTG CCTTTTGGGA	60
	GCTGTGCACT TGTCTGTGCA GGCGCAGATG C/CAATACTC CTTTCGAGCT GTCGGATCAG	120
	ATCGTCTCTG CTCCCACCGA AAGGCAATAC AGGGAGATT TGTGTGCAAAC GAAAGAAAAA	180
	AGGGGGGCGG ATCTTTTCCC GTTGAGCGAT AAGCTGCGCG ATTCGGCCTA TGTTCGTTTC	240
	GGCTCGGCGT ATGGCGATAT TGCGGGCGGAC TATCTTCGT ACAACGGCAA TAACTACTCC	300
30	TCGCTCTCGC TCGAATCGGG TGGTCGCATC AGTGTCCGTA ACTATGGCAC ATGTCAGGGC	360
	AGTGCTTCC TCTCACGTGG CATGCACAAA CGCATCGGCT GGAATGCTCT GCGCAACGCC	420
	GAAGCCTACT ATCCCTATTT GGTGTCCGAT TCGACCGGCG GAGACTATCA TTTCGAAGAC	480
	TATCGGCTTG CCGGCTACTA TTCTTTTCGC GCCGGCCGCT TGCCCCCTCG TATAGGCTTC	540
	TCATACAGGG GCGAAGTTGC TTATCGGCTG ACCGATCCGC GTACGACCAA TACGACCGGT	600
35	GCATTGGAGC TTTCTTGTC TACCTCTTTG ACGCTGCCTC GAGAGAACAG GCTATCGCTT	660
	TCGGCTGCGT ATCTCTATCA TAGACAACAC CTCACACAGT ACAACTGGCG TCCCGGGCAG	720
	CAGGACAAAT TCTTCGTCAG CTACGGTTTC GGTGAGGTGG ATGTCAGCAA CAGCCCTATC	780
	TGGTTCGSTA TCTCCAGAA GAACTACGTC AACGGATGGA AGCTTAGCTC CCGTCTGGAT	840
	ACCCGTAGGG GCGATGCCAT CGGTCTCGAC TACAGCGGCT ACTTCCTCGA TACCGAaGAG	900
40	AGGTCGTCCA TCAATCTCTT TGCTTTGCTT TACAATCGCC TCGCACTCTA TGGTAGCTGG	960
	CATCTGTGCG ACTTCGATTT TTCATTTTCA GCCGACTATG CTCTGCGCCA AGGGATAGAG	1020
	CGGATATACG AAGACTACAA GCCGGATGAT AATTATCATA TCTACGACCT CCGTATCTTG	1080
	GCCATTTCGC GCTGGTATAT GCTCAATGAG TTTTCTGCCC AAGCCCAAGC CTCCTACCGT	1140
	ATTCGCACGG ATAGAGGTTG TGCCCTGAGA GTGAGTGCCG GTAGTGATTT CTACGGCTAT	1200
45	GATGAGACGT ATCGCAAGCA TGGACATCAT ACCATGAGCG GAATGCTACG TCCTTTTGCC	1260
	GGTATAGCCT ATGACCATGC CGGATCCAAA TTGGATTTTG GACTTTGCTT TTCGGCTGCT	1320
	TATCGAATGG TGCTGACGCA TTCGTATAAG ATTTCGTACCA TCCAGAAAGA GCAGCTCGAC	1380
	TATCAGCTGG CCTATTTGCC CTATGCCTAT CGTAATAGAG AAGGCGTGGA GGTGCGTTCC	1440
	TCTCTGTACG TCTCGATTCC GATGCAGAAT ACCACCGCC TGATGACAGA GCTGCGGTTG	1500
50	TATGGCGACC TGATGAAAAG AAAGGACGGT ATAGCCTATG GCAAAACGCC CGGTGTCATC	1560
	TCACATATCC TGTCGGATCC GCAAGCCGAA CGAACGTCCG GCCATACCAT CGGGGCTATC	1620
	TGCAATATCT CCTACCTCTT C	1641

(2) INFORMATION FOR SEQ ID NO:213

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 2250 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:  
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:  
(A) NAME/KEY: misc feature  
(B) LOCATION 1...2250

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## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:213

5	ATGAAAAAAC	TTCACATGAT	TGCCGCTTAA	GCCGCTCTGC	CTTTCTGCCT	GACGGCACAA	60
	GCACCCGTCT	CCAACAGCGA	GATAGATAGT	CTTAGCAATG	TGCAGCTCCA	GACCGTACAG	120
	GTGCTAGCTA	CTCGCGCCAC	GGCGAAAACC	CCTGTCGCTT	ACACCAACGT	TCGCAAGGCC	180
	GAACCTTCCA	AGTCCAATTA	TGGTCTGTGAC	ATCCCTATC	TGCTGATGCT	GACTCCCTCC	240
	GTGGTAGCCA	CCAGCGATGC	CGGTACGGGT	ATCGGATATT	CCGGCTTTCG	CGTGGGTGGC	300
	ACCGATGCCA	ATCGCATCAA	CATAACTACC	AATGGAGTAC	CCCTCAACGA	CTCCGAATCT	360
	CAGTCCGTCT	TTTGGGTGAA	TATGCCCGAC	TTCCCTCTT	CCATCGAAGA	CCTTCAGGTG	420
10	CAGCGAGGTG	TGGGTACTTC	CACCAATGGT	GCCGGAGCTT	TTGGGGCAAG	TGTCAATATG	480
	CGTACGGATA	ATTTGGGACT	GGCTCCTTAT	GGCCGTGTGC	ATTTGAGCGG	AGGTTCTGTT	540
	GGCACATTCC	GCCGATCGGT	CAAACCTCGT	AGCGGACGCA	TCGGTTCGCCA	TTGGGCASTG	600
	GATGCCCGCC	TGTCCAAAAT	CGGTTCGGAC	GGCTACGTGG	ATAGAGGAAG	CGTGGATCTG	660
	AAATCCTATT	TGGCACAGST	GGGCTATTTT	GCTAGCAACA	CGGCTCTCAG	GTTTCATCACT	720
15	TTCCGGAGGAA	AAGAAGTTAC	GGGTATCGCA	TGGAACGGTC	TTTCCAAGGA	GGATGAAGCC	780
	AAATATAGCC	ATCGTACCGG	CAGTGCCGGT	CTTATGTACG	TGGACGCGCA	AGGAGTACCG	840
	CACTACTACC	ACAATACCGA	CAATTACGAG	CAGCGTCACT	ACCATGCCAT	CATGACGCAC	900
	AGCTTCTCTC	CTTCCGTAT	CCTCAACCTC	ACGGCACACT	ACACGGCCCG	ATATGGCTAT	960
	ACGGACGAAT	ATCGTACCGG	ACGTAAACTA	AAGGAATATG	CACCTGCAGCC	CTATGTGGAA	1020
20	AACAGTGTGA	CGGTGAAGAA	AACGGATCTC	ATCCGTGAGA	AGTATCTGGA	CAATGACTTC	1080
	GGAGGACTCA	TGGGTTCGCT	TAACTGGCAC	ACCGGTGCAT	GGGATTGCA	GTTCCGGGGC	1140
	TCGGGCAATA	TGTATAAAGG	AGACCACTTC	GGCCGTATCA	CTTACATCAA	AAAGTACAAT	1200
	CAGCCCTTAG	CTCCCGACTT	CGAATATTAT	CGGAACAGGG	CAGACAAAAG	AGAAGGTGCA	1260
	GCCTTTGCCA	AAGCCAACTG	GCAGATCACT	CCGGAACTGA	ACATGTATGC	CGACCTCCAG	1320
25	TATCGTACCA	TGGGCTACAC	GATAAACGGC	ATCACGGACG	AATATGATGA	GGTACAGGGA	1380
	AGTATGCAGC	ACATCGATTT	GGACAAGACC	TTCCGCTTCC	TCAATCCGAA	GGCCGGTCTT	1440
	ACCTATAGTT	TGACAGATGC	TCATACTGCC	TATGCTTCTG	TTGCCGTAGC	ACACCGCGAG	1500
	CCTAACAGAA	CCAATTACAC	CGAAGCCGGA	ATAGGACAGT	ATCCTACGCC	TGAGCGACTG	1560
30	ATCGACTATG	AGCTGGGCTA	CGGCTATGCT	TCGCCCTCT	TGTCGGCCCG	AGTAGGTCTC	1620
	TATTATATGC	AATACAAGGA	CCAACCTCGT	CTGGATGGCC	GTTTGAGCGA	TGTGGGACAG	1680
	ATGCTCACAA	GCAACGTCCC	CGACAGCTAC	CGTATGGGAC	TGGAGCTGAC	TCTCGGTTGG	1740
	CAGATCCTTC	CTCGTTTGCT	GCGTTGGGAT	GCTTCTTTCA	CTATGAGTGC	CAACAAAATC	1800
	GACCGGTACG	TACAATATAC	ATCCGTATAT	GATGCGGACT	ACAACCTGGCT	CGAACTCAAG	1860
35	GAGGAGACCC	TGGAAGACAC	GGATATAGCC	TACTCGCCCA	ATGTCATTGC	CGGCAGCATG	1920
	CTTACCCTCT	CTCATGCCGG	TTTCGAAATG	GCTTGGACGA	GCCGCTTCGT	CAGCAAGCAA	1980
	TATCTGGACA	ATACACAGCG	CAGCGATCGC	ATGCTTTCCT	CCTATTGGGT	GAACGACCTC	2040
	CGCCTCGGCT	ATGTGCTGCC	GGTTCACCTT	GTTAAGAGAG	TGGCACTGGG	CGTACAGCTC	2100
	AATAATCTCT	TCAACCTCAT	GTATGCGTCC	AATGCCTACA	TCTACGATGC	CGGTTACGTA	2160
40	CAGGCATCCG	GAGAATAAAG	TGCATATGCC	GATCTGCGTT	ATTATCCTCA	GGCCGGATTT	2220
	AATGCACCTG	GTAGTCTGAC	AATCGATTTT				2250

## (2) INFORMATION FOR SEQ ID NO:214

- 45 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1482 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRAINDNESS: double  
 (D) TOPOLOGY: circular
- 50 (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- 55 (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- 60 (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...1482

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:214

65	ATGAAAAGAA	GGTTTCTATC	GCTGTTACTG	CTGTACATAC	TCTCTTCCAT	CAGCCTTCT	60
	GCTCAGCGGT	TTCCGATGGT	GCAGGGAATC	GAGTTGGATA	CCGATTCGCT	TTTCTCTCTG	120
	CCCAAGCGTC	CTTGGCGCGC	CATCGGTAAA	ACGATAGGCG	TCAATCTGGC	CGTATGGGGC	180
	TTGATCATTT	TCATCATGAA	CGAGGACTTT	GCAGACATCA	GTTGGCAGAC	TATCAAGAGC	240
70	AATTTCCAAA	CAGGCTTTGG	CTGGGACAAT	GACAAGTTTG	TCACCAACCT	CTTCGCACAT	300
	CCTTATCAGG	GATCGCTCTA	TTTCAATGCA	GCGAGGTGCA	ACGGTTTGAG	CTTCAGGCAC	360
	TCTGCTCCGT	TTGCCTTCTT	TGGCAGTCTC	ATGTGGGAGC	TGCTTATGGA	AAACGAGCCA	420
	CGAGATATCA	ACGACCTCTG	TGCCACCACC	ATAGGCGGTA	TAGCTTTGGG	GGAGATGGGG	480
	CACAGGCTGT	CGGACCTGCT	CATCGACAAT	CGTACCACAG	GGTGGGAACG	TATGGGGCCG	540
75	GAGGTGGCTA	TCGCTCTGAT	CAATCCGATG	CGCTTCTCTA	ACCGTCTGAC	AGCAGGASAG	600

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	GTGACTTCTG	TCGGGAGTCG	CAGCGGACAG	ATATTTTCAGT	CTGTCCCCAT	AAACATAGTC	660
	GTCGATGCCG	GCTTTTCGCTT	TTTGGCAGAC	AAGCGGCATG	CCCGAACCGG	TGCCACGCT	720
	CTGACCCCTGA	ATCTGAGATT	CGACTACGGC	GATCCATTCC	GAAGCGAGAC	TTTCTCTCCA	780
	TACGATTTCT	TCCAATTCAA	AGCCGGATTG	AGTTTCTCCG	AATCGCAACC	TCTGCTGAGC	840
5	CAGATCAATC	TGATCGGAAT	CCTAAGCGGA	TGCCAACTGC	TGCGCACACGA	ACGAACGGTT	900
	TTGGTGGGAG	GTCTCTTTCA	GCACTTCGAC	TACTACAATT	CGGAAAAACG	AATAAGCAAA	960
	AATTCGGAGG	AGSTACTCGT	CACCCCATAC	CGTATCTCGC	AAGTGGCAGC	TCTGGGAGGC	1020
	GGTCTTATCT	TCCAGCACCA	CGGAAAATTT	CGACGACGTC	CTCTGGAGCT	ATATGCCGAG	1080
	ACCTACCTGA	ATGTGCTCCC	GATGGGAGCC	AGTCTGTCCG	ATCACTACAA	CGTGGACAAT	1140
10	CGGGACTATA	ACCTCGGCAG	CGGATTGAGC	GGCAAGCTAT	ACCTTGGTGC	TACGTACAAT	1200
	GATCTGTGGA	GCTGGCTCTT	GGGAGTCGAA	AGCTATCGGC	TCTACACATG	GATCGGGTAT	1260
	GAAGAGCCCG	ACCAGAAAAA	TACCGATGTC	AGCTCTTTTA	TGGTGCAGGG	GGACGAAAGC	1320
	AAGGCGCGCC	TACTGCTGAC	GAGTTCGAG	TTGCGATTTC	ATCCTGGCCC	CTGGCATGTA	1380
	GCCATCGTCG	CTCGCCGTTT	CATCCGCAAA	ACAGCCTATC	AATTCTACCC	TAAOGTATCA	1440
15	TTGATACCG	GCGACATACA	GCTGCGTGTG	GGATTTCACT	TC		1482

## (2) INFORMATION FOR SEQ ID NO:215

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 882 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...882
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:215

40	ATGAAACGAC	TGATTGTTTT	TCTGGCAATG	GGTGGCTTGC	TGTTCAACCT	TGCGAACGCA	60
	CAAGAAGCAA	ACACTGCATC	TGACACTCCC	AAAAAGGACT	GGACTATAAA	AGGTGTGACC	120
	GGACTAAATG	CCTCTCAGAC	TTCTCTGACC	AACTGGGCTG	CCGGTGGAGA	AAACACGGTG	180
	GCAGGTAACC	TCTATTGAA	CATAGATGCC	AACTACCTGA	AAGATAAATG	GAGTTGGGAC	240
45	AACGTTTTGC	GTACAGACTT	CGGTCTGACC	TACACAACAG	CCAACAAGTG	GAACAAAAGT	300
	GTAGACAAGA	TCGAATCTTT	CACGAAGGCC	GGCTATGAGA	TGGGCAACAA	TTGGTACGGA	360
	AGTGGCTTTT	TCACTTTTCT	CTCACAGTAT	GCCAAAGGAT	ATGAGAAGCC	CTGGGATCAC	420
	TTGACAGGAG	TCAAGCATAT	CTCTAATTTT	TTGCTCTCTG	CATATCTCAC	TCTCGGTATT	480
	GGTGGGACT	ATAAGCCCAA	TGAGAAGTTT	TCTCTCTACC	TCTCTCTAC	AACGGGCAAG	540
50	CTGACTGTAG	TAGCAGACGA	CTACCTCTCA	AGTTTGGGAG	CGTTCCGGGT	GAAAGTTGGT	600
	GAAAAGACAA	TGTTCGAACT	TGGTGCTTTG	GTAAGTGGGT	CGGCCAATAT	AAATCTGATG	660
	GAGAATGTCA	ATTTGATAAC	CAAGGCTTCA	TTCTTCTCGG	CTTATACGCA	CGACTTTGGC	720
	AACATTGACA	TCAATTGGGA	GGCTATGCTG	GCCATGAAGA	TCAACAAGTT	CCTCACGCT	780
	ACGATAGCCA	CCAATCTTAT	CTACGACGAT	GATGTGAAGA	TCAACGATGG	CCCGAAAATC	840
55	CAGTTCAAAG	AAGTTGTGGG	CGTGGGTGTT	GCGTACACTT	TC		882

## (2) INFORMATION FOR SEQ ID NO:216

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 612 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:

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(A) NAME/KEY: misc\_feature  
(B) LOCATION 1...612

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:216

5 ATGAAGAAAA TGATTTTGGC AGCTACTATG CTGCTCGCAA CAATCGGTTT TGCAAATGCT 60  
CAGAGTCGTC CTGCTCTTAG ACTGGATGCT AACTTTGTGG GTAGTAACTT AATGCAAAAA 120  
GTGCGAAACA CGAGCGTGAA CAATAAGATG ATCGTAGGCT TACGTGTGGG TGCTGCTGCT 180  
10 GAGTTCGCTC TTAGCAATGA TGGATTCTAT CTCGCCCCCG GATTGGCCTA TACGATGAGA 240  
GGTGCTAAGA TGGAACTACT AAGTGAAACG ACAACTCGCT TGCATTATCT GCAAATACCG 300  
GTGAATGCCG GTATGAGATT TAGCTTTGCT GACAACATGG CTATTTTCATT GGAAGCAGGT 360  
CCCTATTTCC CATATGGTGT CGCCGGAACG ATTAAGACTA AAGTTGCAGG CGTTACGGCT 420  
TCTGTAGATG CCTTTGGTGA TAACGGATAT AACCGTTTCC ACTTGGGCTT GGGCTTGTCT 480  
GCTGCCTTGA GCTACGACCG TTATTACGTA CAAATTGGAT ATGAGCATGG ATTGCTTAAT 540  
15 ATGTTGAAGG ATGCTCCGGA TAAGACTTCT TTGCGTAATC ATGACTTCTT TGTGGGTCTC 600  
GGTGTTCGCT TC 612

## (2) INFORMATION FOR SEQ ID NO:217

20 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 729 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
25 (D) TOPOLOGY: circular  
(ii) MOLECULE TYPE: DNA (genomic)  
(iii) HYPOTHETICAL: NO  
30 (iv) ANTI-SENSE: NO  
(vi) ORIGINAL SOURCE:  
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS  
35 (ix) FEATURE:  
(A) NAME/KEY: misc\_feature  
(B) LOCATION 1...729

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:217

40 ATGAAAAGGA TTTTACTGT AGCCCTTGTG CTAATTGCTT CCGTCACTAT GGCCATCGGA 60  
CAAAGCCGCC CGGCACTTCG CGTAGATGCC AACTTCGTAG GCAGCAATCA GAGCATGAAA 120  
45 AGAGACGGAT ATGTGTGGGA CACCAAAATG AATGTCGGCC TGCGGGTCGG TGCCGCTGCC 180  
GAATTCATGA TCGSATCAAG AGGATTCTAC TTGGCTCCGG GTCTGAACTA TACGATGAAG 240  
GGCTCCAAAA CGGAATGGGA TATACCCGAA ATGGTTCCGT GTACCTATAT TACGATGGTT 300  
TCCACTCGCT TGCATATCT GCAACTGCCG ATCAATGCCG GCATGCGGTT CGACCTGATG 360  
AATGACATGG CGGTTTCGAT CGAAGCGGGT CCTTTCCTTG CATACGGTAT ATATGGTACA 420  
TATCGGCAGA AGTTGGAAGG ATGGAAGCCG AACAACTACA GCACAGAGTT TTTTGGCCCA 480  
50 ACGCTTGGTG GCCCAACAAA TATCCGCTGG GACATCGGGG CAAACATAAT AGCCGCATTC 540  
CACTATAAGC GTTATTATAT ACAGATAGGC TATGAACATG GATTTGTGGA TATTGTGTCA 600  
GGTGGAGGTT CTGATATTCC CCGACTGAAC GACAATAGGC AATCCTCTTC GACGACCGCT 660  
CTAAGAGAAA AGGGAAATAA CGAATACGCT TATAATCGTG ACTTCTTCGT GGGCATAGGT 720  
55 TACCGCTTT 729

## (2) INFORMATION FOR SEQ ID NO:218

60 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 621 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: circular  
65 (ii) MOLECULE TYPE: DNA (genomic)  
(iii) HYPOTHETICAL: NO  
(iv) ANTI-SENSE: NO  
70 (vi) ORIGINAL SOURCE:  
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS  
(ix) FEATURE:  
75 (A) NAME/KEY: misc\_feature



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(B) LOCATION 1...621

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:218

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5  ATGAAAAGAA TGCTGCTGCT TCTCGTTGTA TTATTATATG GAATTGCAGG CCGATTGGCT 60
   GCACAAGACG TTATCAGACC ATGGTCATTG CAGGTCGGAG CGGGATACTC CGATACGGAG 120
   AACATCCCGG GAGGATTCAC CTATGGTTTC TATTTGGGAA AGCGTATGGG GAGCTTTCTG 180
   GAAGTGGGGG TGTCATGTA CAACGCCACA CGTCAAACAG CCAACAATGC AGACTCCTTT 240
   GCATCGAAGC AAGGAGACGG ATCTTTTCAG GTAAATATGT CTCTCCGAA TGAGAAGTGG 300
10 TCATTCTTCG ATGCAGGCAG TGCCAACTGC TATATGATCG TCGTCGGAGT CAATCCTCTC 360
   CATCTGTTTT GGCAGAATAG CCGGCACAAT TTGTTTCTGG CAGTACAAGC CGGCCTGTCC 420
   AATAAGCACA ATATTCATTT CATCTATGGA GACAAGGGAG CCAAAGTCAG TATCTACACC 480
   AATTGGAATA CCTACATCGG TTACGGAGCA CGTGTAGCCT ACGAATATCA AATTCATAAA 540
   AACGTGGGGG CGGGTGCCGC TGAATGTAC GACCACGGCA ATAAGATGCT TACGGCCATG 600
15 GCCACGCTCT CCACTCATTT T 621

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(2) INFORMATION FOR SEQ ID NO:219

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20  (i) SEQUENCE CHARACTERISTICS:
      (A) LENGTH: 2853 base pairs
      (B) TYPE: nucleic acid
      (C) STRANDEDNESS: double
      (D) TOPOLOGY: circular
25  (ii) MOLECULE TYPE: DNA (genomic)
      (iii) HYPOTHETICAL: NO
30  (iv) ANTI-SENSE: NO
      (vi) ORIGINAL SOURCE:
      (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
35  (ix) FEATURE:
      (A) NAME/KEY: misc feature
      (B) LOCATION: 1...2853

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:219

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40  ATGAGAGTAT CCGATCTCTG TTCCAGACTT TCATGGTTAT TACCCGTAAT CCTTGTGGGA 60
   TTGCTCTGTG CTACTTTGGT CGCTGCGGAA CGTCCTATGG CCGGAGCAGT CGGATTGCAC 120
   CACCGTCGGC ATGCTGCGCT GTCTGATTCT ACAGCGAAAG ACACGGTGCC TCTCGCAAAA 180
   CCTATTCCTG ACASTGCTTT TCGAGATTCC CTTCCTGCCG ATTCCACCGG ATCGATGCGG 240
   CAAGATAGCG TGTATGACGA TGAATTCGAA TTGGAAGATA TAGTGGAGTA CGAAGCTGCC 300
   GATTCCATCG TTTTGCTCGG ACAGAATCGT GCCTATCTTT TCGGCAAGAG CTATGTGAGC 360
   TATCAAAAGA GTCGCTTGGG GGCAACTTTC ATGTATCTCA ATACCGACAG CAGTACGGTT 420
   TATACTCGCT ATGTCTCTGA TACGGCGGGT TATCGGATGG CCTTCTCTGT TTTCAAGGAT 480
   GGAGAGCAAT CGTTCGAAGC CAAGAACTTT ACCTACAAC TCCGCACGGA GAAGGGGATT 540
50  ATCAGCGGAG TGATCACGCA GCAGGGCGAA GGCTATCTGA CTGCCGTAAG GACCAAGAAG 600
   ATGCCCCACA ATATCATGTT TATGCAAGGA GGGCGTTATA CGACCTGCGA CAATCACGAT 660
   CATCCTCACT TCTATATCAA TCTTTCGAAG GCAAAGGTGC ATCCGGAGAA AGACATCGTC 720
   ACAGGTCCGG TCAATCTGGT TATCGCCGAT ATGCCGCTGC CGATAGGTCT TCCTTTCGGC 780
   TATTTTCCCT TTTCCAACAA ATACTCTTCC GGTATATTGA TGCCACGTA CGGAGAGGAC 840
55  AATCGCTATG GATTTTATTT GAGGAATGGT GGATATTATT TTGCCTTCAG CGACTATATC 900
   GATTTGGCAT TGCGTGGGGA GATCTTTTCC AAAGGGTCAT GGGGCATTTT AGCCCAATCG 960
   AAATATAAGA AGAGGTATAA GTACAACGGC TCGTTCGAAG CCAATTATCT GGTATCGAAG 1020
   TCCGGCGACA AATACGTGCC CGGAGACTAC AGCAAGACCA CAGTCTGAA TATCCGATGG 1080
   ACACACAGTC AGGATCGGAA GGCCAACTCT TTGCAAAACG TGTCCGGCAA TGTCAATTTT 1140
60  GCCACCGGGA GCTATTTCGA GAATTCGCTG AATACCACCT ATGATGTCAA TGCCCGTACT 1200
   GCTACGACAC GAAGTTCGGC CGTGAGCTAT TCGCGCAAGT TTCCGGGTAC TCCTTTTTCG 1260
   ATTACGGGTA GCATGGATAT CAGCCAGAAC ATGCCGATA CGACGGTGAG CTTACCTTG 1320
   CCGAATCTTT CGATTAATAT GTCCACGCGT TATCCTTTCA AGCGGAAGAC CCGTGTAGGA 1380
   CCGSAGCGAT GGTACGAGAA GTTGAGTGTG GGCTATTCGG GTCAGCTTCC CAATAGTATC 1440
65  TTGACAAAG AGAAAGATTT GCTCCAGAGC AATCTCGTGC GCGATTGGAA GAATGGTATG 1500
   CGTCATTCCG TACCGATCAG TTTGACTGTC CCTTTGTTGG ATTATATCAA TCTGACTATG 1560
   GGGGTTAACT ACAATGAGTG GTGGTACACG AAAGGCATAC GGAAGTCGTG GAATGAGGAT 1620
   AAGAAAACAT TCCTGCCTTC GGACACGACC TATAAATTCG GCAGACTGTA CGATTACAGT 1680
   CTGTGCGGCA GCTTATCTAC CACATGTGAC GGTATGTTCA AGCCTTGGAA ACCTTTTTC 1740
70  TTCGGAGGCA ATCTCATTAT GATCGTCTAT CGCTTCACGC CCACTGTCAG TTTCTCCTAT 1800
   ATGCCGGGCT TCACGAAACG CCGATATGGC TTTTGGGAAC TTCTTGAGCA TACGGATCAG 1860
   AACGGCAAGC TGCATACGCT GCTCTACTCT CCTTATTTTC AGCAGATATT CGGTGCTCCC 1920
   TCCATGGGCA ATGCGAGGATC TGTCAATTTT TCTTTTGACA ACAACTTAGA GGCCAGATC 1980
   AAATCCAAAT CGGATTTCGAC AGGATCAGCC AAGATCAGCC TGATAGATCA GTTACATGG 2040
75  TCTACATCCT ATAATATGTT TGCCGATTCC ATCCGATGGA GCAATATCTC GGCTTCGCTG 2100

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5 GCACCTCGCC TCTCCAAGAG CTTTACCTTG CGCTTGTCGG GTCTGTTCTGA TCCCTATTG 2160  
ACGAAGTATT ATGAGGGAGA AGATGGGAAG ATCATTCCCT ATAAGAGCAA CGACCTGCGC 2220  
ATTTTAAACG GCAAGGGATG GGCACGCCCTG ATCAGTACGG TACTTCTTT CAGCTATACG 2280  
CTCAACAAAG AGTCGCTCAG CGGATTGATA GCTCTTTTCA GTGGCAAAA GGAGCGGAGA 2340  
GATGAAAAGA AAAACACAGG GGCTACTCCT CATGAAGGAG ACGATGCTGC CGATATACTT 2400  
GAGGGAGGAA GACCGCAAAA TGAAAGTGGG GGGTCGCTCC TCGAGCGCAA CCGTCAGGGC 2460  
GGAGCAGTGG ATCAGGATGG TTACTIONGCA TATTCGATCC CATGGAGCCT GTCTTCGAC 2520  
TATAGTTGGA ATATTGCTAC CGACTACAAT AGGTACAATG TCAATAAGAT GGAGCACTAC 2580  
TACCGGGTAA CGCAGAATCT GAGCTTTCCG GGCATATCC AGCCTACACC GAACTGGAGC 2640  
10 TTCCGATTCA ATGCGAATA CAATTCGAC TTGAAGAAAA TAACATCGCT TACCTGCAAC 2700  
GTCACGCGG ACATGCACTG CTGGGCTATC TCGGCCAGTT TCATCCCTAT AGGAGCATA 2760  
AAGTCCATA ATTCGTCAT ATCGGTGAAG AGTTCACCT TCGAGGATCT GAAGTATCAG 2820  
CAGAGCAATC GTCCCATCAC GAATACTTGG TAT 2853

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(2) INFORMATION FOR SEQ ID NO:220

- (i) SEQUENCE CHARACTERISTICS:  
20 (A) LENGTH: 3678 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- 30 (vi) ORIGINAL SOURCE:  
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:  
(A) NAME/KEY: misc\_feature  
35 (B) LOCATION: 1...3678
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:220

40 ATGATGAAC GATATACAAT AATCTTGCA GTTTTCTTT TATTCTGCAC GGTATTTACC 60  
TTTCAAATAA AAGCTCGCCC TTATGAAAGA TTTCAGATG TAGAGAAGCC TTGGATTCAG 120  
AAACATTCAA TGGATTCTAA ATTGGTGCCT GCAATAAAGG GTAACCTAAT TCAAGCTGAA 180  
ATTGTATACC AATCTGTTTC TGAACATAGT GACTTAGTTA TTTCACCTGT GAACGAAATA 240  
AGGCTGCAA ATCGTTTCCC TTGCGATAGG AAGTCTTTT TTGAGAAAA TCTACGGGCA 300  
TCTCCCCCG TAGTTCCCGT TGCCGTCGAC AAGTATGCGG TACCGGTTGC CAATCCAATG 360  
45 GATCCTGAAA ATCCCAATGC CTGGGATGTG ACGCTAAAA TCACTACTAA AGCGGTAACA 420  
GTACCTGTGG ATGTGGTGAT GGTATCGAC CAGTCTTCGT CAATGGGAGG GCAAAACATT 480  
GCCAGATTAA AGTCTGCCAT TGCATCGGGA CAGCGTTTTC TGAATAAAT GTTGCCTAAG 540  
GGGACGGCTA CAGAAGGGGT GCGTATCGCT CTGTGAGTT ATGACCATGA GCCTCATCGC 600  
TTATCTGATT TTACCAAAGA CACTGCTTT CTCTGTCAA AAATCCGGG TTTGACTCCT 660  
50 ATTTGGGGAA CACATACCCA GGGGGGCTT AAAATGGCGA GAAACATTAT GGCCACTTCT 720  
ACTGCTGTGG ATAAGCATAT CATATTGATG TCTGACGGGT TAGCGACGGA GCAGTATCCT 780  
GTTAAATAAG TAACACTGC AGACTTCATT GGCAAAAGT GAAATGCGAA TGATCCCAT 840  
GATTTGTTA TACAAGGAGC AATTAATTTC CCTACAAATT ATGTTTCCAA CAATCCATCT 900  
ACACCTCTTA CCCCAAATTA TCCAACATCAT TCTTCTAAG TTGGACGGAG AAATCTGCCG 960  
55 GAATCCAAAT TCGATTATAG TAATCTGAGT GCAAGGATTA CTTTGTATGG TGTGCTGGC 1020  
GCATTGGTCT ATGAACCGAG GTTTCCTCAT CCCTATTATT ATTATTCCC TTGTAACGCT 1080  
GCTATCAATG AGGCTCAGTT TCGCAAAAAC TCTGGTTATA CAATCCATAC TATTGGCTAT 1140  
GACCTGGGAG ATTTTGCCTT GGCCAACAAT TCGTTGAAAC TAACCGCTAC AGACGAGAAT 1200  
CACTTCTTTA CGCGGACACC GGCCAATTTA GCTGCAGCGT TTGATAATAT TGCCCAAACT 1260  
60 ATTAATATAG GTATACAGAG GGGGGAGGTG ACGGACTTTG TAGCTCCTGG TTTCTCGTT 1320  
AAAAATCTGA CGCAATCGGG AGATGTTACT CATTTGCTAA ATGTTTCAA TGGAACGGTG 1380  
CACTATGATG TCTCTACTAA AAAACTGACA TGGACTACTG GTACTATCCT GAGCTCATCA 1440  
GAAGCTACCA TAACCTATCG TATTTATGCC GATTTGGATT ATATACAGAA CAATGATATT 1500  
CCGTAAATA CTACTCTGC TATCGGCCG GATCTTGGTG GATTCGATAC CAATACCGAG 1560  
65 GCAAAATTGA CCTATACCAA TTCCAATTGG GAACCGAATC AGCAGTTAAT TTTCCACGT 1620  
CCGACGGTTA AGTTAGGTTA TGSTGTTATT AAGCGGCACT ATGTATTGGT AAATAAGAC 1680  
GGTCAACCCA TACAGGCAA TGAACAGTT GTCAATTCCC TAAGCAGGC TCATGTTCTA 1740  
CAGTCACAAG ATTTCTTTT GCCCTCAGGT GGAGGTCTATA TTGTTCCCAA ATGGATAAAG 1800  
TTGGACAAA CGACCGAAGC ATTACAGTAC TATTCGTAC CGCCGACTAA CACGGTCATC 1860  
70 ACTACTGCCG ATGGTAAACG TTATCGTTT GTCAAGTCC CAGGCTCCAC GCCGAATCCG 1920  
GGCCAAATCG GTATCAGTTG GAAAAACCG GCAGGAACCG CTTACTTCG TTACAAGCTC 1980  
CTCAATTATT GGATGGGAGG AACACAGAC CAACAGAGTG AATGGGATGT GACGTCCAAT 2040  
TGGACAGGAG CCCAAGTACC GCTCACAGGA GAAGATGTAG AGTTTGCAAC GACAGAAAA 2100  
TTGGGTTCTC CGCGGTAGC CGATTTGAT GTCCCGACAA CCAACCCAA AATTATCGGT 2160  
75 AACCTATTA ATAATTCCGA CAAGGATTA GTTGTACCA CAAGCAGTCA ATTGACGATC 2220

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	AACGGCGTGG	TTGAGGATAA	CAATCCGAAT	GTCGGTACGA	TCGTGCTGAA	GTGCTCGAAA	2280
	GACAACTCCTA	CGGGGACATT	GCTTTTTTGCC	AATCCGGGCT	ATAATCAAAA	TGTAGGGGGG	2340
	ACCGTCGAGT	TTTACAAATCA	GGGATATGAT	TGTGCCGATT	GTGGTATGTA	TCGCAGGAGC	2400
	TGGCAGTATT	TCGGTATCCC	TGTCAATGAA	TCAGGTTTTC	CAATTAATGA	TGTGGGCGGA	2460
5	AACGAGACCG	TCAACCAATG	GGTTGAGCCT	TTCAATGGCG	ATAAGTGGCG	GCCAGCACCT	2520
	TATGCACCTG	ATACAGAGCT	TCAAAAATTC	AAGGGCTACC	AGATCACGAA	TGACGTGCAG	2580
	GCACAGCCTA	CGGGAGTTTA	CAGCTTCAAG	GGTATGATTT	GTGTGTGCGA	TGCCTTCCTG	2640
	AATCTGACAC	GCACGTCCGG	TGTCAACTAC	TCGGGCGCCA	ACTTGATCGG	CAACTCATAC	2700
	ACTGGAGCCA	TCGACATCAA	GCAGGGTATT	GTCTTCCCGC	CGGAAGTCGA	GCAGACGGTG	2760
10	TATCTGTTCA	ACACGGGAAC	ACGCGACCAG	TGGCGTAAGC	TTAATGGAAG	CACGGTTTCA	2820
	GGCTATCGAG	CCGGTCAGTA	CCTCTCTGTA	CCTAAGAATA	CAGCGGGTCA	GGACAATCTT	2880
	CCGGATCGTA	TTCCATCGAT	GCATTCCCTC	TTGGTGAAGA	TGCAGAACGG	AGCGTCTTGT	2940
	ACGTTGCAHA	TCTTGTACGA	TAAGCTGCTC	AAGAACAAGA	CTGTAAACAA	CGGTAATGGT	3000
	ACGCAGATCA	CATGGCGATC	CGGCAACTCC	GGATCGGCGA	ATATGCCGTC	ACTTGTGATG	3060
15	GATGTTCTTG	GTAACGAGTC	GGCCGACCGT	TTGTGSACTC	TTACCGATGG	GGTCTTTCTT	3120
	TTCCGATTCT	ACAACGGCTG	GGATGCTCGC	AAGCTGACTG	AAAAAGGTTT	GTCACAACTT	3180
	TATGCATGT	CTGACATCGG	TAATGATAAA	TTCCAGGTTG	CAGGGGTTCC	GGAGTTGAAT	3240
	AACCTGCTGA	TCGGCTTCGA	TGCGGATAAG	GATGGTCAAT	ACACGTTGGA	GTTTGCTCTT	3300
	TCGGATCATT	TTSCGAAAGG	GGCTGTTTAC	CTGCACGATC	TTCACTCAGG	AGCCAAACAC	3360
20	CGTATTACGA	ATTCTACGTC	GTATTCAATC	GATGCCAAGC	GGGGAGATTG	CGGGGCTCGT	3420
	TTCCGCTTGT	CATATGGATG	TGATGAGAAC	GATAGTGATT	CGCATGTCTG	GAGTACAAAT	3480
	GGCCCGTGAAA	TTATAATTCT	GAATCAAGAT	GCTCTTGACT	GCACTGTAACT	CTTATTGACA	3540
	ATAGAAGGTA	AGCTTCTTCG	CCGCTTGAAA	GTATTAGCTG	GTATAGAGAA	AGTCATGAAA	3600
	GTGCAGACCG	GAGGGGCCCTA	TATTGTGCAT	CTTCAAAATG	CTTTCACATA	TGATGTGCAT	3660
25	AAGGTGCTTG	TTGAGTAT					3678

## (2) INFORMATION FOR SEQ ID NO:221

- 30 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 3675 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular
- 35 (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- 40 (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- 45 (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...3675
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:221

50	ATGAAACGAT	ATACAATAAT	TCTTGCACTT	TTTCTTTTAT	TCTGCACGGT	ATTACCTTT	60
	CAAATAAAAG	CTCGCCCTTA	TGAAAGATT	GCAGATGTAG	AGAAGCCTTG	GATTCAGAAA	120
	CATTCAATGG	ATCTCTAATT	GGTGCTTGCA	AATAAGGGTA	ACTTAATTCA	AGCTGAAATT	180
	GTATACCAAT	CTGTTTCTGA	ACATAGTGAC	TTAGTTATTT	CACCTGTGAA	CGAAATAAGG	240
55	CCTGCAAATC	GTTTCCCTTC	GCATAGGAAG	TCTTTTTTTG	CAGAAAATCT	ACGGGCATCT	300
	CCCCCGTAG	TTCCCGTTGC	CGTCGACAAG	TATGCGGTAC	CGGTTGCCAA	TCCAATGGAT	360
	CCTGAAAATC	CCAATGCCTG	GGATGTGACG	CTAAAAATCA	CTACTAAAGC	GGTAACAGTA	420
	CCTGTGATG	TGGTGTGGT	TATCGACCAG	TCTTCGTCAA	TGGGAGGGCA	AAACATTTGCC	480
	AGATTAAAGT	CTGCCATTGC	ATCGGGACAG	CGTTTTGTGA	AAAAAATGTT	GCCTAAGGGG	540
60	ACGGCTACAG	AAGGGGTGCG	TATCGCTCTT	GTGAGTTATG	ACCATGAGCC	TCATCGCTTA	600
	TCTGATTTTA	CCAAAGACAC	TGCTTTTCTC	TGTCAAAAAA	TCCGGGCTTT	GACTCCTATT	660
	TGGGGAACAC	ATACCCAGGG	GGGGCTTAAA	ATGGCGAGAA	ACATTATGGC	CACCTCTACT	720
	GCTGTGGATA	AGCATATCAT	ATTGATGTCT	GACGGGTTAG	CGACGGAGCA	GTATCCTGTT	780
	AAAAATGTAA	CTACTGCAGA	CTTCATTGGC	AAAACTGGAA	ATGCGAATGA	TCCCATTTGAT	840
65	TTGGTTATAC	AAGGAGCAAT	TAATTTCCCT	ACAAATTATG	TTTCCAACAA	TCCATCTACA	900
	CCTCTTACCC	CAAATTATCC	AATCATTTCT	TCTAAAGTTG	GACGGAGAAA	TCTGCCGGAA	960
	TCCAAATTCG	ATTATAGTAA	TCTGAGTGCA	AGGATTACTT	TTGATGGTGT	TGCTGGCGCA	1020
	TTGGTCTATG	AACCGAGGTT	TCCTCATCCC	TATTATTATT	ATTTCCTCTG	TAACGCTGCT	1080
	ATCAATGAGG	CTCAGTTTGC	GAAAACTCT	GSTTATACAA	TCCATACTAT	TGGCTATGAC	1140
70	CTGGGAGATT	TTGCCTTGGC	CAACAATTCT	TTGAAACTAA	CCGCTACAGA	CGAGAATCAC	1200
	TTCTTTACGG	CGACACCGGC	CAATTTAGCT	GCAAGCTTTG	ATAATATTGC	CCAAACTATT	1260
	AATATAGGTA	TACAGAGGGG	GGAGGTGACG	GACTTTGTAG	CTCCTGGSTT	CATCGTTAAA	1320
	AATCTGACCG	AATCGGGAGA	TGTTACTCAT	TTGCTAAATG	TTTCAAATGG	AACGGTGAC	1380
	TATGATGTCT	CTACTAAAAA	ACTGACATGG	CTACTCTGAG	CTATCTGAG	CTCATCAGAA	1440
75	GCTACCATAA	CTTATCGTAT	TTATGCCGAT	TTGGATTATA	TACAGAACAA	TGATATTCGG	1500

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5	GTAAATACTA	CTTCTGCTAT	CGGCCCGGAT	CTTGGTGGAT	TGATACCAA	TACCGAGGCA	1560
	AAATTGACCT	ATACCAATTC	CAATGGCGAA	CCGAATCAGC	AGTTAATTTT	CCCACGTCGG	1620
	ACGGTTAAGT	TAGGTTATGG	TGTTATTAAG	CGGCACTATG	TATTGGTAAA	TAAAGACGGT	1680
	CAACCCATAC	AGGCAAATGG	AACAGTTGTC	AGTTCCCTAA	GCGAGGCTCA	TGTTCTACAG	1740
	TCACAAGATT	TCTTTTGGCC	CTCAGGTGGA	GGTCATATTG	TTCCCAAATG	GATAAAGTTG	1800
	GACAAAACSA	CCGAAGCATT	ACAGTACTAT	TCCGTACCGC	CGACTAACAC	GGTCATCACT	1860
	ACTGCCGATG	GTAAACGTTA	TCGTTTGTGC	GAAGTCCCAG	GCTCCACGCC	GAATCCGGGC	1920
	CAAAATCGGTA	TCAGTTGGAA	AAAACCGGCA	GGAAACGCTT	ACTTCGCTTA	CAAGCTCCTC	1980
10	AATTATTGSA	TGGGAGGAAC	AACAGACCAA	CAGAGTGAAT	GGGATGTGAC	GTCCAATTGG	2040
	ACAGGAGCCC	AAGTACCGCT	CACAGGAGAA	GATGTAGAGT	TTGCAACGAC	AGAAAATTTT	2100
	GGTTCTCCGG	CGGTAGCCGA	TTTGCATGTC	CCGACAACCA	ACCCCAAAT	TATCGGTAAC	2160
	CTTATCAATA	ATTCCGACAA	GGATTTAGTT	GTTACCACAA	GCAGTCAATT	GACGATCAAC	2220
	GGCGTGGTTG	AGGATAACAA	TCCGAATGTC	GGTACGATCG	TCGTGAAAGT	GTCGAAAGAC	2280
15	AATCCTACGG	GGACATTGCT	TTTTGCCAAT	CCGGGCTATA	ATCAAAATGT	AGGGGGGACC	2340
	GTGAGTTTT	ACAATCAGGG	ATATGATTGT	GCCGATTGTG	GTATGTATCG	CAGGAGCTGG	2400
	CAGTATTTCG	GATATCCCTG	CAATGAATCA	GGTTTCCCAA	TTAATGATGT	GGGCGGAAAC	2460
	GAGACCGTCA	ACCAATGGST	TGAGCCTTTC	AATGGCGATA	AGTGGCGGCC	AGCACCTTAT	2520
	GCACCTGATA	CAGAGCTTCA	AAAATTCAAG	GGCTACCAGA	TCACGAATGA	CGTGCAGGCA	2580
20	GACGCTACGG	GAGTTTACAG	CTTCAAGGGT	ATGATTTGTG	TGTGCGATGC	CTTCCTGAAT	2640
	CTGACACGCA	CGTCCGGTGT	CAACTACTCG	GGCGCCAACT	TGATCGGCAA	CTCATACACT	2700
	GGAGCCATCG	ACATCAAGCA	GGGTATTGTC	TTCCCGCCCG	AAGTCGAGCA	GACGCTGTAT	2760
	CTGTTCACAA	CGGGAACACG	CGACCASTGG	CGTAAGCTTA	ATGGAAGCAC	GGTTTCAGGC	2820
	TATCGAGCCG	GTCAGTACCT	CTCTGTACCT	AAGAATACAG	CGGGTCAGGA	CAATCTTCCG	2880
25	GATCGTATTC	CATCGATGCA	TTCTTCTTGT	GTGAAGATGC	AGAACGGAGC	GTCTTGTACG	2940
	TTGCANATCT	TGTACGATAA	GCTGCTCAAG	AACACGACTG	TAAACAACGG	TAATGGTACG	3000
	CAGATCACAT	GGCGATCCGG	CAACTCCGGA	TCGGCGAATA	TGCCGTCACT	TGTGATGGAT	3060
	GTCTTGTGTA	ACGAGTCGGC	CGACCGTTTG	TGGATCTTTA	CCGATGGGGG	TCTTCTTTTC	3120
	GGATTTCGACA	ACGGCTGGGA	TGGTCGCAAG	CTGACTGAAA	AAGGTTTGTC	ACAACTTTAT	3180
30	GCGATGTCTG	ACATCGGTAA	TGATAAATTC	CAGGTTGCAG	GGGTTCCGGA	GTTGAATAAC	3240
	CTGCTGATCG	GCTTCGATGC	GGATAAGGAT	GGTCAATACA	CGTTGGAGTT	TGCTCTTTTC	3300
	GATCATTTTG	CGAAAGGGGC	TGTTTACCTG	CACGATCTTC	AGTCAGGAGC	CAAACACCGT	3360
	ATTACGAATT	CTACGTCGTA	TTTATTTCGAT	GCCAAGCGGG	GAGATTCCGG	GGCTCGTTTC	3420
	CGCTTGTGAT	ATGGATGTGA	TGAGAACGTA	GATGATTGCG	ATGTCGTGAG	TACAAATGGC	3480
35	CGTGAAATTA	TAATTCGTAA	TCAAGATGCT	CTTGACTGCA	CTGTAACCTT	ATTCACAATA	3540
	GAAGGTAAGC	TTCTTCGCGG	CTTGAAAGTA	TTAGCTGGTC	ATAGAGAAGT	CATGAAAGTG	3600
	CAGACCGGAG	GGGCTATAT	TGTGCATCTT	CAAAATGCTT	TCACTAATGA	TGTGCATAAG	3660
	GTGCTTGTG	AGTAT					3675
40	(2) INFORMATION FOR SEQ ID NO:222						
	(i) SEQUENCE CHARACTERISTICS:						
	(A) LENGTH: 1275 base pairs						
45	(B) TYPE: nucleic acid						
	(C) STRANDEDNESS: double						
	(D) TOPOLOGY: circular						
	(ii) MOLECULE TYPE: DNA (genomic)						
50	(iii) HYPOTHETICAL: NO						
	(iv) ANTI-SENSE: NO						
	(vi) ORIGINAL SOURCE:						
55	(A) ORGANISM: PORYPHYROMONAS GINGIVALIS						
	(ix) FEATURE:						
	(A) NAME/KEY: misc feature						
60	(B) LOCATION 1...1275						
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:222						
	ATGGAAGTGA	AGAAAAACAC	AGTGGTGCTA	CGCCTTCTGA	TTTGGTTCGT	GGCCATTCTT	60
65	CTCTTCCACT	CCTCACGGCT	GTGGGGACAG	GAAGGGGAGG	GGAGTGCCCG	ATACAGATTG	120
	AAAGGATTCT	TGGATACCTA	CCATGCCGTA	CGCAGCTCTT	CTCCTTTTGA	TTTCATGAGC	180
	TCGCGTACGA	GAGTGAGAGG	TGAGCTGGAG	AGGTCGTTCG	GTAATTCGAA	AGTAGCCGTA	240
	TCGGTCAATG	CCACCTACAA	TGCTCTACTG	AAAGACGAGA	CCGGCTTACG	TTTACGTGAA	300
	GCCTTCTTCS	AGCATCAGGA	AGAGCATTGG	GGGTTGCGCC	TCGGACGACA	GATTGTCATT	360
70	TGGGGGGGCTG	CCGACGGTGT	GCGCATCACG	GATCTGATCT	CCCCGATGGA	TATGACCGAG	420
	TTTCTGGCAC	AGGATTACGA	TGATATTGCT	ATGCCGCTCA	ATGCATTGCG	TTTCTCTGTC	480
	TTCAACGAAT	CGATGAAAGT	GGAAGTCGTG	GTAAGTCGCTG	TATTCGAGGG	GTACCGTCTG	540
	CCTGTGGATC	CTCGCAATCC	TTGGAATATC	TTCTCCCTTT	CGCCCATTCG	TCAGGGGATG	600
	AATATCGTCT	GGAAAGAAGA	AGCCGGCAAA	CCGGCCTTCA	AGGTTGCCAA	TATCGAGTAC	660
75	GGTGGCGGAT	GGAGCACTAC	GCTCTCCGGT	ATCGACTTCG	CTTTGGCTGC	ATTGCATACA	720
	TGGAACAAGA	TGCCCGTCAT	CGAAGTACAG	GGCATTGTGC	CGACGGAAAT	CATCGTTAGC	780

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5 CCTCGCTATT ATCGTATGGG ATTTGTCGGC GGGGACCTCT CCGTACCCGT CGGACAGTTT 840  
 GTTTTCAGGG GAGAGGCTGC GTTCAATATC GACAAACACT TCACCTATAA GAGTCATGCC 900  
 GAGCAAGAGG GTTTCCAAAC AATCAATTGG TTGGCCGGAG CCGATTGGTA TGCTCCCGGT 960  
 GAATGGATGA TCTCAGGACA ATTCTCAATG GAAAGCATAT TCAGGTATAG GGATTTTCATC 1020  
 TCCCAAAGAC AACATTCTAC CCTGATTACT CTCAATGTTT CCAAGAAATT CTCCGGCAGT 1080  
 ACACCTCCAAC TTTCGGACTT CACCTACTAC GACCTTACGG GCAAAGGATG GTTCAGTCGC 1140  
 TTTGCAGCTG ACTATGCCTT GAACGATCAG ATACATCTGA TGGCCGGATA TGA CTGCTGGTTC 1200  
 AGTAGTAAGG GCAGCGGTAT ATTGATCGC TACAAAGACA ATTCGGAAT CTGGTTCAA 1260  
 GCCCGCTACA GCTTC 1275

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## (2) INFORMATION FOR SEQ ID NO:223

15 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1212 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular

20 (ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

25 (iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

30 (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...1212

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:223

35 ATGTCCTCCT GTGAGGTGGC TTATTTTTCCTA CTAAAGCCGA TCGATCTGCA GAACATCCGC 60  
 GAACGGAATC ACTCTTCCGA CATCGCGCTT TCCAATTTAT TAGACAATTC GAATCAGCTA 120  
 TTAGCTACTA TTCTGATCGG GAATAATGTG ATTAATGTAG CCATCGTTAT CCTTTCAT 180  
 TATGCCATCG AGCAGACATT CGTTTCTCT TCTCCGATCA TTGGATTCT GATCCAGACG 240  
 ATACTCCTGA CCACTGTTCT TTTGCTGTTC GGAGAGATTC TGCCGAAAGT GTATGCGCGG 300  
 40 AAGAATCCGC TGCAATACTC GCGCTTTTCT GCTGCAGCTA TGTCCGTTAT CTATAAGATA 360  
 TTGTCACCGT TTTCAAAAT GCTGGTCAAA AGTACCGGCA TCGTTACCAG AGGTATCAGC 420  
 AAGAAGAAAT ACGATATGTC CGTGGATGAG CTCTCGAAAG CGGTAGCCCT CACCACTACG 480  
 GAGGGAGAGC CGGAGGAGAA AGAAATGATT AACGAAATCA TCAAAATCTA TAATAAGACA 540  
 GCCTGCGAAA TCATGGTTCC GCGTATCGAT ATTGTGGATG TGGATCTGAG CTGGCCATTT 600  
 45 CGTAAGATGC TTGACTTCGT TGTTCGTCG GGTATTCCA GACTTCCCGT TTCAGAGGGG 660  
 TCAGAAGACA ATATCAAAGG GGTGATTTAC ATCAAAGATC TAATCCCACA CATGGATAAA 720  
 GGCGATGAAT TCGACTGGCA TCCTCTGATT CGTAAAGCAT ATTTTGTCCC CGAAAACAAG 780  
 CGCATAGATG ATTTGCTCGA GSAGTTCAGA GCCAATAAGG TGCATGTCTC CATCGTTGTG 840  
 GATGAGTTCC GTGGCACTTG CCGACTGATC ACAATGGAGG ACATATTGGA AGAGATCGTC 900  
 50 GGCGAGATTA CCGACGAGTA CGATGAGGAA GAACTCCCT TTAAGGTTT GGGGATGGC 960  
 AGTTATCTTT TCGAAGGAAA AACGTCTCTC TCCGATSTTC GACACTATCT TGACCTTCG 1020  
 GAAATGCTT TCGGTGAAT GGGGACGAG GTAGATACGC TAAGTGGGCT CTCTTGGA 1080  
 ATCAAGCAGG AACTCCCCCA TGTGGGCGAT ACAGCASTGT ACGAGCCATT CCGCTTTCAA 1140  
 GTGACCCAAA TGGACAAGCG CCGAATCATC GAAATCAASA TTTCCCTTT CGAGCGCACT 1200  
 55 TGGGAGGTGC AA 1212

## (2) INFORMATION FOR SEQ ID NO:224

60 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 780 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular

65 (ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

70 (iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

75 (ix) FEATURE:

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(A) NAME/KEY: misc feature  
(B) LOCATION 1...780

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:224

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ATGAAACTAT	TACTTTATCT	CCTATTGGTC	TTGTGACTC	TATCCCCGAT	GTATTGCGAA	60
ATGCTCTTCT	CAGAGAATCT	CACAATGAAT	ATAGACAGCA	CCAAAACCAT	ACAAGGAAACG	120
ATATTGCCCG	TACTGGATTT	CAAAACCGAA	AAGGAAAATG	TGTTACACCTT	CAAAAATACT	180
GCCAATCTCA	ATCTGCTGAT	AAAGCACGGT	CAAGTAATCA	ACTTAATTAA	TAAGCTTGAG	240
TTTTCTACCT	ATGGCAATAA	AGTAACCGTA	AGTGGAGGAT	ATGTACACAC	CGAATACCGC	300
TATTTGTTCG	ATCATGTTTT	TGAGSTTTAT	CCTTATGTTCG	AGTCGCAATG	GGCAGAAAGT	360
AGAGGAATGA	AATATAAGGT	TTCTACGGGA	TTACAGTCGC	GTATCGGCT	GGTAAATAGT	420
GATAACTGTC	TCATGTTTGC	AACATTGGGG	GTATTTTTCG	AATTCGAAAA	GTGGGAACAG	480
CCAGCCACTA	GCCTCTTTCG	AGGAACGTAT	GCATACAGCC	GAAGTATCAA	AAGCCACCTG	540
TCTATCASTT	TCAGACATCG	GTTGGGTGAA	CATTGGGAAT	TTACAACCTAC	GGCTATTAC	600
CAGGGAAAGC	CTGACAGTTA	TTTAAAGAA	GCACGTTTTC	GAGGAGCTAT	CGACCTCAAA	660
TACCATATCA	CACCTACGAT	AGGAATACGC	GGGGCCTATC	GGATCATCTA	CGATACTGCC	720
CCTATTGTAC	CTGTGCGGAA	AGATTACAAC	ACCGTTGATG	TTGGTATCGA	TATTTCTGTT	780

(2) INFORMATION FOR SEQ ID NO:225

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2502 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc feature  
(B) LOCATION 1...2502

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:225

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ATGAAACGAA	TCGTTTTATC	ATCTTTCCTG	TTGCTTCTGT	CCATACTTTC	TTTGATGGCA	60
CAGAACAAATA	CCCTCGATGT	ACACATATCC	GGTACGATCA	AGGATGCCTC	CTCCGGCGAA	120
CCAGTGCCCT	ATGCCACTGT	AAGCATCCGG	CTGACAGGAG	CAGATACCAC	ACAGGTGTTT	180
CGACAAGTGA	CTGACGGCAA	CGGCTACTTC	GTCTAGGGCC	TGCCGGCAGC	TCCCTCCTAT	240
CACCTGACAG	CTTCGTTCGT	AGGTATGAAA	ACCCATACCA	TGCAGATTAG	TCGSGGAAAT	300
GGACAGCAGC	ACATCAAATC	CATCGACATT	TCTCTCGAAT	CCGAGGACAA	ACAACCTCTC	360
ACCGTCACCG	TATCGGCAGC	ACGACCACTG	GTGAAGATGG	AGATAGACCG	CCTGTCCTAT	420
AATATGAAAG	ATGACCCCGC	AGCCAAGACG	AACAACCTGC	TCGAAATGCT	GCGCAACGTT	480
CCTTTGGTAA	CGGTGGATGG	TCAGGGCAAT	ATCCAGGTGA	AAGGATCTTC	CAACTTCAAA	540
ATCCACCTCA	ATGGCAGGCC	CTCGACCATG	GTGAGCAGCA	ACCCGAAGGA	GGTCTTTCGC	600
TCCATTCCCTG	CCCATACGAT	CAAACGGGTG	GAGGTCATCA	CCGATCCGGG	TGTAAAGTAC	660
GATGCGGAAG	GCACAAGTGC	CATCCTGGAC	ATCGTCACGG	AAGAAGGTAA	GAAGCTGGAA	720
GGATATTTCAG	GTTCCTATCAC	GGCCAGTGTC	AGCAACAATC	CCACAGCCAA	CGGTAGTATC	780
TTTCTGACGG	CAAGTCCGG	CAAAGTCGGG	CTGACTACCA	ACTATAACTA	CTACGGTGGC	840
AAAAACAAGG	GCTCTCGCTA	CTTTACCGAA	CGTACTACAT	CCATGCTCCA	AACGATAGAA	900
GAAGGCAAGG	GGCAAGAAAC	CTTTGGCGGA	CACTTCGGCA	ATGCCCTCCT	CTCATTCGAG	960
ATAGATTCCG	TCAATCTCTT	TACGGTGGGC	GGCAATGTAC	GCCTTTGGGA	GATGACCACC	1020
GACCGGAACA	GCCTAGAAAA	AAGCTTTGCC	GGCAGCAACC	TCATGTCTTA	CATAGACAGA	1080
AAACTCAAAA	CACAGATGGA	TGCCGGATCA	TACGAGCTCA	ATGCCGACTA	TCAGCACAGC	1140
ACTCGCCTGC	CGGGCGAATT	GCTCACCGTT	TCCTACCGCT	TCACTCACAA	TCCTAATAAT	1200
AGCGAGACCT	TCATTGACCA	ATGGAAGCGC	GATCCGCTCA	ACACAGCTAA	TACGATCCAG	1260
TACGCCGGCC	AGCACTCCAA	ATCCGATGCG	GGCATGAGCG	AACATACGGC	ACAAGTGGAC	1320
TATACACGTC	CCTTAGGACA	AGCACATTCT	TTGGAAGCAG	GGCTGAAGTA	CATCTATCGT	1380
CATGCCACGA	GGGATCCTCT	CTATGAGATA	CGACCATCCG	AAGATGCTCC	GTGGCAGCCC	1440
GGCTCTCTAT	ATGCACAGAA	TCCGTCGAAC	GGAAAGTTCC	GCCACGATCA	ATACATCGGA	1500
GCAGCCTATG	CCGGCTACAA	CTATCGTAAG	GATCAGTATT	CTTTGCAAA	CGGCTCCGA	1560
GTGSAAGGCA	GCAGGCTGAA	AGCACTCTTT	CCCGAAAACG	CAGCAGCAGA	TTTCTCCAC	1620
AACTCGTTTCG	ACTGGGTGCC	ACAGCTCAGC	CTCGGCTATA	CCCCCTCGCC	CATGAAGCAG	1680
CTTAAGCTGG	CCTATAACTT	CCGAATCCAA	CGTCTGCA	TGCGCCAACT	GAATCCCTAC	1740
CGGCTACAGA	CCAACGATTA	TCAAGTACAG	TATGGTAATC	CCGACCTAAA	GTCGGAGAAG	1800
CGTCACCAAG	TCGGTCTCTC	CTATAATCAA	TACGGAGCCA	AGGTCTATGCT	TACAGCATCG	1860
CTCGACTACG	ACTTCTGCAA	CAACGCCATC	CAGAATTACA	CCTTCTCCGA	CCCGGCCAAT	1920

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CCCAATCTGT	TCCACCAGAC	CTATGGCAAT	ATCGGACGAG	AGCATTCCTT	CAGCTTGAAT	1980
ACCTATGCCA	TGTACACGCC	GGCCGTATGG	GTCAGGATTA	TGCTCAACGG	AAATATCGAT	2040
CGCACATTCC	AAAAGAGCGA	AGCACTCGGC	ATTGATGTCA	ATTCATGGTC	CGGCATGGTA	2100
TACTCAGGCC	TGATGTTTAC	CCTGCCGAAG	GATTGGACTG	TGAATCTCTT	CGGAGGTTAT	2160
TATCATGGGG	GAAGAAGCTA	CCAGACGAAG	TATGATGGCA	ATGTATTCAA	CAATATCGGT	2220
ATAGCCAAAC	AGCTTTTTCGA	CAAAAAATTG	AGAGTCTCGC	TGAGCGCAAA	CAACATTCAT	2280
GCGAAGTATT	CGACATGGAA	GAGCCGGACC	ATCGGCAATG	GATTACTAT	TTATTCGGAA	2340
AATGCCGGTA	TACAACGGAG	TGTTTCCCTC	AGCCTCACCT	ACAGCTTCGG	TAAGATGAAT	2400
ACACAAGTGC	GCAAGGTAGA	GCSTACGATC	GTCAACGACG	ACCTCAAGCA	AACCTCATCC	2460
CAAGGACAGC	AGGGTGGCGG	ACAAGGAAAT	CCTACCGGCA	AT		2502

## (2) INFORMATION FOR SEQ ID NO:226

- 15 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1197 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular
- 20 (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- 25 (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- 30 (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...1197
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:226

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ATGAGACTCT	CTGCCATTCT	TATCGCTTTG	ATTGTGATGC	TGCCTGCTGT	GCTTAGCGGG	60
CAGCATTATT	ATTCCATGGC	GGGAGAGCGA	CTGGAGACGG	ACAGCATTTC	TCCGAACGAA	120
CTCTCGGCAT	CGATCCGAAG	TGCGCTTTTC	TTTCGGAACA	ATGAATACAA	TGCACGTTCC	180
GTCAAAGGTT	ATACGTTGCC	GGGTGCACGG	GTTTCCGCTT	TTGCCTCTTA	CTCGCTGCCG	240
GCAGCACATG	GTGTGAAGCT	TTGCTCGGA	GTATCTACCC	TGAACTACTG	GGGGGCAAGT	300
CGCTATCCGG	CCGGTATCGC	TTATTCGGAT	TTACCTTATT	GGACGGACTA	TAACGACTAT	360
GTACGCTTGC	GTATCCTGCC	TTATGTACAG	GCCATGCTGA	AGCCGACGGC	CACGACTGCT	420
CTCATGCTGG	GCAATATAGC	CGGTGGTACG	GCTCACGGAC	TGATCGAACC	GATCTACAAT	480
CCTGAGTTGG	ATTTGACGGC	TGATCCTGAA	GCCGGTGTGC	AATTTCGGGG	TGATTGGACA	540
CGTTTCCGAA	TGGATGTTTG	GSTCAATTGG	ATGAGCATGA	TTTTCAAAAA	TGACAAATCAT	600
CAGGAGTCGT	TTGTCTTTGG	CTTGTCCTACT	ACTTCGAAAT	TGTTATCGGG	TGAAGGCAAA	660
TGGCGACTCG	AACTGCCCTT	GCAGGCTATT	GCCACGCATC	GCGGCGGGGA	ATACAACTGG	720
GCGCAGCAGG	ATACCGTGCA	TACATGGGTC	AATGGAGCTG	TCGGACTTAA	GCTTTCGTAT	780
CGCCCTCGTA	CCGACAAACC	CATGCAGATT	TGGGGATCTG	CTTATGGTGT	GGCAGCCTTG	840
TCAAGCGGAG	GATACTTCCC	TTACGAAAAGA	GGGTGGGGCG	GTTATCTTTC	TCTCGGAATG	900
GACTTGGAGC	ACTTCGCTTT	TCGTACCGAC	TATTGGTACG	GCAGGCATTA	CGTTTCTCCC	960
TTTGCTGCAC	CTTTCGCCAA	TTCCCTGACG	TATGACAAAC	AGCCTCTTAC	GAACGGTTTG	1020
GGCGATTATA	TTCGTCTCTA	TGCCGACTAT	TCGTGGCGSA	TGGCACGAAG	TGTTTCGTTG	1080
GCGGCTGTTG	CTCGGGTATG	GTTCACGCCT	TCGGATCGTT	TTGCGATGAG	CCACGCCTTG	1140
GAACTGACGA	TGCGTATCGA	TCCCAAATTC	CCAATAGCTT	TTCTGAAAGG	CAATCAT	1197

## (2) INFORMATION FOR SEQ ID NO:227

- 60 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1146 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular
- 65 (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- 70 (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- 75 (ix) FEATURE:

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(A) NAME/KEY: misc feature  
(B) LOCATION 1...1146

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:227

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ATGAACAAAT	CGCTATTATC	ATTGGCATGC	CTCATCCTGT	GCGGTATGCC	GGCCATCGCC	60
CAACAGACAG	GACCGGCCGA	ACGCAGCGGC	GAGCCTTCTC	TGGCCGAACG	TGTATTCGGT	120
CTGGAGCAGA	ASCAGAAAAA	GCTGAAGGTG	TACTTAGGCA	TACAGTCGTT	CTACGACCAG	180
CCGCTTGTCG	ATGACGAATC	CCATATCGGA	CACTTCAAGG	TACAGGAGCT	GCGGATGTCT	240
GCTCATGGCG	AACTGAACCG	CCACCTCAGC	TTCGACTGGC	GACAACGTCT	CAACCGTGCC	300
GCCGACGSCA	CTTCGTTTGC	CGACAATCTC	TCCAATGCCA	TCGACATCGC	AGGTGTGGAC	360
TGGCACCCGA	ACGACAAGGT	GTCTTTCTTC	TTCGGACGTC	AGTACGCGCG	TTTCGGAGGG	420
ATAGAATACG	ACATGAACCC	CGTAGAGATC	TACCAGTACA	GCGACCTTGT	GGATTACATG	480
ACCTGCTATA	CTTCGGGCGT	GAACCTTCGA	TGGAACCTCC	ACCCCGAACA	GCAGCTGCAG	540
CTACAGGTAC	TCAATGCTTA	CAACAACCGC	TTCGCCGACC	GCTACCACGT	GACACCCGAT	600
GTCGCTACCG	CCACGAGCTA	CCCGCTCCTC	TACTCGGCAC	AGTGGAACGG	TACCCTCCTC	660
GGAGGAGCAC	TGCATATGCG	TTACGCCGTG	TCGATGGCTC	ATCAGGCCCA	AGAGCGTAAT	720
ATGTGGTACT	TCACTGCGGG	CAACCTGTTT	AATCCGGGCA	AACGGATCAA	CGGATACCTC	780
GACCTCACCT	ACTCGATCGA	GGGATTGGAC	GACAAAGGCA	TTATGACTGC	TCGCTACGGC	840
AAGGGCAAGA	CCCTCACGGA	CGTCAAGTAC	TATGCTCTGG	TATCGAAGTG	GAACCTCCGC	900
ATTTTCGATC	AGGTCAATCT	CTTCTCTCAA	GGCATGTACG	AGAACGGCTA	TGCGCCTGCC	960
CAATACGGCG	AGAGCAGCCA	CACGCGCCAC	TCCTACGGCT	ATATGGGAGG	GGTGGAAATAT	1020
TACCTACGG	AGACCAACTT	CCGTCTGTTC	GTCACTTACA	TAGGACGGCA	TTACCGGTAC	1080
AGTGGGACCG	AGACGGAAAG	CACCAATGCT	CTTCGCGCCG	GTCTGATCTA	TCAGATACCT	1140
TTCTTA						1146

(2) INFORMATION FOR SEQ ID NO:228

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(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 666 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:  
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:  
(A) NAME/KEY: misc feature  
(B) LOCATION 1...666

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:228

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ATGAACATT	TGTTAAGTC	GACATTAGTA	CTTCTTTGTG	CTCTTTCTTT	TTCCGGTACC	60
TATACCTTTG	CACAAGAAAA	TAATACAGAA	AAGTCACGAT	TTGATTTTTC	TGTTAGGCTG	120
GGACAGGGAT	ATATTGCAGG	TTCAACTACC	AACCTGATGT	ATGGGTATAC	ATCTGCTAAC	180
GATAGACTTT	TGCTGGTGC	AATTTATCTG	GGCTTGACAC	CAAGTAAGAA	AGAAAAAGCA	240
ACCGGCGTAG	CATTTGTTTT	CTTATCTCCC	TCTCCGGGTT	ATTATGTCTG	TATATCCGGC	300
AAAGAAAATA	CCTTGAATTA	TGCGTTTTAC	GTTGTCGGAG	CATATAATAG	AATAGCCATT	360
CCTATACGCC	CTATCAAAA	TTTTAATTTC	ATCTTCTCTA	CAGAAAGTCG	AATGGCTTGG	420
ATGAGTCGTC	ATGAGCAAA	TTACAATTCT	ACTTCGCAGA	CTTGGGATAA	GCAGCGCAAG	480
TCGAGGTCGG	GACTGGATTT	TGGTCTCGGG	ATGCATCTGC	AATHCCACAT	TAATAAGACC	540
GTTTACTTTA	TGGCAGGAAC	CGATCTTACG	TCTTGCATGT	TCGGAAAAAG	GATCAATGAC	600
TACCAGCAAA	AGGATCGAAC	CTTCATTGCA	CTTATCGACA	ACAGTATTGG	CATAGGATTA	660
AACCTC						666

(2) INFORMATION FOR SEQ ID NO:229

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(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 1173 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO



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(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:  
5 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:  
(A) NAME/KEY: misc\_feature  
10 (B) LOCATION 1...1173

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:229

ATGATTATCA	AGAAAAATGCT	GAAAAATAAA	TTGGCCCCCT	TGGCCATACT	GTTCCCTTTT	60
GCTCCAAAGG	CTATGAAGGC	TCAGGAGCAA	CTGAATGTGG	TACACACCTC	TGTGCCATCG	120
15 CTGAATATCA	GTCCGGATGC	ACGTGCGGGC	GGTATGGGGG	ATATAGGTGT	GGCAACGACG	180
CCGGATGCST	ATTCACAGTA	TTGGAATCCG	AGTAAATATG	CTTTCATGGA	TACGAAAGCC	240
GGTATTAGCT	TCTCATATAC	ACCCTGGCTG	TCCAAGCTGG	TCAATGATAT	TGCCCTGATG	300
CAGATGACCG	GTTCCTACAA	ATTGGGAACA	GACGAGAATC	AGGCTATTAG	TGCTTCTCTG	360
CGTTATTTC	CATTAGGAAA	GTTGGAGACT	TTCGACGAAT	TGGGCGAATC	CATGGGAGAG	420
20 GCCCATCCCA	ATGAATTTGC	TGTCGATTTG	GGCTATAGCC	GCCAGTTGTC	GGAGAACTTC	480
TCCATGGGCTG	TTGCACTGCG	TTACATCCGC	TCAGACCAAA	GCCTCAGCAA	CACCGGAGAG	540
AATCAGGCCG	GAAATGCCTT	TGCGGCGGAT	ATAGCCGGTT	ATTTGCAGAA	GTATGTGCTA	600
CTGGGTAAATG	CGGAGAGCTT	GTGGTCGTTG	GGTTTCAACG	TAAAGAATAT	CGGAACGAAG	660
ATCTCCTATG	ACGGAGGTGT	CACGAGTTTT	TTTCATCCCTA	CTTCGTTGAA	TCTCGGGACG	720
GGGCTGTTGT	ATCCGATCGA	TGACTATAAC	AGCATCAATT	TCAACCTTGA	ACTTASCAAG	780
25 CTGCTTGTAC	CCACTCCTCC	TATCATGGAT	CAAAACGATC	AGGCCGGGTA	TGAGGCTGCA	840
CTCAAGAAAT	ATCAGGAAAC	TTCTTCGATC	AGCGGTATAT	TCTCTTCTTT	CGGTGATGCG	900
CCGGGAGGAC	TCAAGGAAGA	ATTCCGTGAG	ATTACATGGG	GACTTGGGGC	TGAATATAGC	960
TATGACGATA	AATTTTTTGT	TCGTGCCGGA	TATTCATACC	TGCACCCAC	CAAAGGCAAT	1020
30 TTGCAGTACT	TCACGGCCCG	TGCCGCTTC	AAAATGAACA	TATTCGGTAT	CGATGCTTCC	1080
TACCTGTTGT	CTACGATCCA	GAGTAATCCG	TTGGATCAGA	CTCTGCGGTT	TACGCTTGCT	1140
TTCGATATGG	ATGGATTGCG	CAATTTGTTT	CAC			1173

(2) INFORMATION FOR SEQ ID NO:230

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 1338 base pairs  
40 (B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

45 (iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:  
50 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:  
(A) NAME/KEY: misc\_feature  
55 (B) LOCATION 1...1338

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:230

ATGAAACAA	CAGTTCAACA	AATTATTCTG	TGCCTGGCTT	TAATGATGTC	AGGTGTATTG	60
GGCGGAAACG	CACAGAGCTT	TTGGGAAGAA	ATAGCTCCTC	CTTTTATCAG	TAATGAGCCT	120
60 AACGTCAAGT	ATATAATTCC	CAATATGGGG	ATTGATTCAA	AGGGAACAAT	CTATGTAACC	180
GTGACAAAAA	GGATTTCAGCA	GGGAGCAAAT	TATACTTCTG	AGCAATTGGG	TATGTACTAT	240
CGACCATTAG	GTGATAATGA	ACAGTGGTGG	AAACATGATC	CGTATTTTGA	TGACAAGATA	300
GTTGCGGATA	TTCAGACAGA	TGCATATGGC	AGAGTTTATG	TATGTACGAC	TTCTTCTCGA	360
GATCAAGAGT	ATCAACTTTA	TATAAACGAG	AGAACGAAT	GGAGGTGTAT	ATTCAAAACT	420
65 TCTGTGTCTA	CATATGAGCA	TGGTATGGCT	GTTTTCGCT	CTTCGACAGG	GGTGACTTAT	480
ATAGGTACCA	GGCATCACAT	CTTCGCATCA	GGTGTAAATG	ATTTGAGATT	CAACACTATC	540
TATGAAGACT	CTACACCTAT	GAGCTGTGCG	TTTGCAGAGG	CTACGAATAG	TGGCACCATC	600
TATCTGSCAT	TGATGCATGA	AACCACAATG	TCTACGACTA	TCCTTACTTA	TCAAAACGGT	660
GAGTTCGTCG	ATATCTCGGA	AAGTGAATTG	AGTAACTCGA	TTATTGCATC	CATGTGCTCT	720
70 AATAAAGAA	GTGATATAAT	AGCTCTTGTT	ACTTCATATA	CAGGATTTAT	GAGTGGAAAC	780
CTTGCGATCA	GAAAAGCAGA	TGAAGGCAAA	TGGCAACTTG	TTGGCGGAGA	TATACAGAA	840
GCGATCGTTC	AAAATATATG	CATGATGGAC	GACAACAAGA	TTGCTTGTGA	AGTCTTCGGG	900
ACTCCTAAGC	GAGTAGATGG	TCGGACAAGG	GTTTGTGTTT	CTGACGCATC	TGTCTTTGAT	960
75 TTTGAGTGGT	ATGAAGATGA	AATATACGGA	GGCCTGATAT	TTGACACTTT	CTTCTATAGC	1020
CCTTGGGACA	AACTTCTTTA	TGCGAAATTT	GGTGGGATTA	TGCTCAGGAS	TAAAGAGTCT	1080

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5 TTTATAACCT CTTTCATTTC TCCGACAGTT GTACAAGGAG TGGATGTCTA TACTTTGGCC 1140  
 GGGGAAGATAA GGATCGAAAG TGAAACTCCG GTGTCTGAGG TGTGCTTTT CGACCTGGCT 1200  
 GGCAGGATGG TACTTCGGCA AACCATTGAT AATAAAATCT ATTCGGACAT AGATACTAAC 1260  
 GGAATAAAGC GAAGCGGTAT TTACGTAGTC TCGGTGCGGC TCTCTCCGG ACAGGTATTC 1320  
 AGTCATAAGG TGCAGGTA 1338

## (2) INFORMATION FOR SEQ ID NO:231

- 10 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 924 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular
- 15 (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- 20 (iv) ANTI-SENSE: NO
- (v) ORIGINAL SOURCE:  
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- 25 (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...924
- 30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:231

ATGATAATCC GGTGTCTTAT CCGTCGTCCG AGAACCGTCC TGTTCCGGTT GATATTCGTG 60  
 GTAGGTCTTT TCTCTGCGAT GCGCGAAGAG AAAAAGGATA GTCTCTCTAC GGTTCAGCCA 120  
 GTGCCGAATA GCAGCATGGT GGAGCAGACC CCTCTCTCT CCATTGATCA CCCCCTCCTG 180  
 CCGGCTTCTT TTCAGAATAC CCGTACACTG AAAAGGTTTA GAGACAAACA TCTTTCCGAT 240  
 35 GCTTTGCTCA ATGGATTGAA GCCTCATCGC TCATCTTTGC AATTGAATGA GGAACCAAC 300  
 TTGCGCGCAG AGCGTCGGGA TTTCGTTTCT CCCCTCTTGC AAACTCGCCA CGCTGCCGGT 360  
 GTCCTTTTCAI GSCGACCGAC CGATAGGATG CATTTTTATA CATCGGGCAA TATCGGTCTT 420  
 GGCCATGATT TATTGACCGG TGTGCGCAAG GACTTCGGAT GGAATGCTGG TGCCGACTTC 480  
 40 TTGCTGAGTC AAAATCTTAC GGCACATGTC CAAGGCGGTT GGCAGCAGAA TTTCCGGCTTT 540  
 ATACCTATGA CGGCTGTCAA TGGCCAACATG CGTTGGCAAG CCACCGAGAG ATTGAGTTT 600  
 ACCACCGGTA TCGATTATCG ACAGGTACAG TGGAAATGCTT TCGATAATAG AACGTCTCG 660  
 CTTAAAGGAA GTGCTCGATA CGAAGTGATG GACAATGTCT TTGTCAATGG ATTTGGCAGC 720  
 TATCCTCTCT ACAGCAGTAC GCGCTCAGGA CTCAATATGG CTGTTCCGAT GCATGGATT 780  
 45 GGCCCTCAGT ACGGTGGATC GCTTGAGCTG AAAGTCTCCG AGCGATTCCG CTTTGCCGTC 840  
 GGTATGGAGC GCGAATACAA TATCTGGACT CGTCGGTGGG AAACGCATTA CTTTGCTTAT 900  
 CCTGTATTCT ATGGCGATAA GAAG 924

## (2) INFORMATION FOR SEQ ID NO:232

- 50 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 945 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular
- 55 (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- 60 (iv) ANTI-SENSE: NO
- (v) ORIGINAL SOURCE:  
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- 65 (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...945
- 70 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:232

ATGAAAACGA ATAGACGATA CGCATTGTGT TTGCCGCTTC TGCTACTCAC CGGATTGTTG 60  
 GCATGGGGGC AGGATTCTTC CCACGGTAGC AATACAGCGT TTGCAACTGA TTCTTCGAGT 120  
 75 AGAGASTTGC CCACGGAGCA GTCCGCCTAC CGCATTCATT CTGCCTATAT GGTCCGTGGT 180  
 GGCGBAAGCA TAACGCGCGA CACCTATTTG TCACCCCTTC GTTATGGAGG ATGGACACTG 240

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5 AATTTGTTGG GAGAGAAGAC GTTCCCTCTC AAAGCCTCCG ATTCCCCTTG GATGATCCGT 300  
 ACCGGGCGATG AGCTGGATTT TGCCCTGATG GACAATCCGG CCAATAATGC TCATTTCTAT 360  
 TCCCTGCTGT ATAACGGTTC CGCTGCGGCT CTTTACCGCC TTGGCGCTAA GCATCTGCGA 420  
 GCCGCGTGGG TGGACAATCT GCGCTTGGCA TTGGGCCCCG GCTTGGAAAT CGGGCTTGGG 480  
 GGAATTTATA GTACACGCAA CGGCAATAAT CCTGCGACAT TGAAGCTCTA CACCAATGCC 540  
 ATCGCCCAAG CCTCGATAGG ATACTACGTC CCTCCGAAA CTTTCCCCT GTATTTTCGG 600  
 TTGCTCTCCC AGATCAATCT CTTGGGTATA GCCTATGGAA ATGGTTTTGG TGAGAGCTAT 660  
 TACGAGAATT TTTTGCTCAA TAACGGCATT GCAGGCTCCC TGCATTTTAC TTATCCGGGC 720  
 AAGTTTACTC GGTTACGAC ACTCATAACG GCGGATATTC CCATTCCGAA CTCTGTACG 780  
 10 CTTCGTGTCG GTTATCGCTA TTCCCATTTG GGCTCTTCGC TTAACGCATT GGATACTCGA 840  
 ATCCACAGTC ATACGGCTTT TATCGGTTTC GTCACGGAGT TTTACCGATT CCGTGGGCGC 900  
 AAAGCCATGA ATACGGGTCG GAGAACCAGT CTTTACTATC ATGAT 945

15 (2) INFORMATION FOR SEQ ID NO:233

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 855 base pairs  
 (B) TYPE: nucleic acid  
 20 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular  
  
 (ii) MOLECULE TYPE: DNA (genomic)  
  
 25 (iii) HYPOTHETICAL: NO  
  
 (iv) ANTI-SENSE: NO  
  
 (vi) ORIGINAL SOURCE:  
 30 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS  
  
 (ix) FEATURE:  
 (A) NAME/KEY: misc feature  
 (B) LOCATION 1...855  
 35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:233

ATGGTAGTGA CGCTGCTCGT AATTGTCGGT ATTGTGGTAG TAGTGCGGTA CTCCTTGCGC 60  
 GTCCACGTAC ATAAGACCGG CACTGTTGTA TCGGCGGCCA TATTTGGCTT CATCCTCCTT 120  
 40 GGAAAAGACCG TTCCATGCGA TACCCGTAAC TTCTTTTCCT CCGAAAGTGA TGAACCTGAG 180  
 AGCCGTGTTG CTACCGAAAT AGCCACCTG TCGGAAATAG GATTTTCAGAT CCACGCTTCC 240  
 TCTATCCACG TAGCCGTCGG AACCGATTTT GGACAGGCGG GCATCCACTG CCCAATGGCG 300  
 ACCGATGCGT CCGCTACCGA GTTTGACCGA TCGGCGGAAT GTGCCGAACG AACCTCCGCT 360  
 45 CAAATCGACA CGGCCATAAG GAGCCAGTCC CAAATTATCC GTACGCATAT TGACACTTGC 420  
 CCCAAAGCT CCGGCACCAT TGGTGGAAGT ACCCACACCT CGCTGCACCT GAAGGTCTTC 480  
 GATGGAAGAG GCGAAGTCGG GCATATTCAC CCAAAGACG GACTGAGATT CGGAGTCGTT 540  
 GAGGGGTACT CCATTGGTAG TTATGTTGAT GCGATTGGCA TCGGTGCCAC GCACGCGAAA 600  
 GCCGGAATAT CCGATACCCG TACCGGCATC GCTGGTGGCT ACCACGGAGG GAGTCAGCAT 660  
 50 CAGCAGATAG GGGATGTCAC GACCATAATT GGACTTGGAA AGTTCGGCCT TGCGAACGTT 720  
 GGTGTAAGCG ACAGGGGTTT TCGCCGTGGC GCGAGTAGCT ACGACCTGTA CCGTCTGGAG 780  
 CTGCACATTG CTAAGACTAT CTATCTCGCT GTTGAGAGCG GGTGCTTGTG CCGTCAGGCA 840  
 GAAAGGCAGG ACGGC 855

55 (2) INFORMATION FOR SEQ ID NO:234

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1797 base pairs  
 (B) TYPE: nucleic acid  
 60 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular  
  
 (ii) MOLECULE TYPE: DNA (genomic)  
  
 65 (iii) HYPOTHETICAL: NO  
  
 (iv) ANTI-SENSE: NO  
  
 (vi) ORIGINAL SOURCE:  
 70 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS  
  
 (ix) FEATURE:  
 (A) NAME/KEY: misc feature  
 75 (B) LOCATION 1...1797

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## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:234

5 ATGGAAACT TAAAGAACAT TCAGCCAGAG GAGGATTTCA ACTGGGAAGA GTTTGAGGCC 60  
GGTGGCGTCC ATGCTGCGGT GAGTCGTCAG GAGCAGGAAG CTGCTTATGA CAAAACGCTC 120  
AATACCATCA AGGAAAAGGA AGTGGTAATG GGTAGGGTAA CTGCTATCAA CAAGCGTGAA 180  
GTGGTTATCA ATGTAGGGTA CAAATCGGAA GGTGTGGTAC CTGCAACAGA ATTCGCTAC 240  
AATCCCGAAC TCAAAGTGGG AGACGAAGTG GAAGTTATA TCGAGAATCA GGAAGATAAG 300  
AAGGGCCAGC TCGTCTTGTC TCACCGCAAG GGTCTGTCCG CTCGCTCTTG GGAGCGCGTG 360  
AACGAGGCTC TCGAAAAAGA CGAAATCGTA AAGGGCTATG TGAAGTGTG TACCAAGGGT 420  
10 GGTATGATCG TCGATGTATT CGGTATCGAG GCTTTCTCC CGGGATCACA GATCGACGTG 480  
CGCCCCATTC GCGACTACGA TGCATTGCTT GAGAAGACGA TGGAGTTCAA GATTGTGAAA 540  
ATCAATCAAG AATATAAGAA TGTAGTTGTT TCCCAACAAG TGCTCATCGA AGCAGAGCTC 600  
GAACAACASA AGAAAGAAAT CATCGCAAG CTCGAAAAAG GGCAGGTAAT CGAAGGTATC 660  
GTCAAGAATA TTAATTCTTA CGGAGTATTT ATCGACCTCG GTGGAGTGGG TGGTCTTATC 720  
15 CATATCACTG ACCTTTTCATG GGGTCGTGTG GCTCATCCGG AAGAAATCGT ACAGCTGGAT 780  
CAGAAGATCA ATGTCTGTAT CCTCGACTTT GATGAAGATC GCAAGCGTAT CGCTCTCGGA 840  
CTCAACAGC TGATGCCTCA TCCTTGGGAT GCTCTCGACA GCGAGCTTAA GGTAGGCGAT 900  
AAGGTGAAGS GTAAAGTTGT GGTGATGGCA GATTACGCTG CTTTCGTTGA GATTGCACAG 960  
GGCGTTGAGG GTCTTATCCA CGTAAGCGAA ATGTCATGGA CACAGCACTT GCGTCTGCT 1020  
20 CAGGACTTCC TGCATGTAGG CGACGAAGTG GAAGCCGTGA TCCTGACGCT CGACCGCGAA 1080  
GAACGCCAAA TGTCGCTCGG TCTGAAGCAA CTCAGCCCGG ATCCTTGGGC TGATATCGAA 1140  
ACTCGTTTCC CTGTAGGCTC TCGTCACCAT GCTCGTGTTC GCAACTTCAC CAATTTCTGG 1200  
GTATTCGTTG AGATCGAAGA GGGCGTAGAT GGCCTTATCC ATATTTCCGA CCTTCTTGG 1260  
ACGAAGAAGA TCAACACCCC CAGCGAGTTT ACGGAAGTAG GTGCTGATAT CGAAGTTTCA 1320  
25 GTAATCGAGA TCGACAAGGA AAACCGTCGT CTCAGCTTGG GTCACAAACA GTTGAAGAG 1380  
AATCCTTGGG ATGTATTCTGA GACGGTATTC ACTGTAGGAT CTATCCACGA AGGAACGGTA 1440  
ATCGAAGTGA TGGACAAGGG TGCTGTCTGT TCTCTGCTT ACGGTGTGGA AGGTTTTCGC 1500  
ACTCCGAAGC ACATGGTGA GGAAGATGGC TCACAGGCTG TACTCGAAGA GAAGTTACCT 1560  
TTCAAGGTGA TTGAGTTCAA TAAGGATGCC AAGCGAATCA TTGTATCTCA TAGCCGTGTA 1620  
30 TTCGAAGATG AGCAGAAAAT GGCTCAGCGT GAAGCCAATG CAGAGCGTAA GGCTGAAGCC 1680  
AAAGCGGCTC AGAAAGAAAC TGCTGCCGAA GCTGCCAATC CTGCACAGGC TGTAGAGAAA 1740  
GCCACTCTCG GAGACCTCGG CGAGCTGGCC GCTTTGAAAG AAAAGCTTTC AGAAAAAC 1797

## 35 (2) INFORMATION FOR SEQ ID NO:235

## (i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 1650 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: circular

## (ii) MOLECULE TYPE: DNA (genomic)

## 45 (iii) HYPOTHETICAL: NO

## (iv) ANTI-SENSE: NO

## (vi) ORIGINAL SOURCE:

- 50 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

## (ix) FEATURE:

- 55 (A) NAME/KEY: misc feature  
(B) LOCATION 1...1650

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:235

60 ATGGGTAGGG TAACTGCTAT CAACAAGCGT GAAGTGGTTA TCAATGTAGG GTACAAATCG 60  
GAAGGTGTGG TACCTGCAAC AGAATTCCGC TACAATCCCG AACTCAAAGT GGGAGACGAA 120  
GTGGAAGTTT ATATCGAGAA TCAGGAAGAT AAGAAGGGCC AGCTCGTCTT GTCTCACC GC 180  
AAGGGTCGTS CCGCTCGCTC TTGGGAGCGC GTGAACGAGG CTCTCGAAAA AGACGAAATC 240  
GTAAAGGGCT ATGTGAAGTG TCGTACCAAG GGTGGTATGA TCGTGGATGT ATTCGTTATC 300  
GAGGCTTTCC TCCCGGGATC ACAGATCGAC GTGCGCCCCA TTCGCGACTA CGATGCATTC 360  
GTTGAGAAGA CGATGGAGTT CAAGATTGTG AAAATCAATC AAGAATATAA GAATGTAGTT 420  
65 GTTTCCACAC AGGTGCTCAT CGAAGCAGAG CTCGAAACAC AGAAGAAAGA AATCATCGGC 480  
AAGCTCGAAA AAGGGCAGGT ACTCGAAGGT ATCGTCAAGA ATATTACTTC TTACGGAGTA 540  
TTTATCGACC TCGGTGGAGT GGATGGTCTT ATCCATATCA CTGACCTTTC ATGGGGTCTG 600  
GTGGCTCATC CGGAAGAAAT CGTACAGCTG GATCAGAAGA TCAATGTCTG TATCCTCGAC 660  
TTTGATGAAG ATCGCAAGCG TATCGCTCTC GGAATCAAAC AGCTGATGCC TCATCCTTGG 720  
70 GATGCTCTCG ACAGCGAGCT TAAGGTAGGC GATAAGGTGA AGGGTAAAGT TGTGGTGATG 780  
GCAGATTACG GTGCTTTCGT TGAGATTGCA CAGGGCGTTG ASGGTCTTAT CCACGTAAGC 840  
GAAATGTCTT GGACACAGCA CTTGCGTTCT GCTCAGGACT TCCTGCATGT AGGCGACGAA 900  
GTGGAAGCCG TGATCTTGAC GCTCGACCGC GAAAGACGCA AAATGTCGCT CGGTCTGAAG 960  
CAACTCAAGC CGGATCCTTG GGCTGATATG GAAACTCGTT TCCTGTAGG CTCTCGTCA 1020  
75 CATGCTCGTG TTCGCAACTT CACCAATTTT GGTGTATTCT TTGAGATCGA AGAGGGCGTA 1080

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5 GATGGCCTTA TCCATATTTC CGACCTTTCT TGGACGAAGA AGATCAAACA CCCAGCGAG 1140  
 TTTACGGAAG TAGGTGCTGA TATCGAAGTT CAGGTAATCG AGATCGACAA GGAAAACCGT 1200  
 CGTCTCAGCT TGGGTCACAA ACAGTTGGAA GAGAATCCTT GGGATGTATT CGAGACGGTA 1260  
 TTCACTGTAG GATCTATCCA CGAAGGAACG GTAATCGAAG TGATGGACAA GGGTGCTGTC 1320  
 10 GTTTCCTCTGC CTTACGGTGT GGAAGGTTT GCCACTCCGA AGCACATGGT GAAGGAAGAT 1380  
 GGCTCACAGG CTGTACTCGA AGAGAAGTTA CCTTTCAGG TTATTGAGTT CAATAAGGAT 1440  
 GCCAAGCGAA TCATTGTATC TCATAGCCGT GTATTCGAAG ATGAGCAGAA AATGGCTCAG 1500  
 CGTGAAGCCA ATGCAGAGCG TAAGGCTGAA GCCAAAGCGG CTCAGAAAGA AGCTGCTGCC 1560  
 GAAGCTGCCA ATCCTGCACA GGCTGTAGAG AAAGCCACTC TCGGAGACCT CGGCGAGCTG 1620  
 15 GCCGCTTTGA AAGAAAAGCT TTCAGAAAAC 1650

## (2) INFORMATION FOR SEQ ID NO:236

- 15 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1374 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular  
 20 (ii) MOLECULE TYPE: DNA (genomic)  
 (iii) HYPOTHETICAL: NO  
 25 (iv) ANTI-SENSE: NO  
 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS  
 30 (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...1374  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:236

35 ATGATCGTCG ATGTATTGGG TATCGAGGCT TTCCTCCCGG GATCACAGAT CGACGTGCGC 60  
 CCCATTCCGG ACTACGATGC ATTCGTTGAG AAGACGATGG AGTTCAAGAT TGTGAAAATC 120  
 AATCAAGAAT ATAAGAATGT AGTTGTTTCC CACAAGGTGC TCATCGAAGC AGAGCTCGAA 180  
 CAACAGAAGA AAGAAATCAT CGGCAAGCTC GAAAAGGGGC AGGTACTCGA AGGTATCGTC 240  
 40 AAGAATATTA CTTCCTACGG AGTATTTATC GACCTCGGTG GAGTGGATGG TCTTATCCAT 300  
 ATCACTGACC TTTCATGGGG TCGTGTGGCT CATCCGGAAG AAATCGTACA GCTGGATCAG 360  
 AAGATCAATG TCGTTATCCT CGACTTTGAT GAAGATCGCA AGCGTATCGC TCTCGGACTC 420  
 AAACAGCTGA TGCTCATCC TTGGGATGCT CTCGACAGCG AGCTTAAGGT AGGCAGATAAG 480  
 GTGAAGGGTA AAGTTGTGGT GATGGCAGAT TACGGTGCTT TCGTTGAGAT TGCACAGGGC 540  
 45 GTTGAGGGTC TTATCCACGT AAGCGAAATG TCATGGACAC AGCACTTGCG TTCTGCTCAG 600  
 GACTTCCTGC ATGTAGGCGA CGAAGTGGAA GCCGTGATCC TGACGCTCGA CCGCGAAGAA 660  
 CGCAAAATGT CGCTCGGTCT GAAGCAACTC AAGCCGGATC CTTGGGCTGA TATCGAAACT 720  
 CGTTTCCCTG TAGGCTCTCG TCACCATGCT CGTGTTCGCA ACTTCACCAA TTTGCTGTGA 780  
 TTGCTTGAGA TCGAAGAGGG CGTAGATGGC CTTATCCATA TTTCCGACCT TTCTTGGACG 840  
 50 AAGAAGATCA AACACCCAG CGAGTTTACG GAAGTAGGTG CTGATATCGA AGTTCAGGTA 900  
 ATCGAGATCG ACAAGGAAAA CCGTCGTCTC AGCTTGGGTC ACAACAGTT GGAAGAGAAT 960  
 CCTTGGGATG TATTCGAGAC GGTATTTACT GTAGGATCTA TCCACGAAGG AACGGTAATC 1020  
 GAAGTGATGG ACAAGGGTGC TGTGTTTCT CTGCCTTACG GTGTGGAAGG TTTTGCCACT 1080  
 CCGAAGCACA TGGTGAAGGA AGATGGCTCA CAGGCTGTAC TCGAAGAGAA GTTACCTTTC 1140  
 55 AAGGTTATTG AGTTCAATAA GGATGCCAAG CGAATCATTG TATCTCATAG CCGTGTATTC 1200  
 GAAGATGAGC AGAAAATGGC TCAGCGTGAA GCCAATGCAG AGCGTAAGGC TGAAGCCAAA 1260  
 GCGGCTCAGA AAGAAGCTGC TGCCGAAGCT GCCAATCCTG CACAGGCTGT AGAGAAAGCC 1320  
 ACTCTCGGAG ACCTCGGCGA GCTGGCCGCT TTGAAAGAAA AGCTTTCAGA AAAC 1374

60

## (2) INFORMATION FOR SEQ ID NO:237

- 65 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1278 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular  
 (ii) MOLECULE TYPE: DNA (genomic)  
 70 (iii) HYPOTHETICAL: NO  
 (iv) ANTI-SENSE: NO  
 75 (vi) ORIGINAL SOURCE:

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(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc\_feature

(B) LOCATION: 1...1278

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:237

10 ATGGAGTTCA AGATTGTGAA AATCAATCAA GAATATAAGA ATGTAGTTGT TTCCACAAG 60  
GTGCTCATCG AAGCAGAGCT CGAACAACAG AAGAAAGAAA TCATCGGCAA GCTCGAAAAA 120  
GGGCAGGTAC TCGAAGGTAT CSTCAAGAAT ATTACTTCTT ACGGAGTATT TATCGACCTC 180  
GGTGGAGTGG ATGGTCTTAT CCATATCACT GACCTTTCAT GGGGTCGTGT GGCTCATCCG 240  
GAAGAAATCG TACAGCTGGA TCAGAAGATC AATGTGTTA TCCTCGACTT TGATGAAGAT 300  
CGCAAGCGTA TCGTCTCTCG ACTCAAACAG CTGATGCCTC ATCCTTGGGA TGCTCTCGAC 360  
15 AGCGAGCTTA AGGTAGGCGA TAAGGTGAAG GGTAAAGTTG TGGTGATGGC AGATTACGGT 420  
GCTTTCGTTG AGATTGCACA GGGCGTTGAG GGTCTTATCC ACGTAAGCGA AATGTCTATG 480  
ACACAGCACT TGGCTTCTGC TCAGGACTTC CTGCATGTAG GCGACGAAGT GGAAGCCGTG 540  
ATCCTGACGC TCGACCGCGA AGAAGCGCAA ATGTCGCTCG GTCTGAAGCA ACTCAAGCCG 600  
GATCCTTGGG CTGATATCGA AACTCGTTTC CCTGTAGGCT CTCGTACCA TGCTCGTGT 660  
20 CGCAACTTCA CCAATTTCTG TGTATTCGTT GAGATCGAAG AGGGCGTAGA TGGCCTTATC 720  
CATATTTCTG ACCTTCTCTG GACGAAGAAG ATCAAACACC CCAGCGAGTT TACGGAAGTA 780  
GGTGTGATA TCGAAGTTCA GGTAAATCGAG ATCGACAAGG AAAACCGTCG TCTCAGCTTG 840  
GGTCACAAAC AGTTGGAAGA GAATCCTTGG GATGTATTTC AGACGGTATT CACTGTAGGA 900  
TCTATCCACG AAGGAACGGT AATCGAAGTG ATGACAAAGG GTGCTGTCTG TTCTCTGCCT 960  
25 TACGCTGTGG AAGGTTTTGC CACTCCGAAG CATATGGTGA AGGAAGATGG CTCACAGGCT 1020  
GTACTCGAAG AGAAGTTACC TTTCAAGGTT ATTGAGTTCA ATAAGGATGC CAAGCGAATC 1080  
ATTGTATCTC ATAGCCGTGT ATTCAAGAT GAGCAGAAAA TGGCTCAGCG TGAAGCCAA 1140  
GCAGAGCGTA AGGTGAAGC CAAAGCGGCT CAGAAAGAAG CTGCTGCCGA AGCTGCCAA 1200  
CCTGCACAGG CTGTAGAGAA AGCCACTCTC GGAGACCTCG GCGAGCTGGC CGCTTTGAAA 1260  
30 GAAAAGCTTT CAGAAAAC 1278

(2) INFORMATION FOR SEQ ID NO:238

35 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 720 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: circular  
40 (ii) MOLECULE TYPE: DNA (genomic)  
(iii) HYPOTHETICAL: NO  
45 (iv) ANTI-SENSE: NO  
(v) ORIGINAL SOURCE:  
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS  
50 (ix) FEATURE:  
(A) NAME/KEY: misc\_feature  
(B) LOCATION: 1...720

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:238

55 ATGAAAAAAG CTATTCTTTC CGGAGCGGCC TTGCTCCTCG GCCTATGTGC CAACGCACAA 60  
AACGTGCACT TGCACTACGA TTTGCGTCAT TCCATCTACG ACGAACTAGA TGGACGTCCC 120  
AAACTGACTA CCACAGTGGA AACTTTCACA CCGACAAAT GGGGAAGCAC CTTCTTCTTC 180  
ATCGACATGG ATTACACGGG CAAGGGTATC CAGTCGGCCT ATTGGGAGAT TTCGCGCGAA 240  
60 CTGAAGTTTT GGCAGCTCC CGTTTCCATT CATTTGGAGT ACAACGGAGG CCTCTCCACA 300  
AGCTTTACTT TCGACACGA TGCTCTAATC GGTGCCACCT ACACCTACAA CAACCCCTCC 360  
TTTACACGTG GATTACGAT CAGCCCCATG TACAAGCATC TGGGTGCGCA CGACTTCCAC 420  
ACCTATCAGA TCACCGGCAC TTGGTACATG CACTTTCCTG ACGGTCTGCT TACCTTCAAC 480  
GGCTTCTCTG ATCTTTGGGG TTTCCCCCAA GAGAACCCTA TCGGGGGCCC TGTGCTCAAA 540  
65 GAAGGGGATA AGTTCTGATT CCTGTCCGAA CCGCAGTTCT GGATCAACCT CAATCGCATC 600  
AAAGGCATCG ACAAGGATTT CAATCTCAGC ATAGGGACAG AGATGGAAAT CAGCAGGAAC 660  
TTCGCTCGCA TGGACAAATT CTCTGCATC CTAATCTTTC CGGTCAAATG GACTTTCAAC 720

(2) INFORMATION FOR SEQ ID NO:239

70 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 1302 base pairs  
(B) TYPE: nucleic acid  
75 (C) STRANDEDNESS: double

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(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

5 (iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

10 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc\_feature

15 (B) LOCATION 1...1302

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:239

ATGTATAAAG	ACTATAAGGG	TTTGTATGCG	TGGCTTCGGT	GGTATGCCCT	GATCATTGGG	60
TTGCTATTTG	CAGCAGACGG	TATACAGGCT	CAGAACAACA	ACTTTACCGA	GTCGCTTAC	120
20 ACTCGCTTCG	GCCTTGGCCG	TCTCGGAGAA	CGSACGACTA	TTAGTGGGCA	TTCCATGSGA	180
GGACTCGGCG	TGGTCTGCG	TCAGGGCACA	TACGTCAATG	CCGTCAATCC	TGCTTCATAC	240
TCGGCTGTGG	ATTGATGAC	GTTTATCTTC	GATTTCGGTG	CATCTACCGG	AATTACGTGG	300
TATGCCGAGA	ACGGGAAAAA	GGACAATAGG	AAAATGGGAA	ACATTGAGTA	TTTCGCCATG	360
CTTTTTCCTA	TTTCCAAATC	CATTGCTATG	AGTGCGGGAG	TGCTTCCTTA	CTCCGCATCC	420
25 GGGTACCAGT	TGGGATCCGT	TGATCAAGTG	GAAGGAGGCA	GCGTCCAGTA	CACCCGTAAA	480
TACTTGGGGA	CAGGCAATCT	GAACGATCTC	TATGTCGGTA	TAGGTGCAAC	CCCGTTCAAA	540
AACTTCTCAA	TAGGAGCCAA	TGCTTCATCC	CTTTTGGGGC	GATTACACAC	CAGCAGGCAG	600
GTAATCTTCT	CCACGGAGGC	TCCTTACAAT	CCCGTACATC	TCTCGACGCT	GTAATTGAAG	660
30 GCTGCCAAGT	TGGACTTCGG	TATGCAGTAT	CACCTTCTTC	TCAAATCAGA	TCGTTGCTTC	720
GTTATCGGTG	CCGTCTATTC	TCCGCGGGTG	AAGATGCATA	GCGAGCTGAC	TCAGATAAAG	780
AATCAGGTTT	AGAACGGTGT	AGTAGTGGAG	AGCGAAACCC	AAGAATATAT	CAAGGGAATG	840
GACTATTATA	CCCTGCCTCA	TACATTGGGG	ATAGGTTTTT	CTTATGAAAA	GAAAGATAAA	900
CTTCTCTTAG	GAGCAGACGT	CCAATATAGT	AAATGGAAAG	GCGAGAAATT	TTATAAATCC	960
35 GATTGCAAAAT	TCCAGGACAG	AATACGGGTA	TCTCTCGGCG	GAGAGATCAT	ACCGGATATA	1020
AATGCCGTTG	GGATGTGGCC	TAAAGTTCGC	TATCGCTTCG	GTTTACATGG	TGAAAATTCT	1080
TACCTGAAAG	TGCCGACTAA	AGGCGGTGTA	TATCAAGGAT	ACCATATCGT	AGGTGCTGTA	1140
TTGCTATAG	GAATCCGCT	CAATGACAGA	CGTTCGTTCG	TAAATGTCTC	TCTTGAATAT	1200
GACCGATTGA	TCCCGAAGGA	GGGTATGATC	AAAGAAAATG	CTCTGAAATT	GACCTTCGGC	1260
40 CTCACGTTCA	ACGAGTCATG	GTTTAAAAAG	CTGAAACTGA	AC		1302

(2) INFORMATION FOR SEQ ID NO:240

(i) SEQUENCE CHARACTERISTICS:

45 (A) LENGTH: 2778 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

50 (iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

55 (vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

60 (A) NAME/KEY: misc\_feature

(B) LOCATION 1...2778

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:240

65 ATGCGATCGA	TTTATCAATT	ACTGTGTGCA	ATACTCCTTG	CTTCTCTTGG	TTTCGTGGGG	60
CTGGAAGCCC	AACAAGCCGG	AGTAGCAGGT	AGAGTATTGG	ACGAAGAAGG	CAACCCCATG	120
ATTCAAGCCA	ACGTACAGCT	TGTACAGAGT	ACCGGCCAAG	TAGCCGTTCG	CGCAGGTGCC	180
ACTAATGAAA	AAGGGTTGTT	CAGCCTGAAA	ACGTACAGG	AGGGTGACTA	CATTCTGCGC	240
70 GTTTCATATG	TAGGTTACAC	TACCCACGAC	GAAAAAATAT	CTCTTAGAAA	CGGGCAAACC	300
ATTACGCTCA	AAGATATATC	CATGAACGAA	GATGCCCGTC	TTCTACAGAG	TGTGACGGTG	360
CAGGCTAAAG	CGGCAGAGGT	CGTGGTACGC	AACGATACGC	TGGAATTCAA	TGCCGGATCC	420
TATACCGTAG	CACAGGGAGC	TTCTATCGAG	GAAGTATCA	AGAAGCTACC	CGGAGCAGAG	480
ATCGGATCCG	ATGGGAAGAT	CACCATCAAC	GGCAAGGACA	TTAGCAAGAT	CCTTGTCGAT	540
75 GGCAAGAGAT	TTTTCTCCAA	AGATCCACAG	GTGGCAATAA	AGAATCTTCC	GGCCGATATG	600
GTCAATAAAG	TACAGGTACT	GAACAAACTG	AGCGAGCTGT	CGCGGATGAG	CGGTTTCGAT	660

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	GATGGAGAAG	AGGAGACCGT	AATCAACCTG	ACGGTGAAGC	CGGAAAAAAA	GAAAGGCCTC	720
	TTCGGAAACG	TTCAGGCGCG	CTACGGTACC	GACCAACGCT	ATATGGCCGG	AGGGAACGTC	780
	AATCGGTTTC	ATGGAAATTA	GCAATGGACA	TTGATCGGTA	GTGCGAACAA	TACGAACAAT	840
	ATGGGCTTTA	GCGAGATGGA	CAGCGAGATG	GGATCCATGA	CCTTCTTCTC	TCCCAAGGC	900
5	GGTGTCTGAC	GCGGCTTCGG	CAATAGTGA	GGTGTACGT	CTTCGTCGAT	GCTGGGCGGC	960
	AACCTTCAGT	TCAATTTCTC	CTCTGCCCTT	AATACAGGAG	GCGATGCACG	CTACGGATAC	1020
	AACGACAAGG	CCATAGAGAC	GACCAAAACG	GTGGAATA	TCCTCGCCGA	AGGGAATACT	1080
	TATATGGACG	AAAATATATT	GGAACGCTCT	TTCTCTCACA	ATGGTCAGGC	GCGATTTAGG	1140
	ATGCAATGGA	AACCGTCCGA	ACGTACCGAA	GTGTATTTCG	AGCCGGATCT	TTGATATACC	1200
10	AAGATCGATG	GGTCTTTTAA	CGACACATAC	GAGACGAAAG	ATGCCACCGG	AATCTCTATC	1260
	AACAAAGGTT	CTATCCACCA	AATACACAA	GGAAACAAC	TCAGACTGAA	CGGAGAATTG	1320
	GATATCAGTC	ACAAGCTCAA	CGACGAAGGC	CGTACGATCA	GTGCCTCCGT	CAGTGGCGST	1380
	CTGACCGAGG	AAGACGGAGA	TGGCATATAT	CAGGCTGTGC	TCCAAAGCGT	GGAGACGAAT	1440
	CAAAAGCAAT	TCAACGACAA	CTCCAACCTG	CAATATCGGC	TTGCGCTCTC	GTATGTGGAA	1500
15	CCGTGGGGTA	AAAATACTTT	CGCACAAAGG	ATTCTGAACA	GACGTTTCTC	CCGTGCAAT	1560
	TCGGATCGTG	AGGTGTACCG	ACTGGGCGAT	GACGGGCAAT	ACTCCATATT	AGACAGTCAG	1620
	TACGGACTCT	CCTACAGTAA	CGAGTTTACC	CAGTATCGCA	TCGGACTCAA	CCTCAAGAG	1680
	ATTGCCAAAA	CGTGGGACTA	CACCGTAGGA	TTCAATGTGG	ATCCCAACAG	AATGTGACG	1740
	TATCGGAGCG	TAGCCGGAGT	AGAGCAGGAC	AACTGGGCTT	TCAATCGTGT	CAATCTCTCC	1800
20	CCGATGCTCC	GAATCAACTA	CAAACCGAGC	AGGACTACCA	ACCTCCGAGT	GGACTACCGA	1860
	GGACGCACGA	CACAACCATC	CATCAATCAG	ATCGCTCCCG	TTGAGGACAT	CACGAATCCG	1920
	CTATTCGTGA	CGGAAGGCAA	TCCCGGTCTG	AAGCCGAGCT	ATTCCAACAA	TGTGATGGCC	1980
	ATGTTCTCGG	ACTTCGATGC	CAAAAGTCAG	CGAGCTTTCA	ACATTGTTTT	CTTCGSCAAC	2040
	TATACATTCC	ACGACATCGT	CCCCAATACG	CAGTACGATC	CGTCTACAGG	GATCCGTACC	2100
25	ACTCGTTACG	AAAACGCCCTC	CGGTACGTGG	CAAGCGAATC	TTGATGGGAC	ACTATCGCTT	2160
	CCACTCAAGA	ACAGGGGCTT	TTCTTTTCTG	TCAACAGGTT	GGCCGAAGGA	GGCCGAAGGA	2220
	CAAAGCTTCA	TCAATGAGCA	TAAGAACAAA	GCTCTCTCTT	TCCGAACGAG	GGACCGCTTG	2280
	ACGCTGACCT	ATCGCAACAA	TTGGATCGAT	ACGAGTATCG	GTGGCAATAT	CGGATTCTAT	2340
	ATGGCGAATA	ATAGCTGAG	CGGACAGAAA	GATTCTCGCA	CATACGATTT	TGGCGGCAAT	2400
30	TATCAAGTTG	CCCTAACGCT	TCCCTATGGA	TTCCGTATCG	ACAGCGATGT	TGAATACAAT	2460
	ACGAACTCCG	GTTACAGCGG	AGGATTCAGT	CTGGACGAAT	GGCTTTGGAA	TGCTTCGCTT	2520
	TCATACAGCT	TCTCCGTGA	CAAGGCCGGT	ACACTGCGTG	TCAATGGCTA	TGACATCCTC	2580
	GGTCAGCGGT	CAAGTATCAG	CCGTTCTGCT	TCGGCCATCA	ATATAGAAGA	GAGCATGTCC	2640
	AATACGATCG	GACGCTACGT	GATGGTGGAC	TTTATCTACC	GATTCAACGC	CTTCAGTGGT	2700
35	GGTGGATCTC	CGAGCGATCA	TACGCGTGGC	AATATGAATC	GTCCGGGCCC	ACCTTTCGGC	2760
	GSTGGCAGAC	GACCGTCC					2778

## (2) INFORMATION FOR SEQ ID NO:241

- 40 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1200 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular
- 45 (ii) MOLECULE TYPE: DNA (genomic)
- 50 (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- 55 (ix) FEATURE:  
 (A) NAME/KEY: misc feature  
 (B) LOCATION 1...1200
- 60 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:241

	ATGTTATGA	AGCTGATTAA	AAGAAATTG	CTCCTGCTTG	GAGCGGTACT	GCTGATTACG	60
	CTTCTGCGT	ACTCGCAGAA	TGATGACATC	TTGGAAGATG	ACATCTATAC	ATCGCGAAAA	120
	GAAATACGTA	AACAAAACCA	AGTTAAAGAC	TGGCAAAACC	AAGAGGACGG	ATACGGCGAC	180
65	GATACGGAAT	ATACAGTGGC	TTCCGATCGG	GACATTGACG	CCTACAATCG	TAGAGATGGC	240
	CAGTCTACG	ATGGGAAAAA	GTGTGCCAAA	GACAAGAAAA	GAGACTCCAC	TCGTTCTTCT	300
	GTTCGCGGTC	GCTATAGTCG	CCGCTTGGCT	CGATTCTATA	AGCCGAATAC	GATCGTCATT	360
	TCAGTGCCG	ACAATGTATA	TGTAACATGAT	GATGGTGAAT	ATTTCTGCTA	TGGAGACGAA	420
70	TACTATGATG	ACGCGTCGTC	TGTAACATT	TACATCAACA	GTCTTTGGTG	CGATCCGTTT	480
	CCTTATACGT	CATGGTATCC	ATCTTTCTCC	GGCTGGTACA	ACTATACGTG	GAATATCCAA	540
	TGGTTCTACT	ACGGTAGCCA	TATCGGATGG	GGCGGTTATT	ACCCCGGATA	TAATTGGTAT	600
	TGGAGCTACT	ACTATGATCC	TTTCTACAAT	CCCTATGGAA	TCGGTATGGG	TTGGGGATAT	660
	CCTTATGGCT	GGGGCAGCTA	TTACGGTTGG	GGTGGCTATC	CGGGAGTGAT	ACATCACTAC	720
	CACCACTACT	CCAGAAGAC	CTATTTCCAAT	GGTCAGCATT	CGGAGCTTA	CTATTCTTAT	780
75	GGCCGACCGA	ATCGTATCAA	AGGTGGAACG	TCCGGTGCCA	AACTTGGGAC	AGGACGCTAC	840



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5 GATAGAATTC AAAATTTCGTC TTCGCAAAAA AATAAGTTTC GATTGCAGTC GAACAAACCC 900  
 AATAATAATC TGCAAAATGT CAAGTCGGGA CGTACCGGCC GAGCCAATAG AGACCGAAAT 960  
 ATAGAAACGG TAACTCCAAA CAACGGGCAA AAGCAGAATC GTCCCGTATT CCAGCAGAAT 1020  
 CAGTCCGGCA ATGACCGACC GACCGGACGG AATATCCGCA GCGAGAGACA GGGGGAAAT 1080  
 AACGATAGGA CATTTCGAC TCCTTCTCGT AGCAATAGTA ACGGTGGCTT CTCCACGCCT 1140  
 TCTCGCTCTT CTTCGGCTC TATGAGCGGA GGTGSCGGAC GTAGTGCCG GGGACGCAAT 1200

## (2) INFORMATION FOR SEQ ID NO:242

10

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1194 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular

15

(ii) MOLECULE TYPE: DNA (genomic)

20

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

25

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PORPHYROMONAS GINGIVALIS

(ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION: 1...1194

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:242

ATGAAGCTGA TTAAGAAG TTTGCTCTG CTTGGAGCGG TACTGCTGAT TACGCTTCCT 60  
 GCGTACTCGC AGAATGATGA CATCTTCGAA GATGACATCT ATACATCGCG AAAAGAAATA 120  
 CGTAACAACA ACCAAGTTAA AGACTGGCAA AACCAAGAGG ACGGATACGG CGACGATACG 180  
 35 GAATATACAG TGGCTTCCGA TCGGSACATT GACGCTACA ATCGTAGAGA TGGCCAGTCC 240  
 TACGATGGGA AAAAGTTGTC CAAAGACAAG AAAAGAGACT CCCTCGTTC TTCTGTTCCC 300  
 GGTCTGCTATA GTCGCGCTT GGCTCGATT TATAAGCCGA ATACGATCGT CATTCAGGT 360  
 GCCGACAATG TATATGTAAC TGATGATGGT GAGTATTTTCG TCTATGGAGA CGAATACTAT 420  
 GATGACGGGT CGTCTGTAAA CATTTACATC AACAGTCCCTT GGTGCGATCC GTTCCCTTAT 480  
 40 ACGTCATGGT ATCCATCTTT CTCCGGCTGG TACAACATA CSTGGAATA TCCATGGTTC 540  
 TACTACGGTA GCCATATCGG ATGGGGCGGT TATTACCCCG GATATAATTG GTATTGGAGC 600  
 TACTACTATG ATCCTTTCTA CAATCCCTAT GGAATCGGTA TGGGTTGGGG ATATCCTTAT 660  
 GGCTGGGGCA GCTATTACGG TTGGGGTGGC TATCCGGGAG TGATACATCA CTACCACCAC 720  
 TACCCCAAGA AGACCTATT CAATGGTCAG CATTCGGGAG CTTACTATTC TTATGGCCGA 780  
 45 CCGAATCGTA TCAAAGGTGG AACGTCCGGT GCCAAACTTG GGACAGGACG CTACGATAGA 840  
 ATTCAAATTT CGTCTTCGCA AAAAAATAAG TTCCGATTGC AGTCGAACAA ACCCAATAAT 900  
 AATCTGCAAA ATGTCAAGTC GGGACGTACC GGCCGAGCCA ATAGAGACCG AAATATAGAA 960  
 ACGGTAACTC CAAACAACGG GCAAAAGCAG AATCGTCCCG TATCCAGCA GAATCAGTCC 1020  
 GGCAATGACC GACCGACCGG ACGGAATATC CGCAGCGAGA SACAGGGGGA AAATAACGAT 1080  
 50 AGGACATTTT CGATCCTTC TCGTAGCAAT AGTAACGGTG GCTTCTCCAC GCCTTCTCGC 1140  
 TCTTCTTCCG GCTCTATGAG CGGAGGTGGC GGACGTAGTG GCCGGGGACG CAAT 1194

55

## (2) INFORMATION FOR SEQ ID NO:243

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1743 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular

60

(ii) MOLECULE TYPE: DNA (genomic)

65

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

70

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PORPHYROMONAS GINGIVALIS

(ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION: 1...1743

75

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:243

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5 ATGATCCGCA AGTTGATCTT ACTGCTTGCT CTGATGCCGG TAGCCTCTGT GGCTTTTGCG 60  
GTACCAAGCG ACAGCACGGA ATCGAAAGAC AATCGTATCC TTACAAGCAT GCAATCCTCC 120  
TCTTTGAATA GGGATGATGC TCCGGATAAA TGGCAACCTA TGCATGCCAA TTTCAGTATT 180  
CAGAGCGATA TGCTGCTTTC TACTGCCCAA AAGTCCAAGA ACACCTGGTT CGGCAACTCC 240  
TATATCATGG GTATAATCAA GAACAATTAT CTGGAGTTTG GTGCCCGTTT CGAGGATCTC 300  
TATAAGCCCC TGCCCGGACA TGAACCCGAG ATGGGGCGTG GCGTTCCTCA CATGTATGTG 360  
AAGGGAAGCT ATCATTGGGC GGAGCTGACT ATGGGAGACT TCTACGATCA GTTCGGTAGC 420  
GGTATGGTAT TCCGCACCTA TGAAGAGCGC AACCTCGGTA TAGACAACGC GGTTCGCGGC 480  
10 GGACGTATAG TACTCACTCC TTITGATGGA GTGCGTGTCA AGGGTATTGC AGGACAGCAG 540  
CGTAACCTACT TCGACCGCAC GGGCAAGGTA TTCAATTCGG GCCGAGGCTA CCTACTGGGT 600  
TCTGATCTGG AGCTGAATGT AGAGCGTTGG AGCAGTGCCA TGGCGGACAA TGAATATCAT 660  
TTGGCTATCG GGGGATCGTT CGTTTCCAAA CACGAAGCAG ACGAAGATAT ATTTGTGGGT 720  
GTAGGCGAAG ATCGCAAGCG ACTCAACCTG CCGCTCAATG TCCCGATTAT GGGCCTGCCG 780  
15 ACCAACTTTC AAAAAGGAGG TCTCGCCCTC TACGCAGAGT ATGGATACAA ATACAACGAT 840  
CCCTCGGCAG ACAATGACTA TATCTACCAC GACGGACAGG CTGCACTCCT CTCTGCCTCA 900  
TACTCCAAAA AAGGGATGAG TATCCTGTTG CAGGCCAAAC GTTGTGAGAA CTTTGCTTTC 960  
CGCAGCAAGC GAAGTGCCCA GCTCACACCG CTTATGATCA ACTATATGCC GGCTTTTACC 1020  
20 CAAGCTCACA CTTATACGCT GCGGCCATC TACCCCTATG CTACTCAGCC TCAGGGAGAA 1080  
TGGGCTTTCC AAGGTGAAC GCGTTACAAC TTTGCTCGCC GGCAGCTCT CGGTGGACGC 1140  
TACGGTACCG GCTTGCGTAT CAACGTTTCG CATGTGCGTG GTCTGGACAA AAAGATGCTC 1200  
AAAGAGAATC CCGACGAAT GATCGGAACG GATGGCTACA CCGTTTCTTT CTTCGGCATG 1260  
GGCGACCTCT ATTATTGCGA TATAGATGTG GAGATTACTA AAAAGGTAAG CCCAGGATTC 1320  
AACTTTACGC TCACCTACTT GAATCAGATC TACAATAACA AGGTACTGCA CGGTGCAGCC 1380  
25 GGAGAGAAGC CTGAGAAGAT CTATGCCAAT ATCTTCGTCT ATGATGGTAA GTATAAGCTG 1440  
AGTAATAAGG TAGCCCTCCG TACCGAAGTG CAATATTTGC ACACGAAGCA GGATCAGGCT 1500  
GACTGGATCT ACGGCATGGC CGAGCTCTCT ATCCTGCCTT CTCTGATGCT TTCCCTCTCG 1560  
GAGCAGTATA ATATCGGAGA GACCAAGAAA CATTATGTCA TGGGGTCTGT CACCTATACT 1620  
CACGGAGCAC ATCGAGTAGC TTTCTCTGCA GGCAAAACCC GTGCAGGGAT GAACTGCTCG 1680  
30 GGAGGTGTAT GTCGTGTGGT CCTGAGACT CAGGGATTCT ACCTTTCTTA TAGCACC AAT 1740  
CTG 1743

## (2) INFORMATION FOR SEQ ID NO:244

- 35 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 717 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
40 (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- 45 (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:  
50 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:  
(A) NAME/KEY: misc\_feature  
(B) LOCATION 1...717

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:244

55 ATGCGTTCTT TATTTTGTAG CGCGTTGCGC AGCTCCTCTC TCCATGGTTC AGAGCGACGC 60  
AGTCGGATAA GTTCTTCTGT AGTCATGTCA ATAAGGCAGA AAATAAGGTT ATTCCATCTC 120  
TCGGTATGCG CCCAAACGCA TGATCATCTC ATCGAAATCC ACTTGGTGTG CATCGAATTC 180  
60 GGGGCCATCG ACACAGACGA ATTTCTGTCTG TCCTCCACCG CTTATACGAC AAGCCCCACA 240  
CATACCGGTG CCATCCACCA TAATTGTATT GAGAGAAGCT ATGGTCGGTA TCTCGTAAAC 300  
TTTGGTTCAGG AGAGAAACGA ACTTCATCAT CACAGCCGCG CCGATCGTAA CGCAGAGGTC 360  
TACCGTTTCC CGTTTGATAA CGCTTTCCAC TCCATCCGTT ACGAGGCCTT TCGTCCCAT 420  
AGACCCATCG TCTGTCTATG TGATCACTTC ATCGCTATTG GCTCGCATTT GTTCTTCAAG 480  
65 GATAACCCAG TCTTTAGTTC TGGCAGCCAA TACGACAATT ACACGGTTGC CTGCTTTGTG 540  
GAAAGCCTCC ACGATCGGGA GCAAAGGAGC CACACCCACA CCGCTCCGG CACAAACCAC 600  
TGTGCCGACC TTTTCGATAT GCGTACTCTG TCCAGCGGGA CCTACCACAT CCGTGATATA 660  
70 GTCGCCGACT TCGAGTTCCG CCAATTTCTT GGAAGATTG CCCACGGCCT GAACCAC 717

## (2) INFORMATION FOR SEQ ID NO:245

- 75 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 633 base pairs  
(B) TYPE: nucleic acid

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(C) STRANDEDNESS: double  
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:  
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:  
(A) NAME/KEY: misc\_feature  
(B) LOCATION 1...633

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:245

20	ATGTCAATAA GGCAGAAAAT AAGGTTATTC CATCTCTCGG TATGCGCCCA AACGCATGAT	60
	CATCTCATCG AAATCCACTT GGTGTGCATC GAATTCGGGG CCATCGACAC AGACGAATTT	120
	CGTCTGTCTT CCCACGCTTA TACGACAAGC CCCACACATA CCGGTGCCAT CCACCATAAT	180
	TGTATTGAGA GAAGCTATGG TCGGTATCTC GTAACGTTTG GTCAGGAGAG AAACGAACCT	240
	CATCATCACA GCGGGCCCGA TCGTAACGCA GAGGTCTACC GTTTCCTGTT TGATAACGCT	300
	TTCCACTCCA TCCGTTACGA GGCCTTTCGT CCCATAAGAC CCATCGTCTG TCATGATGAT	360
25	CACTTCATCG CTATTGGCTC GCATTGTGTT TCAAGGATA ACCAGATCTT TAGTCTGGC	420
	AGCCAATACG ACAATACAC GGTTCCTGCT TTTGTGGAAA GCCTCCACGA TCGGGAGCAA	480
	AGGAGCCACA CCCACACCGC CTCGGGCACA AACCCTGTG CCGACCTTTT CGATATGCGT	540
	ACTCTGTCCC AGCGGACCTA CCACATCGT GATATAGTCG CCGACTTCGA GTTCGGCCAA	600
30	TTTCTTGGA GATTTGCCCA CGGCCTGAAC CAC	633

(2) INFORMATION FOR SEQ ID NO:246

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 2343 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:  
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:  
(A) NAME/KEY: misc\_feature  
(B) LOCATION 1...2343

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:246

55	ATGGATCGTC CTAAGCCTTC ATATATTGTT CGAATAGCAG CCATTCTCTG CTTGTTTGTC	60
	GGCAGGCCCTT TGTTTGCGCA GAGCTATGTG GACTACGTCG ATCCGCTGAT CCGGACGCTA	120
	AGTTCCTTTTG AGCTGAGTGC GGGCAATACC TATCCGCTGA TCGGTTTACC GTGGGGAATG	180
	AATAGCTGGA CACCGATGAC CCGGTGTACCC GGTGACGGCT GGCAATATAC CTACTCGGCA	240
	CACAAGATTG GCGGATTCAA ACAGACCCAC CAACCCAGTC CTTGGATCAA CGACTACGGC	300
60	CAATTCTCCC TTCTTCCCTT TACGGCACCG CAGAAGCCAT CATCGAACGA CTCCATAGCT	360
	CTGACTAAAT GGTGCAAGCA ACTCTTTTCG GACGAACAGA CCTCGTGGTT CTCGCACAAA	420
	GCGGAGACGG CGACGCCATA CTATTATAGT GTCTATTGG CCGATTACGA CACACGCTG	480
	GAGATGGCTC CGACCGAGCG TGCAGCTATC TTTCGCATAC GTTATTCCGG CAATACCGAA	540
	AGTGGCTCCG GTCGATGGCT TCGTCTTGAT GCCTTTACCG GTGGTTCGGA GATTAGCATC	600
65	GTGGATCCTC ACACCGTAGT GGGCATATCT CGCAAGAATA GCGGAGGTGT GCCGGCTAAC	660
	TTCCGCTGTT ATTTTCATCTT GCACTCCGAT ACTCCTATGG CCGATGTCCT GCTTGAGACA	720
	GATACCGGCA AGTCAGACGA AGGCACAAGG GCATGGGCAG CCTGTCGCTT CGATTGCGAA	780
	GAAGTTACCG TCCGGGTGGC ATCTTCTTTT ATCAGTGTG AGCAGGCCGA AAGAAATCTT	840
	GCGGAAGTCA AAGGGCAGAG TTTCGACCGG ATCAGACTTG CCGGTCGCGA AGCTTGAAT	900
70	AAGGTGCTCG GACGCATACA TGTGGAAGGA GGAACGAAGG ATGAGCGCAC TACATTCTAT	960
	TCCGCACTCT ATCGCTGTCT GCTTTTTCCT CGTCGCTTCT ATGAGGAGGA TGCTTCCGGC	1020
	AATTTTGTGC ATTACAGCCC CTACAATGGA GAGGTACTTC CCGGTTATCT CTATACCGAT	1080
	ACCGGATTTT GGGACACTTT TCGAGCCCTT TTCCCTCTGC TCAATCTGCT GTATCCCGAT	1140
	GAAAACATTA AAATTCAGGA AGGTCTGCTG AATGTATATC GCGAGAGTGG CTTTTTCCCT	1200
75	GAATGGGCCA GTCCGGGCCA TCGGGATTGT ATGATAGGCA ACAACTCTGC TTCTGTTCTG	1260

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5 GCGGATGCCT ACCTCAAGGG TGTTCGGGTA GAAGATACCC GTACACTGAT GAACGGACTC 1320  
TTGCATGCTA CGAAGCCGCT CCATCCGAAA ATCTCCTCCA CGGGTCGCAA AGGTTGGGAG 1380  
TGGTACAACCT CCTTAGGTTA TGTTCGGGCT GATGCAGGCA TCGACGAAAG TGCTGCCCGT 1440  
ACGCTCGAAT ATGCTTATAA CGATTGGTGC ATCCTCCGAC TGGGGCGCAC ATTGGGTTGG 1500  
GATAGAGCTG CATTGGACAC GTTGGCTCAT CGTTCGATGA ACTATCGTCA TCTGTTCGAT 1560  
CCGGAACCA AACTCATGCG CGGTAGAAAT CAGGATGGTA GTTTCGGAC ACCTTTTCC 1620  
CCTTTCAAAT GGGGAGATGT ATTACGGAG GGCATGCCT GGCACACAC TTGGTCGGTC 1680  
TTTCATGATG TGCAGGGGCT TATCGACCTG ATGGGAGGAG ATCGCCCGTT CGTGTCTATG 1740  
CTCGATTCCG TATTCAATAC TCCTCCTATG TTCGATGAGA GCTATTACGG ATTTGTCATC 1800  
10 CACGAAATCA GAGAGATGCA AATAGCGGAT ATGGGCAATT ATGCTCATGG CAATCAACCC 1860  
ATACAGCATA TGATATATCT GTATAATCAT GCCGGTCATC CATGGAAAGC TCAGGAGAGA 1920  
CTACGCGAAG TGATGGGGCG GCTCTATCGT CCTACTCCGG ATGGGTATTG CGGCGATGAA 1980  
GACAACGGAC AGACTTCGGC TTGGTACGTT TTCTCTGCTT TAGGCTTCTA TCCTGTTACA 2040  
CCCGCTACGG ATCAGTATGT GCTCGGTTCC CCGATTTTTT CCAAGGTAAT ACTCTCTTTT 2100  
15 CCGGACGGAC ACAAAACGGT GTTGCATGCT CCGGCCAACA GTGCCGATAC GCCTTACATC 2160  
CGCTCGATCA CGGTAGAAGG AAAAGAATGG AGCTGCAATT ACCTGACTCA CGAACAGCTT 2220  
CGCTCTTCTG CATCCATTCA ATGGATGATG GACACGAAAC CCAATTATAA TCGTGGTATG 2280  
AAGGAAAGTG ACAGACCTTA TTCTTCTCC ACGGAGCAAC AGCGTCGCGC TAATCACAGT 2340  
20 AAT 2343

## (2) INFORMATION FOR SEQ ID NO:247

- 25 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 813 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: circular
- 30 (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- 35 (iv) ANTI-SENSE: NO
- (v) ORIGINAL SOURCE:  
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- 40 (ix) FEATURE:  
(A) NAME/KEY: misc\_feature  
(B) LOCATION 1...813
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:247

45 ATGATGAAAT CCATGCGCAG CGTGTGTTG CTACTCTTTC CATTGTCTTT GATCACTGCT 60  
TTGGGCTGTA GCAATAACAA AGCTGCCGAA TCGAAGTCTG TCTCTTTCGA TTCGGCCTAT 120  
CTCGAAGCGT ACATCCCTCT GCGGGCAGAC ATAGATACGC CATCGCTGCA TGTGATGATC 180  
AGCTACGTCT ATCCTTCGGG AGATGATATG CTCACAGAGA TTTTCAACGG TTTGCTCTTC 240  
GGCGACAGCC TGATGGATTG CTCTTCGCGG GAGAATGCCA TGGGAGGCTA TGCACAGATG 300  
50 CTGGGAGAAG ACTATCGCTC TAACAATGCC GAAGCCAATC TGCAAGGGCT TCCTTCTGAC 360  
CTTTTGGACT ATATCTACAA GCAGGAAAAT ACCATCGCTT ATTGCGATAC GGGATTGATC 420  
TCCACGCGCA TCAATACATA TACTTACGAA GGCGGTGCAC ATACGGAGAA TACAGTCCGG 480  
TTTGCCCAAC TCCTTCGCAC CACCGGCAAG GTGCTCGAAG AGCGAGATAT ATTCAAGATC 540  
GACTATGCGG AAAGGCTGTC CGCACTCATC ATAGGACAAT TGGTGCACGA TTTGCGCAAG 600  
55 ACCACACCTG CCGAATTGGA TGCAATAGGT TTCTTCAACG CAGAAGAAAT ACAGCCCAAT 660  
GGCAATTTA TGATCGATGA CAAAGGTCTC ACATACTGTT TCAATGAGTA TCAGATAGCT 720  
GCTTATGCCA GAGGTGCTGT CTATGTCCGT CTCGGATATG ACGTATTGGC TCCTTTGCTA 780  
AGGGATGATT CCCCATAAA GCGTTACTTG CCG 813

60

## (2) INFORMATION FOR SEQ ID NO:248

- 65 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 810 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: circular
- 70 (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- 75 (vi) ORIGINAL SOURCE:

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(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc\_feature

(B) LOCATION 1...810

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:248

10 ATGAAATCCA TGCGCAGCGT GCTGTGCTA CTCTTTCCAT TGTCTTTGAT CACTGCTTTG 60  
GGCTGTAGCA ATAACAAAGC TGCCGAATCG AAGTCTGTCT CTTTCGATTC GGCCTATCTC 120  
GAACGCTACA TCCCTCTGCG GGCAGACATA GATACGCCAT CGCTGCATGT GATGATCAGC 180  
TACGCTATC CTTTCGGGAGA TGATATGCTC ACAGAGATT TCAACGGTTT GCTCTTCGGC 240  
GACAGCCTGA TGGATTCTCT TTCGCCGGAG AATGCCATGG AAGGCTATGC ACAGATGCTG 300  
GGAGAAGACT ATCGCTCTAA CAATGCCGAA GCCAATCTGC AAGGGCTTCC TTCTGACCTT 360  
15 TTGGACTATA TCTACAAGCA GGAATAATACC ATCGCTTATT GCGATACGGG ATTGATCTCC 420  
ACGCGCATCA ATACATATAC TTACGAAGGC GGTGCACATA CGGAGAATAC AGTCCGGTTT 480  
GCCAACATCC TTGCGACCAC CGGCAAGGTG CTCGAAGAGC GAGATATATT CAAGATCGAC 540  
TATGCCGAAA GGCTGTCCGC ACTCATCATA GGACAATTGG TGCACGATT CGGCAAGACC 600  
ACACCTGCCG AATTGGATGC AATAGGTTTC TTCAACGCAG AAGAAATACA GCCCAATGGC 660  
20 AATTTTATGA TCGATGACAA AGGTCTCACA TACTGTTTCA ATGAGTATCA GATAGCTGCT 720  
TATGCCAGAG GTGCTGTCTA TGTCCGTCTC GGATATGACG TATTGGCTCC TTGCTAAGG 780  
GATGATTCCC CACTAAAGCG TTAATTGCCG 810

25 (2) INFORMATION FOR SEQ ID NO:249

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 801 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

35 (iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc\_feature

(B) LOCATION 1...801

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:249

ATGCGCAGCG TGCTGTTGCT ACTCTTTCCA TTGCTTTTGA TCACTGCTTT GGGCTGTAGC 60  
AATAACAAAG CTGCCGAATC GAAGTCTGTC TCTTTGATT CGGCCTATCT CGAACGCTAC 120  
10 ATCCCTCTGC GGGCAGACAT AGATACGCCA TCGCTGCATG TGATGATCAG CTACGTCTAT 180  
CCTTCGGGAG ATGATATGCT CACAGAGATT TTCAACGGTT TGCTCTCGG CGACAGCCTG 240  
ATGGATTCTT CTTCGCCGGA GAATGCCATG GAAGGCTATG CACAGATGCT GGGAGAAGAC 300  
TATCGCTCTA ACAATGCCGA AGCCAATCTG CAAGGGCTTC CTTCTGACCT TTGGACTAT 360  
ATCTACAAGC AGGAAAATAC CATCGCTTAT TGCGATACGG GATTGATCTC CACGCGCATC 420  
55 AATACATATA CTTACGAAGG CGGTGCACAT ACGGAGAATA CAGTCCGGTT TGCCAACATC 480  
CTTCGCACCA CCGGCAAGGT GCTCGAAGAG CGAGATATAT TCAAGATCGA CTATGCGGAA 540  
AGGCTGTCCG CACTCATCAT AGGACAATTG GTGCACGATT TCGGCAAGAC CACACCTGCC 600  
GAATTGGATG CAATAGGTTT CTCAACGCA GAAGAAATAC AGCCCAATGG CAATTTTATG 660  
60 ATCGATGACA AAGGTCTCAC ATACTGTTTC AATGAGTATC AGATAGCTGC TTATGCCAGA 720  
GGTGTCTCT ATGTCCGTCT CGGATATGAC GTATTGCTC CTTTGGCTAAG GGATGATTCC 780  
CCACTAAAGC GTTACTTGCC G 801

65 (2) INFORMATION FOR SEQ ID NO:250

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 777 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

75 (iii) HYPOTHETICAL: NO

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(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:  
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

5 (ix) FEATURE:  
(A) NAME/KEY: misc feature  
(B) LOCATION 1...777

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:250

ATGAAAAAAA	CTACTTTGAC	AGGATCGATA	TGTGCTTTAC	TCCTGTTTTT	GGGTCTCTCG	60
GCCAAATGCC	AATCGAAGTT	AAAGATCAAG	AGCATTGAGG	CAGCTACCAC	TTTCAGTTCCG	120
GCCACGGCCG	GAAATGGTTT	TGGTGGCAAT	ATCTTCGGCA	TGGACATGAG	CATACGGATG	180
AGGGTACACC	ACAGCATTTCT	GCCCCAAGGG	TTGGATTTTT	CGGTAGGAAT	ACATGAAAGA	240
AGAGCACACT	GGGAAGAGGC	CGGAAGTCCG	AAGCTCATGT	ATACGAATGT	CCCAAGTATC	300
ATTGGTATTG	TTGAAAAGGT	AATAGTCTTC	GAAGACGCAG	AAGACTTTTT	TGACAAAAAA	360
GCTCTCGGCC	GCTTCCTCAT	CAGTTTGGGG	ATATCCTATA	CCAAGCATCT	GGGAGCGTAT	420
TGGGGATGGA	CCAATGACGC	CCATATTCTT	TTCTCACCGA	TACCCAAGAG	CAAGGTCCAC	480
TATGACACCT	ACACAAGAGC	TGGCAGTGAC	CTTGTAATTC	AGTCCGAAGA	TGTTGCCACA	540
GTGAGCAATG	GCTTTTCACC	GGGGATCGGA	CTCAAAAAGT	CTATTTGGTG	GAAAATGCCC	600
ATCAAGAGCA	AATATGATTT	TCSCCTCGGT	TTCAAGCCTGG	GCTATGAGTA	TCTGAACCTG	660
CTATATCCGT	ATCGTAATTT	CAAGCTGGAT	GGAAATAAGC	CGCTTTCAGC	ACTATCTCCT	720
CGCATGAACC	ACATCGGCCA	TGTGGGCTTC	AACTTTACCG	TGGGTCTTTG	GACTAAT	777

(2) INFORMATION FOR SEQ ID NO:251

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 3798 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: circular

35 (ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

40 (vi) ORIGINAL SOURCE:  
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:  
(A) NAME/KEY: misc feature  
(B) LOCATION 1...3798

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:251

ATGGGCAAGT	ATAAAAGAGC	TAAGTACCGC	TATTGGCTTT	TTCTTTCTCG	TTGGGATTAT	60
TATACCTTTG	AGGGAGTTAC	TTTTTTATGC	GCATCTGACG	ATATGACAAC	CAAGAAACCC	120
CAAGCCATTT	TAGACTTAGA	GAAGGCCTAT	AACATTGAAA	TTCTTGATCT	CTCCTCACA	180
GAAGGGATAA	GCTGGTCCGT	AAATAGATAT	TTCAAGCAAG	ATTCTCTCCG	TGCAGTCGTT	240
GAGCTTTGCT	TGCGAGAATG	TCAGATAGAA	AGCATGACTT	GGCTTATGTA	TTTTCTTGCT	300
CTAAAAAAGC	TTGATCTATC	GTATAACCAA	ATCAGTAAGC	TAGAGGGTCT	AGAAGCTCTT	360
ACTTCGTTAA	CAAAACTTCG	TCTAAGAAGT	AACCAAATCC	GTAAACTAGA	GGGCCTGGAT	420
AGTCTCACCT	CGCTAACAAA	ACTTTCTCTC	TCCGATAACC	AAATCAGTAA	GCTAGAGGGT	480
CTGGAACGTC	TCACCTCGTT	AGCGGAGCTT	TATCTTTTGG	ATAACCAAAT	CAGTAAACTA	540
GAGGGTCTGG	AACGTCTCAC	GTCTTAGACA	AGCCTTGAAC	TATCGGGTAA	CCAAATCCGT	600
AAGCTGGAGG	GTCTGGAACG	TCTCACGTCC	TTAGCAACGC	TTGAAGTATC	GGSTAACCAA	660
ATCGGTAAGC	TAGAGGGTCT	GGAACGTCTC	ACTTCGTTAA	CAAAGCTTCG	TCTAAGAAGT	720
AACCAAATCA	GTAAGCTAGA	GGGTCTGGAA	CGTCTACGCT	CCTTAGCAAC	GCTTGAACCTA	780
TCGGGTAACC	AAATCCGTAA	GCTGGAGGGT	CTGGAACGTC	TCACGTCCTT	AGCAACGCTT	840
GAAGTCTCGG	GTAACCAAT	CAGTAAGCTA	GAGGGTCTGG	AACGTCTCTC	TTCTGTTAACA	900
AGCTTCTGTC	TAGAAGTAA	CCAGATCAGT	AAACTAGAGG	GCTTGGAAAC	TCTCACCTCG	960
CTAACAAAAA	TTTCTCTCTC	CGATAACCAA	ATCAGTAAGC	TAGAGGGTCT	GGAAGCTCTC	1020
ACCTCGTTAG	CGGAGCTTTA	TCTTTTGGAT	AACCAAATCC	GTAAGCTGGA	GGGCCTGGAA	1080
CGTCTCACCT	CGTTTAACAAA	GCTTCGTCTA	AGAAAGTAACC	AAATCAGTAA	ACTAGAGGGC	1140
CTGGATAGTC	TCACCTCGCT	AACAAAATTT	TCTCTCTCCG	ATAACCAAAT	CAGTAAACTA	1200
GAGGGCCTGG	AACGTCTCAC	GTCTTAGAGC	GAGCTTTATC	TTTTGGATAA	CCAAATCCGT	1260
AAGCTGGAGG	GTCTTGATGG	TCTTGCTTCC	TTAACAAGGC	TTAGTCTAAG	GCGCAACCAA	1320
ATCAAGTAAGC	TGGAAGGACT	AGACAGACTA	AAGGTTTTGA	GAAAACITGA	TGTTTTCGGGC	1380
AATGATATTC	AATCTATTGA	TGATATTAAG	CTATTGGCTC	CGATTCTGGA	GCAAACITTA	1440
GAAAAACTGA	GAATCCATGA	CAATCCATTT	GTTGCATCAT	CAGGCTTGAT	ACTCTCTCCT	1500
TATGATAATC	ATTTGCCGGA	GATTAAAGCT	CTTCTTGAAA	AAGAAAAAGA	AAAACAGAAA	1560

SUBSTITUTE SHEET (Rule 26) (RO/AU)

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5	AAGACTTCAG	TTGAATATCA	CCCATTTTGC	AAAGTAATGC	TATTGGGAAA	TCATTCTTCG	1620
	GGTAAAAACAA	CATTTCCTTAG	TCAATACGAT	ACAAATTATA	CGTATCAGAA	AAATACACAT	1680
	GTGTTGTGCGA	TACATCGAAG	CAATAACCCCT	AATGCGATCT	TTTACGACTT	TGGGGGACAG	1740
	GACTATTATC	ATGGGATTTA	CCAAGCCTTT	TTTACCACCC	AATCGTTATA	CCTTCTCTTT	1800
	TGGGATGCTA	AGAAGGATCG	AAACTTTGTG	AGCGTAGATG	ATAAAGAATA	TCAGACTCTT	1860
	AAATTCGAATC	GCCCTATTG	GTTAGGACAG	ATAGCCTATG	CCTGCAATCG	TTGTATGTCC	1920
	GTTGGAGSAA	ATCCTGATGG	CAAGGACACA	CCACAGACCA	CAGACGATAC	AATTATCATT	1980
	CAGACTCATG	CCGATGAAAC	GGGCGCTAAG	CAGCAAACCT	TAGGCTGTGC	AGCCGAGAAT	2040
10	GGAGTATTGG	AAGAAATCTA	TGTATCCTTA	GAGCCCAAGG	CGAATAGTGC	CGTACATGCG	2100
	CTCAACTATC	TGAATGAGCG	GGTGCAGAA	GTTGTGCGAA	GCAGGAGTAA	ATCAATTCAG	2160
	ATCACAGAAA	AAGATAAGGG	ATTGTACGAA	GCTCTTCCCA	CAATCGCCGG	TGATAATAAA	2220
	CACATCCCTA	TCTCTCTCGA	AGCTCTTGCG	GCTCAATTGA	ATAAGGSAAG	AGCTGAAAAT	2280
	GATCTTTACA	CCATAGAGTA	TCTACAGACC	GAATTGAACC	AGCTTAGTCT	GCGAGGGGAG	2340
	TTGCTTTACT	ATCGTGAGAA	TGAGAAGCTG	AACATTATG	TCTGGTTAGA	TCCGGCAGCT	2400
15	TTTTTCCAAA	TGATTCATGG	AGAAATCCTC	CAAAAAGACA	ACATCAATAG	AGGAACAGTT	2460
	CCTAAAGACA	TTTTTGAATG	CAAACTGCAT	AATCTAAGTT	CCGGAAGTAT	ATTTGAAGAA	2520
	GATGGCCAAA	ATGGTAATAT	GATCTTGCG	CTATTATTGG	AAGAGCTGAT	CGTATATGAA	2580
	GATAAGSACT	GCTATGTGAT	ACCGGGCTAT	CTCCCTTTGC	ATTCGGATGA	CGAAGCCTAT	2640
20	AAATGGCTTA	CTTTGGGATT	CGAGAGGCCC	AATTTTGTCC	TCAAATTCGA	ACGTTTATATC	2700
	CCCTTTGSCC	TGATCAACCA	GATTATAGCC	TACTATGGCC	GGGAAGAAGG	TGCTCTAAAG	2760
	CGGTATTGSC	GAGATCAGST	CATCTTCACA	GCAGGCCSTG	AGATGGATAG	GCAAACGCTT	2820
	GAGCAAGAAG	AAGAGAAAAG	GGGTTTGCCC	AAGACGAATG	CCGAGGATTA	TCAGATCTGG	2880
	ATCAAGCTCG	ACTTTACCGA	CTTGGCCATA	TCCGTATTCA	TCAAAGAGCA	GAGAAAGACA	2940
25	TCAGCTAAGG	ATATGCAGCG	GAAAGAGGCT	ACTATCCTCA	GTGATATGTT	GGATATGTAT	3000
	TGGAAACAATA	TCCCTCCGAG	GGAGCAAATA	GGAGATAAGG	ATACGGAGCA	AACGAGAAGC	3060
	ACTATTCGTG	AAACAAACAG	AAAGAAGAGA	CCCATCCAGG	ATCTCTACCT	CTCCTGTGCC	3120
	CAAGCGGATA	AAGATTTGAC	GGAGTCTCAT	TATATCCATT	TGGGCACGCT	GGACGATGAA	3180
	AGCAAGACTA	CGGCGAGGAT	TGCAGCCTAT	CCGTTGAAGA	ACGGCGTTAT	CGATAAAGAG	3240
30	CGGTGCGAG	AAGTATCGAC	TCGTCCCTAC	AAACATCTTT	CCGTCAATAA	AAATCTGGCT	3300
	ACTGCAAAAC	AGATCTTTAT	TTCTATTCC	AAAGAGGATC	AGACTGAACT	GGAGACCTGT	3360
	CTGCAATTTT	TCAAACCCCT	GGAGAAGAAT	GGTCAGATCG	AGATCTACTA	TGATAAGTTG	3420
	ACTAAGTTTG	AAACACCTAT	TCACCCTGAA	ATAAGAAAGC	GTATTGTGCG	AGCCGACTGT	3480
	ATAATCGCTT	TGATCAGCCA	ACGCTATCTG	GCCACGGATT	ACATCCTGGA	TCATGAGTTG	3540
35	CCTGTATTTC	GGGAGTATAA	CAAGACCATA	GTGCCGATAT	TGATCAAGCC	TTGTACATTG	3600
	GAAGACGATG	AGTTCCTTCG	GGAGAAATAT	TTTGCTCAGA	AAGCTCAAAT	AATCAATCTT	3660
	GGAAAAGAGG	GAAAAACCAT	TAAAGCTTAT	GATAGTATTA	CGGCATCAGC	CCATCGTGAT	3720
	GAAAATTGGS	TGGCAGTAGT	CAGAGAGTTC	AAAGAGAAGA	TATTAAGAAT	AACAAAACAG	3780
	GAGGTAAATA	CAGATGAA					3798

40

## (2) INFORMATION FOR SEQ ID NO:252

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 3696 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...3696
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:252

65	ATGACAACCA	AGAAACCCCA	AGCCATTTTA	GACTTAGAGA	AGGCCTATAA	CATTGAAATT	60
	CCTGATCTCT	CCTCACAAGA	AGGGATAAGC	TGGTCGATAA	ATAGATATTT	CAAGCAAGAT	120
	TCCTCCGCTG	CAGTCGTTGA	GCTTTGCTTG	CGAGAATGTC	AGATAGAAAG	CATGACTTGG	180
	CTTATTGATT	TTCTGCTCT	AAAAAAGCTT	GATCTATCGT	ATAACCAAAAT	CAGTAAGCTA	240
	GAGGGTCTAG	AACGTCCTTAC	TTCTGTTAACA	AAACTTCGTC	TAAGAAGTAA	CCAAATCGT	300
70	AAACTAGAGG	GCCTGGATAG	TCTCACCTCG	CTAACAAAAC	TTTCTCTCTC	CGATAACCAA	360
	ATCAGTAAGC	TAGAGGGTCT	GGAAACGTC	ACCTCGTTAG	CGGAGCTTTA	TCTTTTGGAT	420
	AACCAAATCA	GTAACCTAGA	GGGTCTGGAA	CGTCTCACGT	CCTTAGCAAC	GCTTGAACAT	480
	TCGGGTAACC	AAATCCGTAA	GCTGGAGSGT	CTGGAACGTC	TCACGTCCTT	AGCAAACGCTT	540
	GAACATATCG	GTAACCAAAAT	CCGTAAGCTA	GAGGGTCTGG	AACGTCCTAC	TTCTGTTAACA	600
	AAGCTTCGTC	TAGAAGTAA	CCAAATCAGT	AAGCTAGAGG	GTCTGGAAGG	TCTCACGTCC	660
75	TTAGCAACGC	TTGAACTATC	GGGTAACCAA	ATCCGTAAGC	TGGAGGGTCT	GGAACGTCCT	720

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	ACGTCCTTAG	CAACGCTTGA	ACTGTCGGGT	AACCAATCA	GTAAGCTAGA	GGGCTCTGAA	780
	CGTCTCTCTT	CGTTAACAAA	GCTTCGTCTA	AGAAGTAACC	AGATCAGTAA	ACTAGAGGGC	840
	CTGGAACGTC	TCACCTCGCT	AACAAAACCT	TCTCTCTCCG	ATAACCAAAT	CAGTAAGCTA	900
	GAGGGTCTGG	AACGCTCTAC	CTCGTTAGCG	GAGCTTTATC	TTTTGGATAA	CCAAATCCGT	960
5	AAGCTGGAGG	GCCTGGAACG	TCTCACCTCG	TTACAAAGC	TTCGTCTAAG	AAGTAACCAA	1020
	ATCAGTAAAC	TAGAGGGCCT	GGATAGTCTC	ACCTCGCTAA	CAAAACTTTC	TCTCTCCGAT	1080
	AACCAATCA	GTAACCTAGA	GGGCCTGGAA	CGTCTCACGT	CCTTAGCGGA	GCTTTATCTT	1140
	TTGGATAACC	AAATCCGTAA	GCTGGAGGGT	CTTGATGGTC	TTGCTTCCTT	AACAAGGCTT	1200
	AGTCTAAGGC	GCAACCAAAT	CAGTAAGCTG	GAAGGACTAG	ACAGACTAAA	GGTTTTTGAG	1260
10	AAACTTGATG	TTTCGGGCAA	TGATATTCAA	TCTATTGATG	ATATTAAGCT	ATTGGCTCCG	1320
	ATTCTGGAGC	AAACTTTAGA	AAACTGAGA	ATCCATGACA	ATCCATTTGT	TGCATCATCA	1380
	GGCTTGATAC	TCTCTCCTTA	TGATAATCAT	TTGCCGGAGA	TTAAGACTCT	TCTTGAAAAA	1440
	GAAAAAGAAA	AACAGAAAAA	GACTTCAGTT	GAATATCACC	CATTTTGCAA	AGTAATGCTA	1500
	TTGGGAAATC	ATTCTTCGGG	TAAAACAACA	TTTCTTAGTC	AATACGATAC	AAATTATACG	1560
15	TATCAGAAAA	ATACACATGT	GTTGTCGATA	CATCGAAGCA	ATAACCTTAA	TGCGATCTTT	1620
	TACGACTTTG	GGGGACAGGA	CTATTATCAT	GGGATTTACC	AAGCCTTTTT	TACCACCCAA	1680
	TCGTTATACC	TTCTCTTTTG	GGATGCTAAG	AAGGATCGAA	ACTTTGTGAG	CGTAGATGAT	1740
	AAAGAATATC	AGACTCTTAA	TTTCAATCGC	CCCTATTGGT	TAGGACAGAT	AGCCTATGCC	1800
20	TGCAATCGTT	GTATGTCCGT	TGGAGGAAAT	CCTGATGGCA	AGGACACACC	ACAGACCACA	1860
	GACGATACAA	TTATCATTCA	GACTCATGCC	GATGAAACGG	GCGCTAAGCA	GCAAACTTTA	1920
	GGCTGTGCAG	CCGAGAATGG	AGTATTGGAA	GAAATCTATG	TATCCTTAGA	GCCCCAGGCG	1980
	AATAGTGCCG	TACATGCGCT	CAACTATCTG	AATGAGCGGG	TGCGAGAAGT	TGTCGCAAGC	2040
	AGGAGTAAAT	CAATTCAGAT	CACAGAAAAA	GATAAGGGAT	TGTACGAAGC	TCTTCCCACA	2100
	ATCGCCGGTG	ATAATAAACA	CATCCCTATC	TCTCTCGAAG	CTCTTGCGGC	TCAATTGAAT	2160
25	AAGGGAAGAG	CTGAAAATGA	TCTTTACACC	ATAGAGTATC	TACAGACCGA	ATTGAACCAAG	2220
	CTTAGTCTGC	GAGGGGAGGT	GCTTTACTAT	CGTGAGAATG	AGAAGCTGAA	CAATTATGTC	2280
	TGGTTAGATC	CGGCAGCTTT	TGTCCAAATG	ATTCATGGAG	AAATCCTCCA	AAAAGACAAC	2340
	ATCAATAGAG	GAACAGTTCC	TAAAGACATT	TTTGAATGCA	AACTGCATAA	TCTAAGTTCC	2400
30	GSAAGTATAT	TTGAAGAAGA	TGGCCAAAT	GGAATATATG	TCTTGCAGCT	ATTATTGGAA	2460
	GAGCTGATCG	TATATGAAGA	TAAGGACTGC	TATGTGATAC	CGGGCTATCT	CCCTTTGCAT	2520
	TCCGATGACG	AAGCCTATAA	ATGGCTTACT	TTGGGATTCT	AGAGGCCCAA	TTTTGTCTCT	2580
	AAATTCGAAC	GTTTTATCCC	CTTTGGCCTG	ATCAACCAGA	TTATAGCCTA	CTATGGCCGG	2640
	GAAGAAGGTG	CTCTAAAGCG	GTATTGGCGA	GATCAGGTCA	TCTTCACAGC	AGGCCGTGAG	2700
35	ATGGATAGGC	AAACGCTTGA	GCAAGAAGAA	GAGAAAGAGG	GTTTGCCCAA	GACGAATGCC	2760
	GAGGATTATC	AGATCTGGAT	CAAGCTCGAC	TTTACCGACT	TGGCCATATC	CGTATTCATC	2820
	AAAGAGCAGA	GAAAGACATC	AGCTAAGGAT	ATGCAGCGGA	AAGAGGCTAC	TATCCTCAGT	2880
	GATATGTTGG	ATATGTATTG	GAACAATATC	CCTCCGAGGG	AGCAAATAGG	AGATAAGGAT	2940
	ACGAGAGCAA	CGAGAAGCAC	TATTCGTGAA	ACAAACAGAA	AGAAGAGACC	CATCCAGGAT	3000
40	CTCTACCTCT	CCTGTGCCCA	AGCGGATAAA	GATTTGACGG	AGTCTCATTA	TATCCATTTG	3060
	GGCAGCGTGG	ACGATGAAAG	CAAGACTACG	GCGAGGATTG	CAGCCTATCC	GTTGAAGAAC	3120
	GGCGTTATCG	ATAAAGAGCG	GGTGGAGAG	GTATCGACTC	GTCCCTACAA	ACATCTTTCC	3180
	GTCAATAAAA	ATCTGGCTAC	TGCAAAACAG	ATCTTTATTT	CCTATTCCAA	AGAGGATCAG	3240
	ACTGAACTGG	AGACCTGTCT	GCAATTTTTC	AAACCTTTGG	AGAAGAATGS	TCAGATCGAG	3300
	ATCTACTATG	ATAAGTTGAC	TAAGTTTGAA	ACACCTATTC	ACCCTGAAAT	AAGAAAGCGT	3360
45	ATTGTGGAAG	CCGACTGTAT	AATCGCTTTG	ATCAGCCAAC	GCTATCTGGC	CACGGATTAC	3420
	ATCCTGGATC	ATGAGTTGCC	TGATTTTCGG	GAGTATAACA	AGACCATAGT	GCCGATATTG	3480
	ATCAAGCCTT	GTACATTCTG	AGACGATGAG	TTCTTTCGGG	AGAAATATTT	TGCTCAGAAA	3540
	GCTCAAATAA	TCAATCTTGG	AAAAGAGGGA	AAAACCATTA	AAGCTTATGA	TAGTATTACG	3600
50	GCATCAGCCC	ATCGTGATGA	AAATTGGGTG	GCAGTAGTCA	GAGAGTTCAA	AGAGAAGATA	3660
	TTAAGAATAA	CAAAACAGGA	GGTAAATACA	GATGAA			3696

## (2) INFORMATION FOR SEQ ID NO:253

- 55 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 3525 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular
- 60 (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- 65 (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- 70 (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...3525
- 75 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:253



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	ATGACTTGGC	TTATTGATTT	TCCTGCTCTA	AAAAAGCTTG	ATCTATCGTA	TAACCAATC	60
	AGTAAGCTAG	AGGGTCTAGA	ACGTCTTACT	TCGTAAACAA	AACTTCGTCT	AAGAAGTAAC	120
	CAAAATCCGTA	AAC TAGAGGG	CCTGGATAGT	CTCACCTCGC	TAACAAAAC	TTCTCTCTCC	180
5	GATAACCAAA	TCAGTAAGCT	AGAGGGTCTG	GAACGTCTCA	CCTCGTTAGC	GGAGCTTTAT	240
	CTTTTGGATA	ACCAAATCAG	TAAACTAGAG	GGTCTGGAAC	GTCTCACGTC	CTTAGCAACG	300
	CTTGAACATAT	CGGGTAACCA	AATCCGTAA	CTGGAGGGTC	TGGAACGTCT	CACGTCCTTA	360
	GCAACGCTTG	AACATATCGG	TAACCAAAATC	CGTAAGCTAG	AGGGTCTGGA	ACGTCCTACT	420
	TCGTAAACAA	AGCTTCGTCT	AAGAAGTAAC	CAAAATCAGTA	AGCTAGAGGG	TCTGGAACGT	480
	CTCACGTCCT	TAGCAACGCT	TGAACATATC	GGTAACCAAA	TCCGTAAGCT	GGAGGGTCTG	540
10	GAACGTCTCA	CGTCTTAGC	AACGCTTGAA	CTGTGCGGTA	ACCAAATCAG	TAAGCTAGAG	600
	GGTCTGGAAC	GTCTCTCTTC	GTTAACAAAG	CTTCGTCTAA	GAAGTAACCA	GATCAGTAAA	660
	CTAGAGGGCC	TGGAACGTCT	CACCTCGCTA	ACAAAACCTTT	CTCTCTCCGA	TAACCAATC	720
	AGTAAGCTAG	AGGGTCTGGA	ACGTCTCACC	TCGTAGCGG	AGCTTTACT	TTTGGATAAC	780
	CAAAATCCGTA	AGCTGGAGGG	CCTGGAACGT	CTCACCTCGT	TAACAAAGCT	TCGTCTAAGA	840
15	AGTAACCAAA	TCAGTAAACT	AGAGGGCCTG	GATAGTCTCA	CCTCGCTAAC	AAAACCTTTCT	900
	CTCTCCGATA	ACCAAATCAG	TAAACTAGAG	GGCCTGGAAC	GTCTCACGTC	CTTAGCGGAG	960
	CTTTATCTTT	TGATAACCA	AATCCGTAA	CTGGAGGGTC	TTGATGGTCT	TGCTTCCTTA	1020
	ACAAGGCTTA	GTCTAAGGCG	CAACCAAAATC	AGTAAGCTGG	AAGGACTAGA	CAGACTAAG	1080
	GTTTTGAGAA	AACCTTGATG	TTCGGGCAAT	GATATTCAT	CTATTGATGA	TATTAAGCTA	1140
20	TTGCTCCGA	TTCTGGAGCA	AACCTTAGAA	AAACTGAGAA	TCCATGACAA	TCCATTTGTT	1200
	GCATCATCAG	GCTTGATACT	CTCTCCTTAT	GATAATCATT	TGCCGGAGAT	TAAAGCTCTT	1260
	CTTGAAAAAG	AAAAAGAAAA	ACAGAAAAAG	ACTTCAGTTG	AATATCACCC	ATTTTGCAAA	1320
	GTATGCTAT	TGGGAATCA	TTCTTCGGGT	AAAACAACAT	TTCTTAGTCA	ATACGATACA	1380
	AATTATACGT	ATCAGAAAAA	TACACATGTG	TTGTGATAC	ATCGAAGCAA	TAACCCTAAT	1440
25	GCATCTTTT	ACGACTTTG	GGGACAGGAC	TATTATCATG	GGATTATCCA	AGCCTTTTTT	1500
	ACCACCCAAT	CGTTATACCT	TCTCTTTTGG	GATGCTAAGA	AGGATCGAAA	CTTTGTGAGC	1560
	GTAGATGATA	AAGAATATCA	GACTCTTAAT	TTCAATCGCC	CCTATTGGTT	AGGACAGATA	1620
	GCCTATGCC	GCAATCGTTG	TATGTCCGTT	GGAGGAAATC	CTGATGGCAA	GGACACACCA	1680
30	CAGACCACAG	ACGATACAAT	TATCATTCAG	ACTCATCCCG	ATGAACCGGG	CGCTAAGCAG	1740
	CAAACTTAG	GCTGTGCAGC	CGAGAATGGA	GTATTGGAAG	AAATCTATGT	ATCCTTAGAG	1800
	CCCAAGGCCA	ATAGTGCCGT	ACATGCGCTC	AACATCTGSA	ATGAGCGGGT	GCGAGAAGTT	1860
	GTGCAAGCA	GGAGTAAATC	AATTCAGATC	ACAGAAAAAG	ATAAGGGATT	GTACGAAGCT	1920
	CTTCCCACAA	TCGCCGGTGA	TAATAAACAC	ATCCCTATCT	CTCTCGAAGC	TCTTGCGGCT	1980
35	CAATTGAATA	AGGGAAGAGC	TGAAATGAT	CTTTACACCA	TAGAGTATCT	ACAGACCGAA	2040
	TTGAACCAGC	TTAGTCTGCG	AGGGGAGGTG	CTTTACTATC	GTGAGAATGA	GAAGCTGAAC	2100
	AATTATGTCT	GGTTAGATCC	GGCAGCTTTT	GTCCAAATGA	TTCTATGGAGA	AATCCTCCAA	2160
	AAAGACAACA	TCAATAGAGG	AACAGTTCC	AAAGACATTT	TTGAATGCAA	ACTGCATAAT	2220
	CTAAGTTCCG	GAAGTATATT	TGAAGAAGAT	GGCCAAAATG	GTAATATGAT	CTTGCAAGCTA	2280
	TTATTGGAAG	AGCTGATCGT	ATATGAAGAT	AAGGACTGCT	ATGTGATACC	GGGCTATCTC	2340
40	CCTTTGCATT	CCGATGACGA	AGCCTATAAA	TGGCTTACTT	TGGGATTCGA	GAGGCCCAAT	2400
	TTTGTCTCTCA	AATTGCAACG	TTTTATCCCC	TTTGGCTGSA	TCAACCAGAT	TATAGCCTAC	2460
	TATGGCCGGG	AAGAAGGTGC	TCTAAAGCGG	TATTGGCGAG	ATCAGGTCTAT	CTTCACAGCA	2520
	GGCCGTGAGA	TGGATAGGCA	AACGCTTGAG	CAAGAAGAAG	AGAAAGAGGG	TTTGCCCAAG	2580
45	ACGAATGCCG	AGGATTATCA	GATCTGGATC	AAGCTCGACT	TTACCGACTT	GGCCATATCC	2640
	GTATTTCATCA	AAGAGCAGAG	AAAGACATCA	GCTAAGGATA	TGCAGCGGAA	AGAGGCTACT	2700
	ATCCTCAGTG	ATATGTTGGA	TATGTATTGG	AACAATATCC	CTCCGAGGGA	GCAATAGGA	2760
	GATAAGSATA	CGGAGCAAAC	GAGAAGCACT	ATTCTGTGAA	CAAACAGAAA	GAAGAGACCC	2820
	ATCCAGGATC	TCTACCTCTC	CTGTGCCCAA	CGGSAATAAG	ATTTGACGGA	GTCTCATTAT	2880
	ATCCATTTGG	GCACGCTGGA	CGATGAAAGC	AAGACTACGG	CGAGGATTGC	AGCCTATCCG	2940
50	TTGAAGAACC	CGGTTATCGA	TAAAGAGCGG	GTGCGAGAAG	TATCGACTCG	TCCCTACAAA	3000
	CATCTTTCCG	TCAATAAAAA	TCTGGCTACT	GCAAAACAGA	TCTTTATTTC	CTATTCCAAA	3060
	GAGGATCAGA	CTGAACCTGGA	GACCTGTCTG	CAATTTTTC	AACCTTTGGA	GAAGAATGGT	3120
	CAGATCGAGA	TCTACTATGA	TAAGTTGACT	AAGTTTGAAA	CACCTATTCA	CCCTGAAATA	3180
	AGAAAGCGTA	TTGTGCAAGC	CGACTGTATA	ATCGCTTTGA	TCAGCCAACG	CTATCTGGCC	3240
55	ACGGATTACA	TCCTGGATCA	TGAGTTGCCT	GTATTTCGGG	AGTATAACAA	GACCATAGTG	3300
	CCGATATTGA	TCAAGCCTTG	TACATTGCAA	GACGATGAGT	TCCTTCGGGA	GAAATATTTT	3360
	GCTCAGAAAG	CTCAATAAAT	CAATCTTGSA	AAAGAGGGAA	AAACCATTAA	AGCTTATGAT	3420
	AGTATTACGG	CATCAGCCCA	TCGTGATGAA	AATTGGGTGG	CAGTAGTCAG	AGAGTTCAAA	3480
60	GAGAAGATAT	TAAGAATAAC	AAAACAGGAG	GTAAATACAG	ATGAA		3525

(2) INFORMATION FOR SEQ ID NO:254

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 687 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular

70 (ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

75 (iv) ANTI-SENSE: NO

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(vi) ORIGINAL SOURCE:  
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

5 (ix) FEATURE:  
(A) NAME/KEY: misc feature  
(B) LOCATION 1...687

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:254

10 ATGATGAAAA AAGCATTGT TTTCGTACTA CTGGTTTGCC TATTCTCCTC GTTCAGCAGT 60  
TCCGCCCAAA CAACGACGAA CASTAGCCGG AGTTATTTTA CAGGACGAAT CGAGAAGGTG 120  
AGTTTGAAGT TAGGGGTCCC CCCCCTAAGC ACAGAGGTTT GGGGAATGAC CCATGATGCG 180  
AACGGTCTCC CTTTCGAAAT ACCTATCTCT TCAAGTCGTT TCAACAGCCA GGGAGATATA 240  
GCTACCACTT ATTACATAGC GAATAGCGAG GCAACTTTGA ATGAATGGTG CGACTATGCA 300  
15 CACCCGGGCG GCATCGTGAG GGTAGAAGGT CGTTTTTGGG AAATGACTTA CAACATACCA 360  
ACCTACAATG CASTCTGCAC CCGGATTACA TTCGAAAATC AAGAAATAGA AGGAACGATC 420  
GTCTTGATAC CCAAGCCCAA AGTCTCGCTG CCTCATGTGT CGGAATCGGT GCCTTGCATC 480  
CGAACCGAAG CCGGGAGGGA ATTTATCCTT TGCGAAGAAG ACGACACCTT TGTGTCTCAC 540  
GATGGTAACG AAGTAACGAT AGGCGGTAAA CCTTCTTTCG TCAATACCAA CGTAAAGATT 600  
20 GTGGGGGACG TATCTCAAAA GTATGCCGTG GGGGTAGGAG AAATTCGATT CCTGCAGATT 660  
TGTGCCCAAA CAGTATCACA ACAAAAA 687

(2) INFORMATION FOR SEQ ID NO:255

25 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 684 base pairs  
(B) TYPE: nucleic acid  
30 (C) STRANDEDNESS: double  
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:  
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

40 (ix) FEATURE:  
(A) NAME/KEY: misc feature  
(B) LOCATION 1...684

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:255

ATGAAAAAAG CATTTGTTTT CGTACTACTG GTTTGCCTAT TCTCCTCGTT CAGCAGTTCC 60  
GCCCCAAACA CGACGAACAG TAGCCGGAGT TATTTTACAG GACGAATCGA GAAGGTGAGT 120  
TTGAACCTTAG GGGTCCCCCC CGTAAGCACA GAGGTTTGGG GAATGACCCA TGATGCGAAC 180  
50 GGTCTCCCTT TCGAAATACC TATCTCTTTC AGTCGTTTCA ACAGCCAGGG AGATATAGCT 240  
ACCACTTATT ACATAGCGAA TAGCGAGGCA ACTTTGAATG AATGGTGCGA CTATGCACAC 300  
CCGGGCGGCA TCGTGAGGGT AGAAGGTCGT TTTTGGAAAA TGAATTACAA CATACCAACC 360  
TACAATGCAG TCTGCACCCG GATTACATTC GAAAATCAAG AAATAGAAGG AACGATCGTC 420  
TTGATACCCA AGCCCCAAGT CTCGCTGCCT CATGTGTGCG AATCGGTGCC TTGCATCCGA 480  
55 ACCGAAGCCG GGAGGGAATT TATCCTTTGC GAAGAAGACG ACACCTTGT GTCTCAGAT 540  
GGTAACGAAG TAACGATAGG CGGTAAACCT TTCTTGCTCA ATACCAACGT AAAGATTGTG 600  
GGGGACGTAT CTCAAAGTA TGCCGTGGGG GTAGGAGAAA TTCGATTTCCT GCAGATTGTG 660  
GCCCCAACAG TATCACAACA AAAA 684

(2) INFORMATION FOR SEQ ID NO:256

65 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 1620 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

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(A) ORGANISM: PORIPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc\_feature

(B) LOCATION 1...1620

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:256

10	ATGAAGACAA AAGTTTTACG CAAATTCGTG GTGGCGGCTT TCGCCGTCGC AACCCCTCTGT	60
	CCTCTCGCCC AAGCGCAGAC GATGGGAGGA GATGATGTCA AGGTGGTCCA GTACAATCAG	120
	GAAAAACTGG TACAAACGAG GATGAGTGTG GCGGACAACG GATGGATCTA TGTAATGACC	180
	CACAGTGGAT ACGACACCGG CAATAGCAAT GTGAAGATCT TCCGCTCCAA AGACCAAGST	240
	GCCACATACC AAAAGTTGAG GGATTGGGAT CCATCGGATG ATTATCAGTT TCAAGACTTC	300
15	GATATCGTGG TAACGGGTAA GAATGAATCC GACATCAAGA TTTGGTCGGT AGAGCTCATG	360
	AATAAGCCCG GAGGATATAA GAGTAGAGTT GCGGTCTTCA GTCGCGATGC CAACGCGCAG	420
	AATGCGAAAC TCGTGTATAA GGAAGACTTC TCCAATGTGC AGTTGTACGA TGTGGATATA	480
	GCCTCCAACAT ATCGTTCCGC TTCTTCTCTT AACAATGGTG GCAACCCCTT TGCTTTGGCT	540
	TTGCTTACCA CCGGCTTCAA CAATACGCAC AAAATAAGTT TTGTGGACTA TGTGTCTCT	600
20	CTGAATGGAG GGCAAAATTT CAATAAAAAA TTAATCTTCA GTCAAGATGG AGAGAAGAAA	660
	ATTGACAAGG TGGATCTCTC ATTGGGTAGC ACCTCTGAAT CCATGGGTCA CAATGCCTGG	720
	CCGCTAATGG GTGTGGTATT CGAAATGAAT AAACAAGGGG GAAAAAGCGA TATCGGTTTC	780
	TTGTCTGAAC TTGTCTGACAA TGATCCCGAA TTTCAGTGGT CAGGCCCTAT AAAAGTGAGT	840
	GAAAGCGACA TGTCTGTCAG CCCCAAAATC CAAATGTTGC TGGACGAGGA TAACAATACG	900
25	ATCAATGGGG AGAGTTGCCA CAACTTCATG ATTACGTACA GCGATTATGA TTCTGAATAT	960
	TCGGATTGGG ACATTCCGTA TGTATATCCC AAGAAATCGT TCAAGTATGA AAAAGGAAAA	1020
	ACTCCGACTA TGGATGATCT GGTGGAAGCT TTCCTTACAG CTTCTGTACCA GAGTGAGACC	1080
	AACTCGGGGG TGGGGTATGA CAAGAACGCC AATCACTACC TGATTACATA TGCCAAAAAA	1140
	GAAGAGAACG GTACGAACAC GCTGAAATAC CGCTGGGCCA ATTATGACAA GATTCTAATC	1200
30	AAAGATTGTT GGAGCGACAC ATTTACGTAT ACATCATCTG CCAATGCTCT CTACACACCT	1260
	CAAGTAGACA TCAATCCGAC CAAGGGTCTC GTGTGCTGGT CATGGGTGGA ATATCTGCCG	1320
	GGCAAAACGG TCGTTTGGTC TGATACGCAG TGGACCCATG CCAACGGTGT AGAAGACATC	1380
	GTAATGCAAG AAGGCAGCAT GAAGCTCTAC CCGAATCCGG CTCAAGAATA TGCTGTGATT	1440
	AGCCTGCCGA CGGCAGCAAA CTGCAAGGCT GTTGTTTACG ATATGCAGGG CAGAGTAGTC	1500
35	GCTGAGGCTT CTTTCTCCGG CAACGAATAC AGGCTGAACG TGCAGCACTT GGCTAAGGGT	1560
	ACGTACATAC TCAAGGTCGT ATCCGATACG GAGCGTTTCG TAGAGAAGCT CATCGTGGAA	1620

(2) INFORMATION FOR SEQ ID NO:257

40	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 2313 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
45	(D) TOPOLOGY: circular
	(ii) MOLECULE TYPE: DNA (genomic)
	(iii) HYPOTHETICAL: NO
50	(iv) ANTI-SENSE: NO
	(vi) ORIGINAL SOURCE:
	(A) ORGANISM: PORIPHYROMONAS GINGIVALIS
55	(ix) FEATURE:
	(A) NAME/KEY: misc_feature
	(B) LOCATION 1...2313

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:257

60	ATGCTGACGA TCCGAAACTT CCTCCTCTTT TGTTGTCTGT CGCTGATAGC GTTTGCTGCC	60
	GATGCACAAA GCTCTGTCTC TTCGGGTAGA CGACTGACAG AATATGTCAA TCCCTTTATC	120
	GGAACGSCCA ATTACGGTAC CACGAATCCG GGAGCAGTAT TGCCCAATGG GTTGATGAGC	180
	GTTACCCCTT TCAATGTCTG CGGATCGACA GAGAATCGCT TCGACAAAGA TTCGCGTTGG	240
65	TGGAGTGCGC CTTATTTCGG CGACAATAGT TACTGCATCG GTTTCAGCCA TGTGAATCTG	300
	AGTGGAGTAG GCTGTCCCGA ACTGAGTGGG ATACTGCTGA TGGCCACTTC CGGCACATTC	360
	GATCCTGATT ACTGCTGCTA TGGCTCTTCG CTCAGTCTGAG AATATGCGCG CCCGGGAGAA	420
	TACAAGGCTG TATTTGGACAA ATACGGTATA GATGCAGCCG TGACCGTAAC CGAGCGGACT	480
	GCTTTGACCG AATTTGCTTT TCCGSAAGGA GAAGGCCATA TCCTGCTGAA CCTGGGACAG	540
70	GCCTTAAGCA ATGAATCGGG AGCCTCTGTT CGATTCTTAA ACGACTCCAC AGTCGTCCGG	600
	AGCAGGCTGA TGGGGACGTT CTGCTACAAT CCGCAAGCAG TTTTTCGTCA GTATTTCGTA	660
	CTTCAGGTGA GTCGGCGACC GATCTCTGCC GGCTATTGGA AGAAGCAGCC TCCTATGACA	720
	GTGGAAGCCC AATGGGATTC GACTGCAGGG AAATATAAGC AGTACGACGG CTACAAGCGT	780
	GAGATGAGCG GTGATGACAT CGGTGTCCGA TTCTCTTCA ACTGCGATCA GGGGGAAGAG	840
75	ATCTATGTAC GATCGGCCGT TTCATTCTGC AGCGAAGCCA ATGCGCTCTA TAATCTGGAA	900

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	GCGGAGCAAG	AAGAGGTGTT	CAAAAGTGTC	GGAGGGAATC	CGGCCAAGGC	TTTCTCCGCT	960
	ATACGCTCTC	GCGCTATAGA	GCGTTGGGAG	GAAGCCCTCG	GTACGGTGGA	AGTGGGAAGGA	1020
	GGCACACCGG	ATGAAAAGAC	GATATTCCTAT	ACCGCACTCT	ATCACCTGCT	GATACATCCG	1080
	AATATCCTAC	AAGATGCCAA	TGGAGAATAT	CCTATGATGG	GCAGTGGCAA	AACGGGTAAAT	1140
5	ACGGCTCACG	ACCGCTACAC	CGTGTCTCT	CTTTGGGACA	CGTACCGCAA	TGTACACCCG	1200
	CTGCTCTGCC	TCCTCTATCC	GGAGAAGCAG	TTGGATATGG	TACGGACACT	GATCGACATG	1260
	TACCGAGAGA	GCGGGTGGCT	GCCGAGATGG	GAGCTGTACG	GACAGGAGAC	CCTGACGATG	1320
	GAGGGCGACC	CCTCGCTTAT	CGTCATCAAT	GACACTTGGC	AAAGGGGCCT	TCGTGCTTTC	1380
	GATACGGCAA	CGGCCTATGA	AGCCATGAAA	AAAAATGCTT	CTTCGGCAGG	AGCGACCCAT	1440
10	CCGATCCGTC	CTGACAACGA	CGACTATCTC	ACCCTCGGCT	TCGTACCGCT	TCGCGAACAG	1500
	TACGACAATT	CCGTATCGCA	TGCGCTGGAA	TACTATCTGG	CCGACTGGAA	TCTGTCCCGG	1560
	TTTGCCCAAG	CACTTGGGCA	TAAAGAAGAC	GCAGCTCTAT	TCGGAAAACG	CTCGTTGGGG	1620
	TACAGACACT	ATTATAATAA	GGAGTATGGT	ATGCTGTGTC	CATTGCTGCC	GGATGGATCA	1680
	TTCTCTACTC	CTTTCTGATC	CAAAACAGGT	GAAAACCTCG	AGCCTAATCC	CGGTTTCCAC	1740
15	GAGGGCACTG	CTTATAACTA	TGCTTTTTTC	GTTCCTCCAG	ATATACAAGG	GCTTGCCCGG	1800
	CTGATGGGAG	GAGCAAAGGT	TTTTTCGGAA	AGGTTGCAAG	AAGTCTTCCA	TGAAGSATAT	1860
	TATGATCCGA	CCAACGAGCC	GGACATCGCC	TATCCTTACC	TCTTCTCCTA	TTTCCCCAAG	1920
	GAAGCATGGC	GAACGAGAA	ATTGACCCGG	GAGTTGATAG	ACAAACATTT	TTGCAATGCT	1980
	CCTAACGGCT	TGCCCGGTAA	TGACGATGCC	GGTACGATGA	GTGCTTGGCT	TGTCTATTCC	2040
20	ATGCTGGGAT	CTACCCCTGA	CTGTCCGGGC	AGCCCCACCT	ATACACTGAC	CTCGCCGCTA	2100
	TTCCCCCGAG	TTAGGATTCG	GCTCAATCCG	CAGTATTATC	CTCAGGGGGA	GTGATCATT	2160
	ACGACCAATA	CAGAGAATCA	ACCGACAGAT	TCCATTTACA	TCCATACGGT	TTCTCTTGGC	2220
	AATAAAACAC	TTCCGCATGG	AACAAGGCAT	ATCAGCCATG	CCGATTTGGT	GCGCTGCGGT	2280
25	CACCTCCGTT	ACGAACTAAG	CAATCGTCCT	CGA			2313

(2) INFORMATION FOR SEQ ID NO:258

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 2328 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (v) ORIGINAL SOURCE:  
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:  
(A) NAME/KEY: misc\_feature  
(B) LOCATION 1...2328
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:258

50	ATGTGCAAAA	TAAGATTCAG	CCTCTTGCA	GCTCTTGTC	TCTGCTTATT	GTTCACTCT	60
	TTTTCTCTCC	AAGCTCAAGA	GGAAGGTATT	TGGAATACCC	TCTTGGCTAT	CCACAAGACG	120
	GAAAAGCCG	TAGAAACGCC	CAAGAAAGTC	TTTGCCGTAG	CCAACGGAGT	ACTTTACTCG	180
	GTGGGCAAG	AAGCTCCCCA	TGAGGCAAG	ATCTTCGACC	GTATCAGCGG	ACTCAGCGAT	240
	ACATCGGTAA	GCAGCATAGC	CTACTCCGAG	CAACTAAAT	CCTTGGTCAT	ATACTATGCA	300
55	TCAGGCAATA	TCGACATCTT	GGACGAAGCA	GGCCGTGTGA	CCAACGTACC	TGCATTGAAA	360
	GACAAATATC	ATCTGATAGA	CAAAACGCTC	AATCGCCTTT	TGATCGTAGG	CAACAGGGCT	420
	TATTTGGCAG	GAGGATTCGG	CCTCTCCGTT	CTGGATGTGG	CGGAAGCTCG	CATACCGGCT	480
	ACCTACGCCA	AGGGAACTAA	GGTGACCGAT	GTGGCTAAAT	TGGACAATGA	TCGCTTGCTG	540
	ATGCTGAAAG	AAGGGCAGCT	CTTCATCGGA	AAAGAGACCG	ATAACCTGCA	AGATCCGGCC	600
60	GCATGGACAG	CCTTGCTTTT	GAATTTGCGG	ATGGGCTCGG	TCACCGGTCT	GGGCATTGTC	660
	GGGGAAAGACA	TCTGTTTCTT	GCTCGCCGAT	GGCCGTGTAT	ATGTCGCTGC	AAACCAATCG	720
	TTTGAGCCCG	AGCTATTGCT	CTCTTCCTCC	GCCGATTCA	GACTGTATGT	GACGGATCGT	780
	GGTCTGTTCA	TCTGTGCCGA	GAATCGAATT	TATTTCATAG	AAAAAGGTGG	CAAAACGACA	840
	CAATTTCCTA	TAGCCGACGT	CCTTGGTGTC	GGTGCCATGA	ACGAAAGCAA	TACGGGCATC	900
65	ATAGCATTTG	GAGAAGAAGG	TTTGGCTTCA	CTTCTTCTCG	CAGAGGGGAA	TACGGCCGAA	960
	GCCATGCCCTG	TAGCATTCGA	CGGACCGGGG	GACAATGATT	TCTACGAGAT	GCGGTTTAGT	1020
	CACGGACGTC	TGTATGCAGC	CAGCGGACTC	TGGGGAAACAA	ACCTGATGGG	ACATGCCGGT	1080
	ATGGTGAAG	TATACGACGG	CAACCGATGG	ACTAACCTCG	ACAAGAAGAC	CGTACAGGAA	1140
	CAGTTGGGCG	GCGGATTCAG	TTTCAATGAT	GCTATCGATA	TAGCTGTTTC	CAACGGAGAC	1200
70	CCCGATCACT	TTTTTGTCGG	TACATGGGGA	AACGGTCTGT	TCGAAATCAA	GGATGGCAAA	1260
	GCGATASCTC	GCTATTCTGG	AAACGAAACT	GCTATCGSAG	AATGTAATCC	CGGAGATGCC	1320
	CGTGTGAAAG	CGATTGCCTT	TGACAATAAG	GGCAACCTCT	GGGGGACGCT	CGGTGCCGTA	1380
	GGCAAGAAC	TTCTCATGTA	CGATCCGCG	AGTAGCACAT	GGCATTCTTT	CAGCTATCCG	1440
	GATGTAGCCA	ATCTGGCCTC	CTTCGGCAAT	ATGATTATCC	TACCAACCGG	AGACAAATGG	1500
75	GTAATATATC	TTCAACCGTAG	TGGCGGATCC	ACGCGCAAG	GTGTCTTGAT	CTTCAACGAT	1560

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5 CGGGGTACAC CGGAAACGAC TTCGGACGAC AGCCATCTTT ACGTCGAGCA GTTTGTCAAT 1620  
 CGCCTCGGGG CAGCCATAGG ACATAAGACT ATCTATGCAA TGGCCGTCGA TCATAACGGC 1680  
 TCTGTCTGGA TGGGATCGGA TATAGGCATT TTCGGCGTCT ACAATGCAGC CGGAGTATTG 1740  
 TCCTCGACTT CTACCCCTAT CGCTGTTCGG CCGGTGCGAG GAGAAGAACC CAATTTGTAC 1800  
 TATGTGCTGG ACAAGGTGAC GGTGACAGAC ATCGTCTGCG ACAAACCTCA TCACAAATGG 1860  
 GTTGCCACCC AAGGGACAGG ACTCTATCTC CTTTCGGAAG ATTGCAGTAA GATCCTCGCG 1920  
 CAATTTACCG TAGAAAACAG CCCTTTGCTT TCTAACACA TACTATCCCT GGCCTTAAAT 1980  
 GACGATAACG GACTGCTGTA CATCGGTACG GCGGACGGAC TGATGACGTT CCAAACGGGT 2040  
 10 ACGGGGAGTG GATCAGCTTC CGAACTGGAC GCGGTCTATG TATACCCCAA TCCGCTAAGG 2100  
 CCGGAATATC CCGATGGCGT CACCATTGCC GGAAGTCAAG CCGGTCTAG TGTCAAAATC 2160  
 ACCGATACCA CCGGACAGT GCTATACCAG ACTGAGAGCG TAACCACCGA AGTCAAATGG 2220  
 AATGCTCGAG GTGCCGATGG CAATAGGGTA GCTTCGGGCG TATATGCCGT TGCAGTGTAC 2280  
 GATCCGGTAT CGAAAAAGTC CAACTAATT CGCTTCGCG TGATTGCG 2328

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(2) INFORMATION FOR SEQ ID NO:259

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 3474 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRAINEDNESS: double  
 (D) TOPOLOGY: circular  
 (ii) MOLECULE TYPE: DNA (genomic)  
 (iii) HYPOTHETICAL: NO  
 (iv) ANTI-SENSE: NO  
 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS  
 (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION: 1...3474  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:259

40 ATGAAACGAA TACTTCCAAT AGTCGCATTG CTTTCTCTCT TCCTTGCCCT TGCTTTGCCT 60  
 GCGAAAGCGC AACGAGCTAT GGGGAAGACG GCCGACCGTT CGCTAATGGC TTCGGGACAT 120  
 TGGGTCAAGA TACGTGTGGA TGCAAGTGGA GTGTATCGCC TTACGGACGA ACAGCTCCGT 180  
 GCCAATGSGT TCTCCGATCC GTCCAAGGTA GGTGTGTTGG GTTATGGTGG AGGGGTGCTT 240  
 CCCGAAGATC TGAGCCGGAT CACGACAGAC GATTTGCTTC CCGTACCGGT ACTCCGTCAG 300  
 GSCAATGCGC TGTATTTCTA TGCCGTGGGC CCGGTGACAT GGTCTACAA TCCGGCCAAA 360  
 45 ACCACCATGG AGCATACGGT GAATACATAC AGTACGCATG GCTACTACTT CCTGTCGGAT 420  
 GCTGCCGGAG CACCTTTGCA GATGTCCCAA TATACGGSTG GAGGTGCGTC GGCCGAGGCT 480  
 TTGATCGACT ACTACGATGA GCTGATGCTC CATGAACAGG AATTGTATTG GCCCAAAGAA 540  
 TCGGACGAGC ATCTGTATGG CGAGTCTTTC AGTGCASTCA ATACGCGTAC GGTCAAGTTC 600  
 CCTTTGAGGG GCAACACCCG CTCGTCTGGC GAATCGGTA CCGTATTCTC ATACATAGCC 660  
 50 AAGGCCAGAT CGGCGGSGTG GCGCGGTGAG ATGTCTGCTC CGGCGAATGG CATCTGATC 720  
 TTCAGCGATC CTTTTCCTAT GACATCGAAT GAAGTCTCCA ATTCTATTG GGCCGGCAAG 780  
 AAGCGTCTCT TCTATCACAG TACGCGGATG AACAGCTTGG TCAATGAGTT GCCTTGGAC 840  
 GCGAACTATA GCATGACAGG AGATGCGGTC AATCTGGATT TCATAGAGGT GGCTACACAG 900  
 AACGACCTCC GSTACGATGG CGCACCCATG CATATCAGGC GGTTTTCCAA TTTGCCCGTT 960  
 55 TTGGGGGGGG AGTCCTGCCG GTTCGTTATC AGTGAGGTGC CCGAGTCTCT GGTGGTTTTG 1020  
 CAGGCCAATT CTTCCCTGAC AGCATCGCTT GTTCCCGTTA AGACTGTCCG GGATAAGACC 1080  
 ATTGAGTTCC TGGCTCCGCC GAAGGGTCAG GATCGTAGSA CTATCAATAC GTTTTATGCC 1140  
 GTGGACTTGT CACAGGCTTC TGCTCCGGAG ATCCTCGGAG CGGTACCCAA TCAAAACCTG 1200  
 CATGGAGAGG AAATCCCTGA TCTGATCATT GTCTCTACTC AGGCGCTCCT CCTTGAGGCT 1260  
 60 GATCGACTGG CCACCTATCG TAGAGAGAAA AACGGGCTGA AGGTTTTGGT CGTGTTCGAG 1320  
 GAACAGGTGT TCAACGAGTT TTCGGGTGGA ACTCCCGATG CTACAGCATA CCGCCTCTTT 1380  
 GCCAAATATG TCTACGACAG ATGGAAGGCA AATGCACCTG TGGGAGAGAC CTTCCCGATG 1440  
 CAAATGCTTC TCTTCGGTGA TGGGGCTCAT GACAACAGSA AGSTCTCCGT AGCTTGGCAG 1500  
 AAACCGTATC TCCAAACAAAC GGAGTTCCTG CTGACATTCG AAGCCGTCAG TCCGACGAAC 1560  
 65 GTAAACAGTT ATGTGACGGA TGATTACTTC GGCTCTGCTG ATGATCAGCC GGCCTCGGTC 1620  
 AATATCGSTT GCGCAATTA TAATATGGCT GTAGGGCGAT TCCCGGTACG TACTCCGGCC 1680  
 GAAGTCTGCA TCGCAGTGGG CAAGACCATC CGATATGAGG AGGATCGAGA GAGTGGTGCC 1740  
 TGGCGTATTG GTGCTGTTT TGCGGCAGAC AACGGGGACA AGCAGCGAAC CGAGACTTCC 1800  
 CGTTTTGATG ATACCGTCAA GCGTTATGCT CCTGCCATCA TGCCGGTACG CGCCTTTTCAG 1860  
 70 GACGTATATC CGCATGTGAT CGAGAACGGG TTGCACAACA TTCCGGGTGC AAAGAAAAG 1920  
 ATGCTGGAAA CCCTTCAGTC GGGTATTATC CTGCTTAATT ATGCTGGTCA TGGCGGCTCT 1980  
 GCCGGATGCT CCGACGAGCA TTTGCTGACG CTCAACGATA TACACAAATT CAATTATAAG 2040  
 CATATGCCCA TTTGGATTAC TGCCACGTGC GACTTTGCCA ACTATGACAG TCAGACGACC 2100  
 TCGGCAGGGG AGGAGGTTTT CCTCCATGAG AAGAGTGGCA CTCGATCAT GTTCTCGACT 2160  
 75 ACGCGTGTCT TTTACAATAC GCAGAATGAG AAGATCAATG GTTTTATGCT TCGGCGTATG 2220

SUBSTITUTE SHEET (Rule 26) (RO/AU)

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5 TTCGAGAAAG CTAAGGATGG GCGTTATCGT ACGATGGGCG AGATTATCCG ATCGGCCAAA 2280  
CAGGGGATGC TCAGTACTGT TTTCCCGGAT TCGATCAACC AGTTGAGTTT CTTTCTGATG 2340  
GGTGATCCGT CCGTGCGTAT GAATCTTCCT ACCCACAAG TGCAATTGAC CGCAATCAAC 2400  
GGGCAGGATC CCGAAGGGCA GTATGGAAC ATTATGCTCA AGTCTTTGGA ACGGGTAGCT 2460  
CTGAAGGGTA AGGTAACCGA TGAAAAGGGG ACATTGACG AGACATTGAG TGGCAAGGTT 2520  
TTCTTGACCG TCTTCGATGG CAGAAAGAAA ATGACAGCTT TGGGAAGAGGA GGGAAACGAT 2580  
CTCTCTCTG TATATTATGA CTATCCTAAC GTGATGTATG CCGGTATTGC CGAGGTGAAA 2640  
GACGGACTCT TCGAAACTTC GTTTATCGTA CCCAAGGATG TGAACATTTC CGAGCACGAA 2700  
GGCCGGATCA ATCTTTATGC TTATAACGAG AGCACAAAGG CGGAAGCCAT GGGGGTAGAC 2760  
10 TTCTCCATCA GASTCCAAAC GGGTATTCCT GATGAGGTAA CGGAAGATAA TACCCGCCT 2820  
GAAATCATAA GCTGCTTCCT CAATGACAGT ACATTCCSAT CGGGAGATGA GGTAAATCCT 2880  
ACTCCTCTGT TTATGGCCGA AGTATTCGAC TTGAATGGAA TCAATATCAC GGGTAGCGGA 2940  
GTAGGGCATG ATATTACGCT TTGTATCGAT GGCCGTGCGG ACCTGACCTA CAACCTCAAT 3000  
GCATATTTCA CAAGTTCGGC TACGGATGCA GGTGTGGGCA CTATCTCTT CATGATACCG 3060  
15 GCTTTGGCCG AAGGAGATCA TACTGCCCGA CTGACGGTTT GGGACATTTT CAATAATGCC 3120  
GTCCATCATG ACTTTTCATT CAGAGTGGTA GATGGCATTG CTCGGGATGT GGCTGATGTG 3180  
ATTCTATTCC CGAATCCGGT ACGCGAGAGT GCTACGTTCC GAATCTTCCA CAATCGCCCC 3240  
GGAAGCGATT TGAACGTGGC CGTGGAGATC TATGACTTCA CCGGTGCTCT TGTGAACAGT 3300  
TTGCCAGTCA AGACCTATTG GTCTTCTTAC GGAGAACCTA TAGAGATCAA GTGGGATCTG 3360  
20 ACCTCCAAAT ACGGAGTGAA GATCGGAAAC GGATTCTACC TCTATCGTTG TGTGGTGAAC 3420  
TCTCCCGGAG GACAGACGGC CTCCATGGCC AAGAAATGA TCGTGGTAGG ACAA 3474

## (2) INFORMATION FOR SEQ ID NO:260

- 25 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 2883 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: circular  
30 (ii) MOLECULE TYPE: DNA (genomic)  
(iii) HYPOTHETICAL: NO  
35 (iv) ANTI-SENSE: NO  
(vi) ORIGINAL SOURCE:  
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS  
40 (ix) FEATURE:  
(A) NAME/KEY: misc feature  
(B) LOCATION 1...2883  
45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:260

ATGAAGAAAC TTTTCCCAT ATTATTACTC ATATTGTGCA TTTTGGTCGG ATGTGGAAAA 60  
AAAGAAAAAC ACTCTGTAAC TGAAATCGCC CGAGAGAAAA AGCGTATTAC TGCATTGCTG 120  
TAGCAAAAAG AACTCCCCAC TGATTCTGTT AAACAGCTTT ACGGAAACAG CGTACAGAAC 180  
50 AAGAACCCTG TGGGACAAAT GTTATTCGCG ATCGAGGTG GCAAACGGAT GCGTAATATG 240  
TCCCAATACA CAGATCGCAT GCTATATCAC CAAAAAGGTT TGAACGCTGC ATTGAATCTA 300  
AGGGACACCA TCGTAGCCGC ACAAGCATGG AATCATCTCG GAACGGATAG CCGTCGTATC 360  
GGTGCTTTGG CAGAAGCTTC GGATTATCAT TACAAGGCTC TTTCTTGAT AGAATCTTTT 420  
AGCGGAAACC AGAATAGGCC TCGGATCAAA GCCAGATCGG CGGCCCTGAA CGGCATCGGC 480  
55 AACATCAATC TTGAGTTAGG ATACCATGAT GAGGCCGAAA AGAATTCCT GAAAGCACTG 540  
CAAGGTGAGA AAGAATCGA CAGTCTCTC GGGCAAGCTA TCAACTATGC GAACCTCGGA 600  
CGTATCTATC GACAACGCAA AGAATACGAC AAGGCTCGTA CCTACTTCCT CTTGTCTCTG 660  
GAGCAGACAA ATATGGCAGA GAATCTGATG GGTATCGGAC TCTGTAGCAT CAATCTCGGA 720  
60 GAAGTAGACG AAGAAAAAGG GGATTATCAA AAGGCTTTGC AAGAGTATGC CACGGCATAC 780  
AAACTGATGG AACAGTTGTC CGATCGATGG CACTGGCTGA ATTCTGTAT CCCGATGGCA 840  
CGTATCAATC TCAACAAGG TAACGAAAGG CTCTACCAGC ATTTCAATTC TTTGGCCGAA 900  
GGGACTGCGA AAGAAATTA TTCGACTTCA CATCTGATAG AAATATACAA TCTTCAATAC 960  
GAGAATCTCG AGCGTAAAAA AGAATACAAA CAAGCCCTCG AAGCATTCTG TCTGAGCAAG 1020  
65 ACGTTGAGCG ACAGCATGTC CATTGCGCAC AAGGTCAGCA GCATACAAGA AACGCGATTG 1080  
AACTACGAAC GAAACAAGTC CCAAAAAGAG CTTGAAGAAA TACAGCAAGT AAGCAAGGCA 1140  
AAACAAGASA AATCGAAGTT TATCTCTCTG AGCACTCTTT TTGCCCTTTT CATCTCGATT 1200  
CTTTTGATT CTGTTCTGAC ATATGCATAC CGTCAGGSCA AGAAGCATAA CAAGCTGATC 1260  
AAAGAGACGG ATAACTTCTG CTCGGGCTTT TTACCCGSTA TTACACACGA ATTCGTACG 1320  
70 CCTATACCCG TCATACAAGG TTTGAATGAG AAAATGAGTT CAAGTCCTGA TCTCCAAGCA 1380  
TCGGACAGAA CCGAGCTGCA CAAGATAATA GACAGACAGA GTAGCCATAT GCTGAATTTG 1440  
GTGAACGAGC TGTGTGATAT TTGCAAGATC AGAAGCGGAG TATCCACGCC CGAATGGCGC 1500  
AATGGCGACA TCGTCTCCTT CGTACAGATT CTCATCGATT CGTTGCAACC ATACGCACAG 1560  
GCTCAAGACA TGACCTTGGA GCTACAAACC GAGAGCAAAC CTATTGTCTG GGAATTCGTC 1620  
CCCTCTTACT TAACAAAAAT CATATCCAAT CTTTGTGTTA ATGCCATCAA GTATTCTTTA 1680  
75 GCCGGAGGGA GAGTGTCAT ATCTCTGGCA AAAACCAAGA ATGAAAAAAA TCTGATCATA 1740

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5 CGCGTTGCAG ACAATGGCAT AGGAATAGAT AAAACTGATC AGGCTCATAT CTTCGACATC 1800  
 TTCTATCGAG GACAGTCCGC TACCGAAAAG CATGGATCAG GCGTCGGACT CTCGTTTACC 1860  
 AATATACTGG TCGAAAACCT TCGAGGTACG ATCAAAGTGG AAAGCCAGCC GGGGAAAAGGA 1920  
 AGTGCCTTCA CCATCAGTAT TCCTACACAA AACCAGTCCT CTTCGGCAGA GATTCTTCCT 1980  
 TGGCTACCTT CCTCCGATGA CATTTGTCATG CCTGTCCACA TCGCGCCCGA TGAATCACCG 2040  
 ACATCTCCGA TGGTAGCAGC TCTGAATCAT CGCTTCGAGG ACGAACGTCC GACCATACTG 2100  
 CTCGTCGAGG ACAATAAGGA TATCAACCTG CTGTCAAAC TACTCCTTTG CGATCGCTAC 2160  
 AATGTGCTAT CCGCCGCAAA CGGAAAAGAG GGTATAGCCC TCGCTACCGA GCATATTCCC 2220  
 GACATTATCA TTACGGATAT TATGATGCCG ATAATGGATG GGATAGAAAT GACAATCCGG 2280  
 10 ATGAAGCAAT CGCTCTGCT CTGTACATTT CCATTGTTCG CTTTGACGGC CAAGAGTACC 2340  
 GAACAGGACA GATTGGAAGG AATCAAAAGC GGTGTAGTCT CTTATCTATG CAAGCCATTC 2400  
 TCTCCGGAGG AGCTTTTGAT GCGGATCGAG CAGCTTCTGA AAGACCGTGA GTTGCTCAAG 2460  
 AAGTTCTATA TGCAAAACT CATGCTGGAT CGGAAGCCGG AGGAGGAGCC TCAACCGATA 2520  
 GATGACAGCA GTATGCAGTT TCTCCTTGCT GCCAAAGATG CAGTGTCCGG TGGAAATCAA 2580  
 15 CAAAATCCGG ATTTTTCGC TCAAGACTTG CCGGAAAAAA TGTGCATGAG TCCATCCCAA 2640  
 CTCAACAGAA AGCTCACGAG TGTCGTAGGT TGCTCCACCA TCGGCTACAT ACAGCAGATC 2700  
 AAGATAAATG TGCCCTGCAA GCTCCTTGCC GATGAGAGCA AAAACATCTC CGACATTAGC 2760  
 ATTGAGGCAAT GCTTTTCGGA TCCGGCTTAC TTCTCTCGCA CCTTCAAACG CTACATGAAC 2820  
 20 TGCTCTCCCT CCCAATATCG GCAAAACTC CTGCCATGC CGGGGAGCGA CAAGGAGACA 2880  
 GTT 2883

## (2) INFORMATION FOR SEQ ID NO:261

- 25 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1668 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 30 (D) TOPOLOGY: circular  
 (ii) MOLECULE TYPE: DNA (genomic)  
 (iii) HYPOTHETICAL: NO  
 35 (iv) ANTI-SENSE: NO  
 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS  
 40 (ix) FEATURE:  
 (A) NAME/KEY: misc feature  
 (B) LOCATION 1...1668  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:261

45 ATGAAAAAGC TTTTACAGGC TAAAGCCTTG ATTCTGGCAT TGGGACTCTT CCAACTGCC 60  
 GCAATCGCCC AAACGCAAT GCAAGCAGAC CGAACAAACG GTCAATTTGC AACAGAAGAG 120  
 ATGCAACGAG CATTCACAGA AACGAATCCC CCTGCAGGTC CTGTGCGTGC TATCGCTGAG 180  
 TACGAACGCT CTGCAGCCGT TTTGGTACGC TACCCCTTCG GTATCCCGAT GGAATTGATC 240  
 50 AAAGAGCTGG CCAAGAACGA CAAGGTGATT ACCATTGTGG CGAGTGAAAG CCAAAAAAAC 300  
 ACCGTTATTA CCCAGTACAC CCAAGCGGCT GTGAATCTCT CTAATTGCGA TTTCATCATT 360  
 GCGAAAACCT ACTCTTACTG GACACGCGAC TATACCGGTT GGTTCGCAAT GTACGATACG 420  
 AACAAAGTAG GTCTCGTGGA CTTTATTTAT AACCGCCCTC GTCTTAACGA TGATGAATTC 480  
 CCCAAATACG AAGCACAAAT TCTGGGCATC GAGATGTTTC GGATGAAGCT CAAGCAGACC 540  
 55 GGTGGCAACT ACATGACGGA CGGATATGGA TCCGCTGTGC AGTCACATAT CGCATATACG 600  
 GAGAACTCCT CTCGTCTCA AGCTCAAGTA AATCAAAAGA TGAAGACTA TCTCGGCATC 660  
 ACACATCATG ATGTGGTACA AGATCCGAAC GCGGAATATA TCAACCATGT GGAATGTTGG 720  
 GGCAAGTATT TGGCACGGA CAAAATCCTC ATCAGGAAAG TGCTGACAA TCACCCTCAG 780  
 CACCAAGCCC TGAAGATAT GGCAGCCTAC TTGCAGCAC AGACCTGCCG ATGGGGAACG 840  
 60 AAGTACGAGG TATATCGCGC TTTGGCCACC AATGAACAA CGTACACGAA CTCTCTGATT 900  
 CTGAACAACA GGGTATTGT TCTGTCAAT GGCCCGCCT CCGTGACAA CGATGCTCTG 960  
 AACGTCTATA AGACGGCAAT GCCCGGTTAC GAAATTATAG GTGTCAAAGG GGCTTCAGGA 1020  
 ACACCTTGGT TAGGAACAGA TGCCCTGCAT TGTCGTACTC ACAGGAGTAG GGATAAGGGC 1080  
 TATCTCTATA TCAAGCACTA CCCGATACTG GCGGAACAGG CAGGCCCTGA TTATAAGATC 1140  
 65 GAAGCAGATG TCGTCTCATG CGCCAATGCT ACTATCTCGC CGGTACAATG TTACTATCGT 1200  
 ATCAATGCTT CCGGTAGCTT TAAGGCTGCT GATATGACGA TGGAAATCAAC AGGTCACTAT 1260  
 ACTTATAGCT TTACAGGTCT TAACAAGATG GATAAGGTAG AATACTATAT CTCTGCCGCT 1320  
 GACAATAGTG GTCCGAAAGA GACTTATCCC TTTATCGGCG AACCTGATCC TTTCAAGTTT 1380  
 ACCTGTATGA ACGAAACCAA TACATGTACT GTGACCGGAG CTGCCAAAGC TCTTCGTGCA 1440  
 70 TGGTTCAACG CCGGTCGTTT AGAAGTGGCT GTTTCGGTAA GTTTGAATAT TGCCGGCACA 1500  
 TATCGGATAA AGCTTTTATA CACCGCAGGA GAAGAAGTGC CTGCAATGAC CAAGGAATTA 1560  
 GTAGCAGGGA CGAGTGTCTT CAGTATGGAT GTGTATTCTC AGGCTCCGGG CACATATGTT 1620  
 CTGGTTGTTG AAGGAAATGG AATCCGTGAG ACAATGAAA TTCTCAA 1668

75

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## (2) INFORMATION FOR SEQ ID NO:262

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 1284 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:  
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:  
(A) NAME/KEY: misc feature  
(B) LOCATION 1...1284
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:262

ATGAACTTT CATCTAAGAA AATCTTAGCA ATCATTGCAT TGCTGACGAT GGGACATGCT 60  
GTGCAGGCAC AGTTTGTTC GGCTCCCACC ACAGGGATTC GCATGTCTGT CACTACAACC 120  
AAGGCCGTAG GCGAAAAAT CGAATTGTTG GTTCATTCCA TAGAGAAGAA AGGCATCTGG 180  
ATCGATCTCA ATGGGGATGC CACTTACCAA CAAGGAGAGG AAATAACCGT ATTGGATGAG 240  
GCATACCACG AATACACGAT CGGGACGCAA ACCCTCACTA TCTATGGTAA TACGACCCGA 300  
TTGGGCTGTC GATCTACCGG TGCAACGGCT GTCGATGTAA CGAAAAACCC TAATCTGACC 360  
TATCTCGCAT GCCCGAAAAA TAATCTGAAA TCATTGGACT TGACGCAAAA CCCAAAGCTG 420  
CTGCGAGTTT GGTGCGACTC TAACGAAATA GAAAGTTTGG ACCTGAGTGG CAATCCGGCT 480  
TTGATCATCC TCGGCTGTGA CAGGAATAAG CTGACTGAGC TGAAGACCGA TAACAACCCC 540  
AAGTTGGCCT CTCTTTGGTG TTCTGATAAT AACCTGACGG AGTTGGAACT CAGTGCCAAT 600  
CCTCGTCTCA ATGATCTTTG GTGCTTCGGT AATCGGATCA CGAAACTCGA TCTGAGTGCC 660  
AATCCTCTAT TGGTAACACT TTGGTGCACT GACAATGAGC TTTTCGACCTT GGATCTTTCC 720  
AAGAATTCCG ACGTTGCTTA CCTTTGGTGT TCATCGAACA AACTTACATC CTTGAATCTG 780  
TCGGGGGTGA AGGGACTGAG TGTTTTGGTT TGTCAATCCA ATCAGATCGC AGGTGAAGAA 840  
ATGACGAAAG TGGTGAATGC TTTGCCACA CTATCTCCCG GCGCAGGGCG TCAGAGCAAG 900  
TTCTCGTTG TAGACCTCAA GGACACTGAT GAGAAGAATA TCTGTACCGT AAAGGATGTG 960  
GAAAAAGCTA AAAGTAAGAA CTGGCGAGTA TTGACTTCA ACGGTGATTC TGACAATATG 1020  
CTTCATACG AAGGAAGTCC GACATCGAAC TTGGCAGTAG ATGCTCCAC TGTCAGGATA 1080  
TATCCCAATC CGGTAGGAAG ATATGCGCTC GTCGAGATCC CCGAGTCTCT TTTAGGGCAG 1140  
GAAGCTGCTT TATACGATAT GAATGGGGTA AAAGTCTATA GTTTCGCGGT AGAGTCTCTT 1200  
CGTCAGAACA TTGACCTGAC ACATCTTCCC GACGGCACTT ATTTCTTCCG TCTCGATAAC 1260  
TATACCACTA AGCTCATCAA ACAG 1284

## (2) INFORMATION FOR SEQ ID NO:263

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 930 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:  
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:  
(A) NAME/KEY: misc feature  
(B) LOCATION 1...930
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:263

ATGAGAAAA CAATAATTTT CTGCTTGTG CTGCGCCTAT TTGGCTGTTT TTGGGCACAA 60  
GAAAGAGTCG ATGAAAAAGT ATTCTCCGCA GGAACAAGTA TTTTATAGGG CATCCTTGAA 120  
AAGGTGAAAG CACCGCTTAT GTATGGAGAT CGTGAGGTAT GGGGTATGGC TCGTGCGAGC 180  
GAGGATTTCT TTTTATACT TCCCGTTACG GATGACCTCA CTCCCGTGCT TTTCTATAAC 240  
CGTCTTACAA ACGAACCCCTG CTTTGTGTCA GACCAAGGAA TAACTGAGTA TTTCAAATTC 300



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5 GCTCAAGAAG GTGATTACAT TGAAGTCGAA GGAAGCTCTG TATTCATGGC GAATCTTTTG 360  
 TACTATCGTT TTTTCCCGAC AAGAATTACC TCCTATAATG CTCCCATTTGA AGGTGTTGTG 420  
 AGCAAGACGG GAAATCCTGC TTTTACAATC CCGATGCTCC CGGGGGTTTC TGATTGCATA 480  
 GAAATCTCAA ACAACCGCAA AGTCTTTCTG ACCAATCAAT TAGGGGTGTG AAACATCACT 540  
 GACGGGATGG AACCTCCGAT TATTGCCGGA GTCTCTGCTT CCTATGGATC TTCCGTCCGG 600  
 GTGTATGGTC ATGTCTCACA GCGGTGGGAC ATCATAGGCC ATTGCTATTT GGATATCTAC 660  
 CCAACCAATT GCTATCCGCT CAGCACGAAA CCCGTTGCAG GAGACGATGA GGTTTTGTG 720  
 AAACAACAAG GCAGGCAAT AGAGATCGAT AGCAACAGCC CCATAGTCCA AGTGGTCGTA 780  
 TACGATCTTG AGGGGAAAAG TGTTTTTCGC AAAAGAATGA CCGAAAACGC TTATACCCTA 840  
 10 TCCTTTAGAG CACCCATGCT CGGCTTTATG ACCATCATGA TCGAAACACA AAATTCGATT 900  
 ATCAATAAAA AACTTAATGT TACACAGCTA 930

## (2) INFORMATION FOR SEQ ID NO:264

15

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1215 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 20 (D) TOPOLOGY: circular

20

(ii) MOLECULE TYPE: DNA (genomic)

25

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

30

(v) ORIGINAL SOURCE:  
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...1215

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:264

ATGAAAAAAA CAACCATTAT TTCTTTGATT GTCTTCGGTG CTTTCTTTGC AGCCGTGGGC 60  
 CAAACCAAGG ACAATTCTTC TTACAAACCT TTTTCGAAAG AAGATATTGC CGGAGGAGTT 120  
 40 TACTCTCTCC CGACTCAAAA TCGTGCGCAG AAGGACAATG CCGAGTGGET TCTTACAGCG 180  
 ACCGTCTCCA CAACCCAGTC TGCGATACT CACTTTATCT TCGATGAGAA CAACCGCTAT 240  
 ATCGCTCGTG ACATAAAAAGC CAATGGGGTA AGAAAAATCCA CGGACTCCAT TTACTACGAT 300  
 GCCAAGCGGC GAATATCGCA TGTGGATCTT TATATCTCGT TCAGTGGCGG AGAGCCTGCA 360  
 CTCGACACCC GATTCAAGTA CACCTATGAT GACGAGGGAA AGATGACCGT GAGGGAAGTA 420  
 45 TTCATGCTGG TAATGGATCC GAATACACCT ATCTCACGCT TGGAAATATCA TTATGATGCA 480  
 CAGGSCAGAC TGACCCACTG GATTTCTTTT GCTTTCGGGG CAGAATCCCA AAAGAATACG 540  
 TATCACTATA ATGAAAAAGG TCTGTTGGTC AGCGAAGTGC TGAGCAATGC AATGGGGACA 600  
 ACCTATTGAG ACACCGGCAG AACGGGAATAC AGCTATGACG ATGCAGATAA TATGGTGAAG 660  
 GCCGAGTACT TCGTCTGTTCA GCAAGGAAAG GCATGGCAAG TACTCAAAAG AGAGGAATAC 720  
 50 ACCTATGAGG ACAATATCTG CATACAATAT TTGGCTATTA ACGGTACCGA CACAAAGGTG 780  
 TACAAGCGAG ACATCGAGAG CGATAAGTCC ATCTCCGCAA ATGTCATTGA CATTCCGTCA 840  
 ATGCCGGAAC AGACCTGGCC TAATATGTAC GGATTCAACG CAAAGCGACT GAAAGAGACT 900  
 TATTCTCTCT ACGAAGGAGA TGTGGCTACT CCTATATTCG ACTATATCTA TACGTACAAG 960  
 55 GCTCTTACCT CAATGGCAAC ACCTTCGACA GAAGCTCAGG TAGCAGTCTA TCTCAATCCG 1020  
 TCAACGGACC GGTTAGTGAT TCTGGCCAAC GGCATCACAC ATCTGAGCAT GTACGACTTG 1080  
 CAGGTAAGC TTATCCGTGA TTGTGCCTTG AGCGGCGATA AGGTGGAAAT GGGTGTGCGA 1140  
 TCTTTGACCA AAGGGACATA CCTGCTTAAA GTGAATACGG ATCAGGGAGC CTTTGTGAGA 1200  
 AAAGTCGTGA TTCGA 1215

60

## (2) INFORMATION FOR SEQ ID NO:265

65

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 454 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

70

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:  
 (A) NAME/KEY: misc\_feature

75

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(B) LOCATION 1...454

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:265

5 Phe Cys Val Met Ala Lys Val Ile Lys Thr Lys Lys Gly Leu Ala Leu  
 1 5 10 15  
 Asn Leu Lys Gly Lys Pro Leu Pro Glu Met Leu Ala Glu Pro Ala Gln  
 20 25 30  
 10 Ser Pro Thr Tyr Ala Val Val Pro Asp Asp Phe Glu Gly Val Ile Pro  
 35 40 45  
 Lys Val Thr Ala Arg Pro Gly Asp Lys Val Arg Ala Gly Ser Ala Leu  
 50 55 60  
 Met His His Lys Ala Tyr Pro Glu Met Lys Phe Thr Ser Pro Val Ser  
 65 70 75 80  
 15 Gly Glu Val Ile Ala Val Asn Arg Gly Ala Lys Arg Lys Val Leu Ser  
 85 90 95  
 Ile Glu Val Lys Pro Asp Gly Leu Asn Glu Tyr Glu Ser Phe Pro Val  
 100 105 110  
 20 Gly Asp Pro Ser Ala Leu Ser Ala Glu Gln Ile Lys Glu Leu Leu Leu  
 115 120 125  
 Ser Ser Gly Met Trp Gly Phe Ile Lys Gln Arg Pro Tyr Asp Ile Val  
 130 135 140  
 Ala Thr Pro Asp Ile Ala Pro Arg Asp Ile Tyr Ile Thr Ala Asn Phe  
 145 150 155 160  
 25 Thr Ala Pro Leu Ala Pro Asp Phe Asp Phe Ile Val Arg Gly Glu Glu  
 165 170 175  
 Arg Ala Leu Gln Thr Ala Ile Asp Ala Leu Ala Lys Leu Thr Thr Gly  
 180 185 190  
 30 Lys Val Tyr Val Gly Leu Lys Pro Gly Ser Ser Leu Gly Leu His Asn  
 195 200 205  
 Ala Glu Ile Val Glu Val His Gly Pro His Pro Ala Gly Asn Val Gly  
 210 215 220  
 Val Leu Ile Asn His Thr Lys Pro Ile Asn Arg Gly Glu Thr Val Trp  
 225 230 235 240  
 35 Thr Leu Lys Ala Thr Asp Leu Ile Val Ile Gly Arg Phe Leu Leu Thr  
 245 250 255  
 Gly Lys Ala Asp Phe Thr Arg Met Ile Ala Met Thr Gly Ser Asp Ala  
 260 265 270  
 40 Ala Ala His Gly Tyr Val Arg Ile Met Pro Gly Cys Asn Val Phe Ala  
 275 280 285  
 Ser Phe Pro Gly Arg Leu Thr Ile Lys Glu Ser His Glu Arg Val Ile  
 290 295 300  
 Asp Gly Asn Val Leu Thr Gly Lys Lys Leu Cys Glu Lys Glu Pro Phe  
 305 310 315 320  
 45 Leu Ser Ala Arg Cys Asp Gln Ile Thr Val Ile Pro Glu Gly Asp Asp  
 325 330 335  
 Val Asp Glu Leu Phe Gly Trp Ala Ala Pro Arg Leu Asp Gln Tyr Ser  
 340 345 350  
 50 Met Ser Arg Ala Tyr Phe Ser Trp Leu Gln Gly Lys Asn Lys Glu Tyr  
 355 360 365  
 Val Leu Asp Ala Arg Ile Lys Gly Gly Glu Arg Ala Met Ile Met Ser  
 370 375 380  
 Asn Glu Tyr Asp Arg Val Phe Pro Met Asp Ile Tyr Pro Glu Tyr Leu  
 385 390 395 400  
 55 Leu Lys Ala Ile Ile Ala Phe Asp Ile Asp Lys Met Glu Asp Leu Gly  
 405 410 415  
 Ile Tyr Glu Val Ala Pro Glu Asp Phe Ala Thr Cys Glu Phe Val Asp  
 420 425 430  
 60 Thr Ser Lys Ile Glu Leu Gln Arg Ile Val Arg Glu Gly Leu Asp Met  
 435 440 445  
 Leu Tyr Lys Glu Met Asn  
 450

(2) INFORMATION FOR SEQ ID NO:266

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 201 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

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(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

(A) NAME/KEY: misc\_feature

(B) LOCATION 1...201

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:266

10 Glu Leu Ser Lys Cys Tyr Met Asp Lys Val Ser Tyr Ala Leu Gly Leu  
 1 5 10 15  
 Ser Ile Gly Asn Asn Phe Lys Ser Ser Gly Ile Asp Ser Val Val Met  
 20 25 30  
 Asp Asp Phe Met Gln Gly Leu Ser Asp Val Leu Glu Glu Lys Ala Pro  
 35 40 45  
 15 Gln Leu Ser Tyr Asp Glu Ala Lys Arg Glu Ile Glu Ala Tyr Phe Met  
 50 55 60  
 Asp Leu Gln Gln Lys Ala Val Lys Leu Asn Lys Glu Ala Gly Glu Glu  
 65 70 75 80  
 Phe Leu Lys Ile Asn Ala His Lys Glu Gly Val Thr Thr Leu Pro Ser  
 85 90 95  
 20 Gly Leu Gln Tyr Glu Val Ile Lys Met Gly Glu Gly Pro Lys Pro Thr  
 100 105 110  
 Leu Ser Asp Thr Val Thr Cys His Tyr His Gly Thr Leu Ile Asn Gly  
 115 120 125  
 25 Ile Val Phe Asp Ser Ser Met Asp Arg Gly Glu Pro Ala Ser Phe Pro  
 130 135 140  
 Leu Arg Gly Val Ile Ala Gly Trp Thr Glu Ile Leu Gln Leu Met Pro  
 145 150 155 160  
 Val Gly Ser Lys Trp Lys Val Thr Ile Pro Ser Asp Leu Ala Tyr Gly  
 165 170 175  
 30 Asp Arg Gly Ala Gly Glu His Ile Lys Pro Gly Ser Thr Leu Ile Phe  
 180 185 190  
 Ile Ile Glu Leu Leu Ser Ile Asn Lys  
 195 200

(2) INFORMATION FOR SEQ ID NO:267

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 279 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

(A) NAME/KEY: misc\_feature

(B) LOCATION 1...279

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:267

55 Gln Lys Asn Lys Arg Lys Met Lys Lys Ala Leu Leu Ile Gly Ala Ala  
 1 5 10 15  
 Leu Leu Gly Ala Val Ser Phe Ala Ser Ala Gln Ser Leu Ser Thr Ile  
 20 25 30  
 60 Lys Val Gln Asn Asn Ser Val Gln Gln Pro Arg Glu Glu Ala Thr Ile  
 35 40 45  
 Gln Val Cys Gly Glu Leu Ala Glu Gln Val Asp Cys Ile Gly Thr Gly  
 50 55 60  
 65 Asn Ser Ala Ile Ile Ala Ala Ala Lys Phe Glu Ser Asp Asp Leu  
 65 70 75 80  
 Glu Ser Tyr Val Gly Trp Glu Ile Met Ser Val Asp Phe Phe Pro Gly  
 85 90 95  
 Tyr Lys Ala Cys Lys Tyr Thr Ser Ala Val Trp Ala Asp Asp Met Thr  
 100 105 110  
 70 Ile Leu Gly Gln Ser Glu Asp Ser Asp Pro Glu Met Gln Thr Ile Asn  
 115 120 125  
 Asn Leu Ala Leu Lys Thr Ser Val Lys Ile Glu Ala Gly Lys Asn Tyr  
 130 135 140  
 75 Ile Val Gly Tyr Ile Ala Asn Thr Ala Gly Gly His Pro Ile Gly Cys  
 145 150 155 160

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Asp Gln Gly Pro Ala Val Asp Gly Tyr Gly Asp Leu Val Ser Ile Ser  
 165 170 175  
 Glu Asp Gly Gly Ala Thr Phe Pro Pro Phe Glu Ser Leu His Gln Ala  
 180 185 190  
 5 Val Pro Thr Leu Asn Tyr Asn Ile Tyr Val Val Val His Leu Lys Lys  
 195 200 205  
 Gly Glu Gly Val Glu Ala Val Leu Thr Asn Asp Lys Ala Asn Ala Tyr  
 210 215 220  
 10 Val Gln Asn Gly Val Ile Tyr Val Ala Gly Ala Asn Gly Arg Gln Val  
 225 230 235 240  
 Ser Leu Phe Asp Met Asn Gly Lys Val Val Tyr Thr Gly Val Ser Glu  
 245 250 255  
 Thr Ile Ala Ala Pro Gln Lys Gly Met Tyr Ile Leu Arg Val Gly Ala  
 260 265 270  
 15 Lys Ser Ile Lys Leu Ala Ile  
 275

(2) INFORMATION FOR SEQ ID NO:268

- 20 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 157 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
 25 (ii) MOLECULE TYPE: protein  
 (iii) HYPOTHETICAL: YES  
 (vi) ORIGINAL SOURCE:  
 30 (A) ORGANISM: Porphyromonas gingivalis  
 (ix) FEATURE:  
 (A) NAME/KEY: misc feature  
 (B) LOCATION 1...157  
 35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:268

Arg Unk Phe Leu Pro Glu Lys Ala Leu Tyr Ile Gly Cys Arg Val Glu  
 1 5 10 15  
 40 Thr Gln Glu Gly His Ala Val Gly Phe Gly Leu Asp Asp Gly Pro Ala  
 20 25 30  
 Met Lys Gly Lys Gly Asp Leu Val Gly Ser Tyr Leu Pro Gly Ala Ala  
 35 40 45  
 45 Pro Met Pro Phe Val Pro Leu Ser Asp Ile Pro Ala Arg Ser Met Asp  
 50 55 60  
 Ala Asn Phe Tyr Ile Tyr Ser Arg Ile Ser Leu Gly Ser Gly Thr Gln  
 65 70 75 80  
 Asp Val Leu Gln His Arg Met Lys Val Tyr Pro Asn Pro Ala Thr Thr  
 85 90 95  
 50 Glu Leu His Val Glu Ala Leu Ser Ala Trp Val Gly Glu Gln Ala Ala  
 100 105 110  
 Val Tyr Asp Met Arg Gly Arg Arg Val Ser Ala Arg Thr Val Asp Ser  
 115 120 125  
 55 Glu Lys Leu Cys Ile Asp Ile Ala Ser Leu Pro Val Gly Val Tyr Met  
 130 135 140  
 Leu Arg Ile Gly Ser Tyr Ser Ala Lys Phe Glu Lys Arg  
 145 150 155

(2) INFORMATION FOR SEQ ID NO:269

- 60 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 562 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
 65 (ii) MOLECULE TYPE: protein  
 (iii) HYPOTHETICAL: YES  
 70 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Porphyromonas gingivalis  
 (ix) FEATURE:  
 (A) NAME/KEY: misc feature  
 75 (B) LOCATION 1...562

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:269

5	Thr	Arg	Asn	Val	Ser	Leu	Ile	Lys	Met	Pro	Arg	Ile	Met	Lys	Leu	Lys
	1				5					10				15		
	Ile	Ala	Leu	Arg	Leu	Leu	Leu	Ala	Thr	Phe	Ala	Ile	Val	Leu	Phe	Ser
			20						25					30		
	Pro	Leu	Ala	Lys	Ala	Gln	Met	Asp	Ile	Gly	Gly	Asp	Asp	Val	Leu	Ile
			35					40					45			
10	Glu	Thr	Met	Ser	Thr	Leu	Ser	Gly	Tyr	Ser	Glu	Asp	Phe	Tyr	Tyr	Lys
		50					55					60				
	Met	Ala	Val	Ala	Asp	Asn	Gly	Trp	Ile	Tyr	Val	Met	Leu	Asp	Phe	Ser
		65				70					75				80	
	Arg	Ile	Tyr	Phe	Asp	Asp	Val	Arg	Leu	Tyr	Arg	Ser	Lys	Asp	Gly	Gly
15					85					90				95		
	Ala	Thr	Tyr	Gln	Lys	Leu	Gly	Ser	Leu	Gly	Ser	Leu	Val	Pro	Tyr	Asp
				100					105					110		
	Phe	Asp	Val	Ser	His	Cys	Asp	Phe	Ile	Val	Thr	Gly	Lys	Asp	Glu	Asp
			115						120				125			
20	Asp	Ile	Asn	Val	Trp	Thr	Val	Met	Thr	Ala	Phe	Glu	Tyr	Val	Gly	Gly
		130					135						140			
	Thr	Ile	Gly	Asn	Gly	Val	Leu	Met	His	Arg	His	Asp	Ala	Asp	Ile	
		145				150					155				160	
25	Asn	Asn	Thr	Glu	Cys	Val	Tyr	Lys	Lys	Asp	Phe	Pro	Asn	Asn	Arg	Leu
					165					170					175	
	Met	Gly	Val	Ala	Ile	Ala	Ser	Asn	Tyr	Arg	Ala	Pro	Ser	Pro	Tyr	Gly
				180					185					190		
	Leu	Gly	Gly	Asp	Pro	Phe	Ala	Leu	Ala	Val	Ala	Val	Ser	Gly	Ser	Gly
			195					200					205			
30	Ser	Asp	His	Ser	Phe	Leu	Asp	Tyr	Ile	Phe	Ser	Leu	Asp	Gly	Gly	Val
		210					215						220			
	His	Phe	Glu	Gln	Lys	Arg	Ile	Tyr	Thr	Arg	Pro	Gln	Lys	Leu	Thr	Ile
					230						235				240	
35	Asn	Arg	Val	Asp	Leu	Ser	Leu	Gly	Ser	Thr	Ser	Pro	Ser	Leu	Gly	Phe
					245					250					255	
	Asn	Thr	Trp	Pro	Leu	Met	Gly	Val	Val	Phe	Glu	Met	Asn	Lys	Asn	Leu
				260					265					270		
	Asp	Gly	Phe	Asp	Ile	Gly	Phe	Ile	Ser	Asn	Phe	Val	Asp	Tyr	Asp	Pro
			275					280					285			
40	Arg	Tyr	Ala	Trp	Ser	Glu	Pro	Ile	Ile	Ile	Glu	Glu	Asp	Cys	Gly	Trp
		290					295						300			
	Thr	Asp	Phe	Asn	Pro	Leu	Gly	Ala	Leu	Ser	Ile	Glu	Ile	Gln	Met	Met
						310					315				320	
45	Leu	Asp	Asp	Asn	Ser	Asp	Asn	Thr	Val	Gly	Gly	Glu	Arg	Ser	His	Asn
					325					330					335	
	Phe	Leu	Ile	Thr	Tyr	Pro	Gly	His	Tyr	Val	Tyr	Pro	Lys	Gln	Ser	Phe
				340					345					350		
	Asn	Tyr	Ser	Pro	Gly	His	Thr	Pro	Thr	Lys	Lys	Asp	Leu	Val	Phe	Lys
			355					360					365			
50	His	Cys	Ile	Gly	Ile	Pro	Ala	Leu	Ala	Tyr	Asp	Lys	Glu	Gly	Asp	Arg
			370				375					380				
	Tyr	Leu	Thr	Thr	Phe	Gln	Asp	His	Asn	Leu	Met	Arg	Tyr	Arg	Trp	Ile
					390						395				400	
55	Lys	Tyr	Asp	Asp	Ile	Asn	Ser	Phe	Tyr	Gly	Trp	Ser	Trp	Pro	Tyr	Val
					405					410					415	
	Tyr	Ala	Lys	Glu	Ala	Lys	Asp	Lys	Lys	Arg	Arg	Arg	Pro	Gln	Val	Ala
				420					425					430		
	Leu	Asn	Pro	Thr	Asn	Gly	Lys	Ala	Cys	Trp	Val	Trp	His	Thr	Arg	Lys
			435					440					445			
60	Ser	Pro	Tyr	Asp	Glu	Thr	Lys	Pro	His	Pro	Thr	Pro	Val	Ile	Ile	Lys
			450				455					460				
	His	Phe	Leu	Trp	Ser	Asp	Thr	Glu	Trp	Val	His	Ala	Leu	Asp	Val	Gly
					470						475				480	
65	Asp	Val	Leu	Gln	Lys	Glu	Gly	Ser	Met	Lys	Leu	Tyr	Pro	Asn	Pro	Ala
					485					490					495	
	Lys	Glu	Tyr	Val	Leu	Ile	Asn	Leu	Pro	Lys	Glu	Gly	Gly	His	Glu	Ala
				500					505					510		
	Val	Val	Tyr	Asp	Met	Gln	Gly	Arg	Ile	Val	Glu	Lys	Val	Ser	Phe	Ser
				515				520					525			
70	Gly	Lys	Glu	Tyr	Lys	Leu	Asn	Val	Gln	Tyr	Leu	Ser	Lys	Gly	Thr	Tyr
			530				535					540				
	Met	Leu	Lys	Val	Val	Ala	Asp	Thr	Glu	Tyr	Phe	Val	Glu	Lys	Ile	Ile
					550						555				560	
75	Val	Glu														

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## (2) INFORMATION FOR SEQ ID NO:270

5

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 391 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

10

- (ii) MOLECULE TYPE: protein

- (iii) HYPOTHETICAL: YES

15

- (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Porphyromonas gingivalis

- (ix) FEATURE:  
 (A) NAME/KEY: misc feature  
 (B) LOCATION 1...391

20

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:270

Gln Met Lys Arg Leu Leu Pro Phe Leu Leu Leu Ala Gly Leu Val Ala  
 1 5 10 15  
 Val Gly Asn Val Ser Ala Gln Ser Pro Arg Ile Pro Gln Val Asp Val  
 20 25 30  
 His Thr Arg Ile Ala Arg Asn Ala Arg Tyr Arg Leu Asp Lys Ile Ser  
 35 40 45  
 Val Pro Asp Ser Arg Gln Ile Phe Asp Tyr Phe Tyr Lys Glu Glu Thr  
 50 55 60  
 Ile Pro Thr Lys Ile Gln Thr Thr Thr Gly Gly Ala Ile Thr Ser Ile  
 65 70 75 80  
 Asp Ser Leu Phe Tyr Glu Asp Asp Arg Leu Val Gln Val Arg Tyr Phe  
 85 90 95  
 Asp Asn Asn Leu Glu Leu Lys Gln Ala Glu Lys Tyr Val Tyr Asp Gly  
 100 105 110  
 Ser Lys Leu Val Leu Arg Glu Ile Arg Lys Ser Pro Thr Asp Glu Thr  
 115 120 125  
 Pro Ile Lys Lys Val Ser Tyr His Tyr Leu Cys Gly Ser Asp Met Pro  
 130 135 140  
 Phe Glu Ile Thr Thr Glu Met Ser Asp Gly Tyr Phe Glu Ser His Thr  
 145 150 155 160  
 Leu Asn Tyr Leu Asn Gly Lys Ile Ala Arg Ile Asp Ile Met Thr Gln  
 165 170 175  
 Gln Asn Pro Ser Ala Glu Leu Ile Glu Thr Gly Arg Met Val Tyr Glu  
 180 185 190  
 Phe Asp Ala Asn Asn Asp Ala Val Leu Leu Arg Asp Ser Val Phe Leu  
 195 200 205  
 Pro Leu Gln Asn Lys Trp Val Glu Met Phe Thr His Arg Tyr Thr Tyr  
 210 215 220  
 Asp Asn Lys His Asn Cys Ile Arg Trp Glu Gln Asp Glu Phe Gly Thr  
 225 230 235 240  
 Leu Thr Leu Ala Asn Asn Phe Glu Tyr Asp Thr Thr Ile Pro Leu Ser  
 245 250 255  
 Ser Val Leu Phe Pro Thr His Glu Glu Phe Phe Arg Pro Leu Leu Pro  
 260 265 270  
 Asn Phe Met Lys His Met Arg Thr Lys Gln Thr Tyr Phe Asn Asn Ser  
 275 280 285  
 Gly Glu Gly Leu Ser Glu Val Cys Asp Tyr Asn Tyr Phe Tyr Thr Asp  
 290 295 300  
 Met Gln Gly Asn Ala Leu Thr Asp Val Ala Val Asn Glu Ser Ile Lys  
 305 310 315 320  
 Ile Tyr Pro Arg Pro Ala Thr Asp Phe Leu Arg Ile Glu Gly Ser Gln  
 325 330 335  
 Leu Leu Arg Leu Ser Leu Phe Asp Met Asn Gly Lys Leu Ile Arg Ala  
 340 345 350  
 Thr Glu Leu Thr Gly Asp Leu Ala Ile Ile Gly Val Ala Ser Leu Pro  
 355 360 365  
 Arg Gly Thr Tyr Ile Ala Glu Ile Thr Ala Ala Asn Ser Lys Thr Ile  
 370 375 380  
 Arg Ala Lys Val Ser Leu Arg  
 385 390

## (2) INFORMATION FOR SEQ ID NO:271

75

- (i) SEQUENCE CHARACTERISTICS:

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(A) LENGTH: 428 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

5 (ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

10 (vi) ORIGINAL SOURCE:

(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

(A) NAME/KEY: misc\_feature

(B) LOCATION 1...428

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:271

Lys Arg Asn Pro Leu Pro Leu Thr Ala Ser Asn Arg Lys Ile Phe Ile  
 1 5 10 15  
 20 Lys Met Arg Gln His Leu Ser Leu Phe Pro Phe Ile Leu Phe Leu Leu  
 20 25 30  
 Leu Ala Phe Ser Tyr Val Gly Cys Arg Thr Val Arg Gln Thr Pro Lys  
 35 40 45  
 25 Gln Ser Glu Arg Tyr Val Val Val Leu Ser Leu Asp Gly Phe Arg Pro  
 50 55 60  
 Asp Tyr Thr Asp Arg Ala Arg Thr Pro Ala Leu Asp Arg Met Ala Gln  
 65 70 75 80  
 Glu Gly Leu Ser Gly Ser Leu Gln Pro Cys Phe Pro Ser Leu Thr Phe  
 85 90 95  
 30 Pro Asn His Tyr Ser Met Ala Thr Gly Leu Tyr Pro Asp His His Gly  
 100 105 110  
 Ile Val Ala Asn Glu Phe Val Asp Ser Leu Leu Gly Ile Phe Arg Ile  
 115 120 125  
 35 Ser Asp Arg Lys Ala Val Glu Thr Pro Gly Phe Trp Gly Gly Glu Pro  
 130 135 140  
 Val Trp Asn Thr Ala Ala Arg Gln Gly Ile Arg Thr Gly Val Tyr Phe  
 145 150 155 160  
 Trp Val Gly Ser Glu Thr Ala Val Asn Gly Asn Arg Pro Trp Arg Trp  
 165 170 175  
 40 Lys Lys Phe Ser Ser Thr Val Pro Phe Arg Asp Arg Ala Asp Ser Val  
 180 185 190  
 Ile Ala Trp Leu Gly Leu Pro Glu Lys Glu Arg Pro Arg Leu Leu Met  
 195 200 205  
 45 Trp Tyr Ile Glu Glu Pro Asp Met Ile Gly His Ser Gln Thr Pro Glu  
 210 215 220  
 Ser Pro Leu Thr Leu Ala Met Val Glu Arg Leu Asp Ser Val Val Gly  
 225 230 235 240  
 Tyr Phe Arg Lys Arg Leu Asp Ser Leu Pro Ile Ala Ala Gln Thr Asp  
 245 250 255  
 50 Phe Ile Ile Val Ser Asp His Gly Met Ala Thr Tyr Glu Asn Glu Lys  
 260 265 270  
 Cys Val Asn Leu Ser His Tyr Leu Pro Ala Asp Ser Phe Leu Tyr Met  
 275 280 285  
 55 Ala Thr Gly Ala Phe Thr His Leu Tyr Pro Lys Pro Ser Tyr Thr Glu  
 290 295 300  
 Arg Ala Tyr Glu Ile Leu Arg Ala Ile Pro His Ile Ser Val Tyr Arg  
 305 310 315 320  
 Lys Gly Glu Val Pro Lys Arg Leu Arg Cys Gly Thr Asn Pro Arg Leu  
 325 330 335  
 60 Gly Glu Leu Val Val Ile Pro Asp Ile Gly Ser Thr Val Phe Phe Ala  
 340 345 350  
 Ile Asn Glu Asp Val Arg Pro Gly Ala Ala His Gly Tyr Asp Asn Gln  
 355 360 365  
 65 Ala Pro Glu Met Arg Ala Leu Leu Arg Ala Val Gly Pro Asp Phe Arg  
 370 375 380  
 Pro Gly Ser Arg Val Glu Asn Leu Pro Asn Ile Thr Ile Tyr Pro Leu  
 385 390 395 400  
 Ile Cys Arg Leu Leu Gly Ile Glu Pro Ala Pro Asn Asp Ala Asp Glu  
 405 410 415  
 70 Thr Leu Leu Asn Gly Leu Ile Arg Asp Lys Arg Pro  
 420 425

(2) INFORMATION FOR SEQ ID NO:272

75

(i) SEQUENCE CHARACTERISTICS:

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(A) LENGTH: 282 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

5 (ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

10 (vi) ORIGINAL SOURCE:

(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

(A) NAME/KEY: misc\_feature

(B) LOCATION 1...282

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:272

Leu Ser Arg Gly Val Phe Pro Leu Met Tyr Gly Arg Arg Gly Ser Ile  
 1 5 10 15  
 20 Arg Ala Ser Ser Gly His Arg Asp Lys Ile Phe Lys Asn Thr Ile Ile  
 20 25 30  
 Arg Phe Ile Thr Met Lys Val Gly Leu Phe Ile Pro Cys Tyr Val Asn  
 35 40 45  
 25 Ala Val Tyr Pro Glu Val Gly Ile Ala Thr Tyr Lys Leu Leu Lys Ser  
 50 55 60  
 Leu Asp Ile Asp Val Asp Tyr Pro Met Asp Gln Thr Cys Cys Gly Gln  
 65 70 75 80  
 Pro Met Ala Asn Ala Gly Phe Glu Gln Lys Ala Gln Lys Leu Ala Leu  
 85 90 95  
 30 Arg Phe Glu Glu Leu Phe Glu Ser Tyr Asp Val Val Val Gly Pro Ser  
 100 105 110  
 Ala Ser Cys Val Ala Phe Val Lys Glu Asn Tyr Asp His Ile Leu Arg  
 115 120 125  
 35 Pro Thr Gly His Val Cys Lys Ser Ala Ala Lys Val Arg Asp Ile Cys  
 130 135 140  
 Glu Phe Leu His Asp Asp Leu Lys Ile Thr Ser Leu Pro Ser Arg Phe  
 145 150 155 160  
 Ala His Lys Val Ser Leu His Asn Ser Cys His Gly Val Arg Glu Leu  
 165 170 175  
 40 His Leu Ser Thr Pro Ser Glu Val His Arg Pro Tyr His Asn Lys Val  
 180 185 190  
 Arg Arg Leu Leu Glu Met Val Gln Gly Ile Glu Val Phe Glu Pro Lys  
 195 200 205  
 45 Arg Ile Asp Glu Cys Cys Gly Phe Gly Gly Met Tyr Ser Val Glu Glu  
 210 215 220  
 Pro Glu Val Ser Thr Cys Met Gly His Asp Lys Val Leu Asp His Ile  
 225 230 235 240  
 Ser Thr Gly Ala Glu Tyr Ile Thr Gly Pro Asp Ser Ser Cys Leu Met  
 245 250 255  
 50 His Met Gln Gly Val Ile Asp Arg Glu Lys Leu Pro Ile Lys Thr Ile  
 260 265 270  
 His Ala Val Glu Ile Leu Ala Ala Asn Leu  
 275 280

55 (2) INFORMATION FOR SEQ ID NO:273

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 251 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

60

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

65

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

(A) NAME/KEY: misc\_feature

(B) LOCATION 1...251

70

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:273

75

Pro Leu Lys Lys Arg Met Asp Ile Val Ser Met Ala Asp Lys Ala Leu



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```

1      5      10      15
Val Val Glu Met Arg Asp Val Thr Leu Cys Gln Glu Glu Asn Val Ile
20      25      30
Phe Gln Asn Leu Asn Leu Thr Leu Ser Ala Gly Asp Phe Val Tyr Leu
35      40      45
Ile Gly Ser Val Gly Ser Gly Lys Ser Thr Leu Leu Lys Ala Leu Tyr
50      55      60
Ala Glu Val Pro Ile Ser Ala Gly Tyr Ala Arg Val Ile Asp Tyr Asp
65      70      75      80
Leu Ala Lys Leu Lys Arg Lys Gln Leu Pro Tyr Leu Arg Arg Asn Leu
85      90      95
Gly Ile Val Phe Gln Asp Phe Gln Leu Leu Asn Gly Arg Thr Val Ala
100      105      110
Glu Asn Leu Asp Phe Val Leu Arg Ala Thr Asp Trp Lys Asn Arg Ala
115      120      125
Asp Arg Glu Gln Arg Ile Glu Glu Val Leu Thr Arg Val Gly Met Ser
130      135      140
Arg Lys Ala Tyr Lys Arg Pro His Glu Leu Ser Gly Gly Glu Gln Gln
145      150      155      160
Arg Val Gly Ile Ala Arg Ala Leu Leu Ala Lys Pro Ala Leu Ile Leu
165      170      175
Ala Asp Glu Pro Thr Gly Asn Leu Asp Ser Val Thr Gly Leu Gln Ile
180      185      190
Ala Ser Leu Leu Tyr Glu Ile Ser Lys Gln Gly Thr Ala Val Leu Met
195      200      205
Ser Thr His Asn Ser Ser Leu Leu Ser His Leu Pro Ala Arg Thr Leu
210      215      220
Ala Val Arg Lys Asn Gly Asp Ala Ser Ser Leu Val Glu Leu Ser Ala
225      230      235      240
Asp Ala Val Ser Arg Lys Asn Thr Glu Ile Asp
245

```

(2) INFORMATION FOR SEQ ID NO:274

- 35 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 238 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear
- 40 (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- 45 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Porphyromonas gingivalis
- (ix) FEATURE:  
 (A) NAME/KEY: misc feature  
 (B) LOCATION 1...238
- 50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:274

```

Thr Arg His Cys Pro Ala Cys Arg Ser Ser Phe His Leu Ile Lys Thr
1      5      10      15
Ser Lys Thr Met Ile Glu Ile Ser Asn Leu Thr Lys Val Phe Arg Thr
20      25      30
Glu Glu Ile Glu Thr Val Ala Leu Asp Gly Val Ser Leu Lys Val Asp
35      40      45
Lys Gly Glu Phe Ile Ala Ile Met Gly Pro Ser Gly Cys Gly Lys Ser
50      55      60
Thr Leu Leu Asn Ile Leu Gly Leu Leu Asp Asn Pro Thr Ser Gly Ile
65      70      75      80
Tyr Lys Leu Asp Gly Ala Glu Val Gly Asn Leu Arg Glu Lys Asp Arg
85      90      95
Thr Ala Val Arg Lys Gly Asn Ile Gly Phe Val Phe Gln Ser Phe Asn
100      105      110
Leu Ile Glu Glu Met Thr Val Ser Glu Asn Val Glu Leu Pro Leu Val
115      120      125
Tyr Leu Gly Val Lys Ala Ser Glu Arg Lys Glu Arg Val Glu Glu Ala
130      135      140
Leu Arg Lys Met Ser Ile Ser His Arg Ala Gly His Phe Pro Asn Gln
145      150      155      160
Leu Ser Gly Gly Gln Gln Gln Arg Val Ala Ile Ala Arg Ala Val Val
165      170      175
Ala Asn Pro Lys Leu Ile Leu Ala Asp Glu Pro Thr Gly Asn Leu Asp

```

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180 185 190  
 Ser Lys Asn Gly Ala Asp Val Met Glu Leu Leu Arg Gly Leu Asn Arg  
 195 200 205  
 5 Glu Gly Ala Thr Ile Val Met Val Thr His Ser Glu His Asp Ala Arg  
 210 215 220  
 Ser Ala Gly Arg Ile Ile Asn Leu Phe Asp Gly Lys Ile Arg  
 225 230 235

## (2) INFORMATION FOR SEQ ID NO:275

10

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 604 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

15

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

20

- (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Porphyromonas gingivalis

25

- (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...604

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:275

30 Ser Thr Glu Thr Asn Ser Lys Ser Glu Met Lys Glu Phe Phe Lys Met  
 1 5 10 15  
 Phe Phe Ala Ser Ile Leu Gly Val Ile Thr Ala Gly Ile Ile Leu Phe  
 20 25 30  
 Cys Ile Phe Leu Phe Ile Phe Phe Gly Ile Val Ala Gly Ile Ala Ser  
 35 35 40 45  
 Lys Ala Thr Gly Gly Thr Ile Pro Lys Ile Glu Ala Asn Ser Ile Leu  
 50 55 60  
 His Ile Unk Asn Ser Ser Phe Pro Glu Ile Val Ser Ala Asn Pro Trp  
 65 70 75 80  
 40 Ser Met Leu Thr Gly Lys Asp Glu Ser Val Ser Leu Ser Gln Ala Val  
 85 90 95  
 Glu Ala Ile Gly Gln Ala Lys Asn Asn Pro Asn Ile Thr Gly Ile Phe  
 100 105 110  
 Leu Asp Leu Asp Asn Leu Ser Val Gly Met Ala Ser Ala Glu Glu Leu  
 115 120 125  
 45 Arg Arg Ala Leu Gln Asp Phe Lys Met Ser Gly Lys Phe Val Val Ser  
 130 135 140  
 Tyr Ala Asp Arg Tyr Thr Gln Lys Gly Tyr Tyr Leu Ser Ser Ile Ala  
 145 150 155 160  
 50 Asp Lys Leu Tyr Leu Asn Pro Lys Gly Met Leu Gly Leu Ile Gly Ile  
 165 170 175  
 Ala Thr Gln Thr Met Phe Tyr Lys Asp Ala Leu Asp Lys Phe Gly Val  
 180 185 190  
 Lys Met Glu Ile Phe Lys Val Gly Thr Tyr Lys Ala Ala Val Glu Pro  
 195 200 205  
 55 Phe Met Leu Asn Arg Met Ser Asp Ala Asn Arg Glu Gln Ile Thr Thr  
 210 215 220  
 Tyr Ile Asn Gly Leu Trp Asp Lys Ile Thr Ser Asp Ile Ala Glu Ser  
 225 230 235 240  
 60 Arg Lys Thr Ala Met Asp Ser Val Lys Met Phe Ala Asp Lys Gly Glu  
 245 250 255  
 Met Phe Gly Leu Ala Glu Lys Ala Val Glu Met Lys Leu Val Asp Glu  
 260 265 270  
 Leu Ala Tyr Arg Thr Asp Val Glu Lys Glu Leu Lys Lys Met Ser Gln  
 275 280 285  
 65 Arg Gly Glu Lys Asp Glu Leu Arg Phe Val Ser Leu Ser Gln Val Leu  
 290 295 300  
 Ala Asn Gly Pro Met Asn Lys Thr Lys Gly Ser Arg Ile Ala Val Leu  
 305 310 315 320  
 70 Phe Ala Glu Gly Glu Ile Thr Glu Glu Ile Ile Lys Lys Pro Phe Asp  
 325 330 335  
 Thr Asp Gly Ser Ser Ile Thr Gln Glu Leu Ala Lys Glu Ile Lys Ala  
 340 345 350  
 Ala Ala Asp Asp Asp Asp Ile Lys Ala Val Val Leu Arg Val Asn Ser  
 355 360 365  
 75 Pro Gly Gly Ser Ala Phe Thr Ser Glu Gln Ile Trp Lys Gln Val Ala

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370 375 380  
 Asp Leu Lys Ala Lys Lys Pro Ile Val Val Ser Met Gly Asp Val Ala  
 385 390 395 400  
 Ala Ser Gly Gly Tyr Tyr Ile Ala Cys Ala Ala Asn Ser Ile Val Ala  
 405 410 415  
 Glu His Thr Thr Leu Thr Gly Ser Ile Gly Ile Phe Gly Met Phe Pro  
 420 425 430  
 Asn Phe Ala Gly Val Ala Lys Lys Ile Gly Val Asn Met Asp Val Val  
 435 440 445  
 10 Gln Thr Ser Lys Tyr Ala Asp Leu Gly Asn Thr Phe Ala Pro Met Thr  
 450 455 460  
 Val Glu Asp Arg Ala Leu Ile Gln Arg Tyr Ile Glu Gln Gly Tyr Asp  
 465 470 475 480  
 15 Leu Phe Leu Thr Arg Val Ser Glu Gly Arg Asn Arg Thr Lys Ala Gln  
 485 490 495  
 Ile Asp Ser Ile Ala Gln Gly Arg Val Trp Leu Gly Asp Lys Ala Leu  
 500 505 510  
 Ala Leu Gly Leu Val Asp Glu Leu Gly Gly Leu Asp Thr Ala Ile Lys  
 515 520 525  
 20 Arg Ala Ala Lys Leu Ala Gln Leu Gly Gly Asn Tyr Ser Ile Glu Tyr  
 530 535 540  
 Gly Lys Thr Lys Arg Asn Phe Phe Glu Glu Leu Leu Ser Ser Ser Ala  
 545 550 555 560  
 25 Ala Asp Met Lys Ser Ala Ile Leu Ser Thr Ile Leu Ser Asp Pro Glu  
 565 570 575  
 Ile Glu Val Leu Arg Glu Leu Arg Ser Met Pro Pro Arg Pro Ser Gly  
 580 585 590  
 Ile Gln Ala Arg Leu Pro Tyr Tyr Phe Met Pro Tyr  
 595 600

(2) INFORMATION FOR SEQ ID NO:276

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 324 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

(A) NAME/KEY: misc\_feature

(B) LOCATION: 1...324

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:276

50 Leu Thr Leu Phe Cys Cys Asn Tyr Phe Lys Gln Met Arg Ala Asn Ile  
 1 5 10 15  
 Trp Gln Ile Leu Ser Val Ser Val Leu Phe Phe Gly Thr Ala Ile  
 20 25 30  
 55 Gly Gln Ala Gln Ser Arg Asn Arg Thr Tyr Glu Ala Tyr Val Lys Gln  
 35 40 45  
 Tyr Ala Asp Glu Ala Ile Arg Gln Met Ser Arg Tyr Asn Ile Pro Ala  
 50 55 60  
 60 Ser Ile Thr Ile Ala Gln Ala Leu Val Glu Thr Gly Ala Gly Ala Ser  
 65 70 75 80  
 Thr Leu Ala Ser Val His Asn Asn His Phe Gly Ile Lys Cys His Lys  
 85 90 95  
 Ser Trp Thr Gly Lys Arg Thr Tyr Arg Thr Asp Asp Ala Pro Asn Glu  
 100 105 110  
 65 Cys Phe Arg Ser Tyr Ser Ala Ala Arg Glu Ser Tyr Glu Asp His Ser  
 115 120 125  
 Arg Phe Leu Leu Gln Pro Arg Tyr Arg Pro Leu Phe Lys Leu Asp Arg  
 130 135 140  
 70 Glu Asp Tyr Arg Gly Trp Ala Thr Gly Leu Gln Arg Cys Gly Tyr Ala  
 145 150 155 160  
 Thr Asn Arg Gly Tyr Ala Asn Leu Leu Ile Lys Met Val Glu Leu Tyr  
 165 170 175  
 Glu Leu Tyr Ala Leu Asp Arg Glu Lys Tyr Pro Ser Trp Phe His Lys  
 180 185 190  
 75 Ser Tyr Pro Gly Ser Asn Lys Lys Ser His Gln Thr Thr Lys Gln Lys

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195 200 205  
 Gln Ser Gly Leu Lys His Glu Ala Tyr Phe Ser Tyr Gly Leu Leu Tyr  
 210 215 220  
 5 Ile Ile Ala Lys Gln Gly Asp Thr Phe Asp Ser Leu Ala Glu Glu Phe  
 225 230 235 240  
 Asp Met Arg Ala Ser Lys Leu Ala Lys Tyr Asn Asp Ala Pro Val Asp  
 245 250 255  
 Phe Pro Ile Glu Lys Gly Asp Val Ile Tyr Leu Glu Lys Lys His Ala  
 260 265 270  
 10 Cys Ser Ile Ser Lys His Thr Gln His Val Val Arg Val Gly Asp Ser  
 275 280 285  
 Met His Ser Ile Ser Gln Arg Tyr Gly Ile Arg Met Lys Asn Leu Tyr  
 290 295 300  
 15 Lys Leu Asn Asp Lys Asp Gly Glu Tyr Ile Pro Gln Glu Gly Asp Ile  
 305 310 315 320  
 Leu Arg Leu Arg

- (2) INFORMATION FOR SEQ ID NO:277
- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 533 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Porphyromonas gingivalis
- (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...533
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:277

40 Arg Ile Pro Asp Glu Gln Thr Gly Arg Ile Met Asp Gly Arg Arg Tyr  
 1 5 10 15  
 Ser Asp Gly Leu His Gln Ala Ile Glu Ala Lys Glu His Val Lys Val  
 20 25 30  
 Glu Ala Ala Thr Gln Thr Phe Ala Thr Ile Thr Leu Gln Asn Tyr Phe  
 35 40 45  
 45 Arg Met Tyr His Lys Leu Ala Gly Met Thr Gly Thr Ala Glu Thr Glu  
 50 55 60  
 Ala Gly Glu Leu Trp Asp Ile Tyr Lys Leu Asp Val Val Ile Pro  
 65 70 75 80  
 50 Thr Asn Lys Pro Ile Ala Arg Lys Asp Met Asn Asp Arg Ile Tyr Lys  
 85 90 95  
 Thr Ala Arg Glu Lys Tyr Ala Ala Val Ile Glu Glu Ile Val Arg Leu  
 100 105 110  
 Val Glu Glu Gly Arg Pro Val Leu Val Gly Thr Thr Ser Val Glu Ile  
 115 120 125  
 55 Ser Glu Leu Leu Ser Arg Met Leu Arg Leu Arg Gly Ile Gln His Asn  
 130 135 140  
 Val Leu Asn Ala Lys Leu His Gln Lys Glu Ala Glu Ile Val Ala Gln  
 145 150 155 160  
 60 Ala Gly Gln Lys Gly Thr Val Thr Ile Ala Thr Asn Met Ala Gly Arg  
 165 170 175  
 Gly Thr Asp Ile Lys Leu Ser Ala Glu Val Lys Lys Ala Gly Gly Leu  
 180 185 190  
 Ala Ile Ile Gly Thr Glu Arg His Glu Ser Arg Arg Val Asp Arg Gln  
 195 200 205  
 65 Leu Arg Gly Arg Ser Gly Arg Gln Gly Asp Pro Gly Ser Ser Ile Phe  
 210 215 220  
 Tyr Val Ser Leu Glu Asp His Leu Met Arg Leu Phe Ala Thr Glu Lys  
 225 230 235 240  
 70 Ile Ala Ser Leu Met Asp Arg Leu Gly Phe Lys Glu Gly Glu Val Leu  
 245 250 255  
 Glu Asn Asn Met Leu Ser Lys Ser Val Glu Arg Ala Gln Lys Lys Val  
 260 265 270  
 Glu Glu Asn Asn Phe Gly Ile Arg Lys His Leu Leu Glu Tyr Asp Asp  
 275 280 285  
 75 Val Met Asn Ser Gln Arg Glu Val Ile Tyr Thr Arg Arg Arg His Ala

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290 295 300  
 Leu Met Gly Glu Arg Ile Gly Met Asp Val Leu Asn Thr Ile Tyr Asp  
 305 310 315 320  
 Val Cys Lys Ala Leu Ile Asp Asn Tyr Ala Glu Ala Asn Asp Phe Glu  
 325 330 335  
 Gly Phe Lys Glu Asp Leu Met Arg Ala Leu Ala Ile Glu Ser Pro Ile  
 340 345 350  
 Thr Gln Glu Ile Phe Arg Gly Lys Lys Ala Glu Glu Leu Thr Asp Met  
 355 360 365  
 10 Leu Phe Asp Glu Ala Tyr Lys Ser Phe Gln Arg Lys Met Asp Leu Ile  
 370 375 380  
 Ala Glu Val Ala His Pro Val Val His Gln Val Phe Glu Thr Gln Ala  
 385 390 395 400  
 15 Ala Val Tyr Glu Arg Ile Leu Ile Pro Ile Thr Asp Gly Lys Arg Val  
 405 410 415  
 Tyr Asn Ile Gly Cys Asn Leu Arg Glu Ala Asp Glu Thr Gln Gly Lys  
 420 425 430  
 Ser Ile Ile Lys Glu Phe Glu Lys Ala Ile Val Leu His Thr Ile Asp  
 435 440 445  
 20 Glu Ser Trp Lys Glu His Leu Arg Glu Met Asp Glu Leu Arg Asn Ser  
 450 455 460  
 Val Gln Asn Ala Ser Tyr Glu Asn Lys Asp Pro Leu Leu Ile Tyr Lys  
 465 470 475 480  
 25 Leu Glu Ser Tyr Glu Leu Phe Arg Lys Met Val Glu Ala Met Asn Arg  
 485 490 495  
 Lys Thr Val Ala Ile Leu Met Arg Ala Arg Ile Pro Val Pro Glu Ala  
 500 505 510  
 Pro Ser Gln Glu Glu Leu Glu His Arg Arg Gln Ile Glu Ile Arg His  
 515 520 525  
 30 Ala Thr Gln Gln Arg  
 530

(2) INFORMATION FOR SEQ ID NO:278

35 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 720 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
 40 (ii) MOLECULE TYPE: protein  
 (iii) HYPOTHETICAL: YES  
 (vi) ORIGINAL SOURCE:  
 45 (A) ORGANISM: Porphyromonas gingivalis  
 (ix) FEATURE:  
 (A) NAME/KEY: misc feature  
 (B) LOCATION: 1...720  
 50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:278

Lys Ser Cys Arg Val Ile Gly Gln Thr Arg Arg Tyr Gly Cys Cys Pro  
 1 5 10 15  
 55 Val Gly Leu Arg Pro Cys His Gln Ser Leu Ser Gly Val Cys Arg Cys  
 20 25 30  
 Leu Phe Gln Ser Arg Pro Ala Val Ala Phe Ala Arg Lys Gly Gln Arg  
 35 40 45  
 60 Arg His Arg Arg Ser Glu Ser Gly Arg Arg Ile Arg Ala Leu Gln Gly  
 50 55 60  
 Val Gln His His Gln Thr Asn Glu His Glu Val Met Ile Ser Val Asn  
 65 70 75 80  
 Asn Leu Thr Val Asp Phe Gly Thr Arg Leu Leu Phe Asp Gln Val Ser  
 85 90 95  
 65 Phe Val Ile Asn Arg Arg Asp Arg Ile Ala Leu Val Gly Lys Asn Gly  
 100 105 110  
 Ala Gly Lys Ser Thr Leu Leu Lys Leu Ile Ala Gly Met Glu Glu Pro  
 115 120 125  
 70 Thr Ser Gly His Ile Ala Arg Pro Lys Gly Ile Arg Ile Gly Tyr Leu  
 130 135 140  
 Pro Gln Val Met Arg Leu Gln Asp Gly His Thr Val Tyr Glu Glu Val  
 145 150 155 160  
 Glu Gln Ala Phe Asn Asp Ile Arg Gln Ile Glu Glu Glu Ile Arg Arg  
 165 170 175  
 75 Leu Ser Asp Glu Met Ala Gly Arg Thr Asp Tyr Glu Ser Asp Asp Tyr

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180 185 190  
 Ile Arg Leu Ile Glu His Tyr Thr Asn Met Ser Glu Thr Leu Ser Leu  
 195 200 205  
 Met Gln Gln Gly Asn Tyr His Ala Ala Ile Glu Gln Thr Leu Ile Gly  
 210 215 220  
 Leu Gly Phe Gly Arg Glu Asp Phe His Arg Pro Thr Ala Asp Phe Ser  
 225 230 235 240  
 Gly Gly Trp Arg Met Arg Ile Glu Leu Ala Lys Leu Leu Leu Gln Arg  
 245 250 255  
 10 Pro Glu Val Leu Leu Leu Asp Glu Pro Thr Asn His Leu Asp Ile Glu  
 260 265 270  
 Ser Ile Gly Trp Leu Glu Gln Phe Ile Ala Thr Asn Ala Gly Ala Val  
 275 280 285  
 15 Ile Leu Val Ser His Asp Arg Ala Phe Ile Asp Asn Thr Thr Thr Arg  
 290 295 300  
 Thr Ile Glu Ile Glu Leu Gly His Ile Tyr Asp Tyr Lys Thr Asn Tyr  
 305 310 315 320  
 Ser His Tyr Val Glu Leu Arg Glu Glu Arg Leu Arg Gln Gln Met Arg  
 325 330 335  
 20 Ala Tyr Glu Asn Gln Gln Lys Met Ile Arg Asp Thr Glu Asp Phe Ile  
 340 345 350  
 Glu Arg Phe Arg Tyr Lys Ala Thr Lys Ser Val Gln Val Gln Ser Arg  
 355 360 365  
 25 Ile Lys Gln Leu Glu Lys Val Glu Arg Val Glu Ile Asp Glu Arg Asp  
 370 375 380  
 Arg Ser Ala Phe His Phe Arg Phe Ile Pro Ala Gln Pro Ser Gly Ser  
 385 390 395 400  
 Tyr Pro Leu Ile Val Asp Asp Leu Ala Lys Ala Tyr Gly Asp His Gln  
 405 410 415  
 30 Val Phe Ser Gly Ala Thr Tyr Thr Ile Glu Arg Gly Glu Lys Val Ala  
 420 425 430  
 Phe Val Gly Lys Asn Gly Ala Gly Lys Ser Thr Met Val Lys Cys Ile  
 435 440 445  
 35 Met Gly Glu Leu Thr Asp Tyr Thr Gly Lys Leu Glu Leu Gly His Asn  
 450 455 460  
 Val Gln Leu Gly Tyr Phe Ala Gln Asn Glu Ala Gln Glu Leu Arg Gly  
 465 470 475 480  
 Asp Leu Thr Val Phe Asp Thr Ile Asp Arg Glu Ala Val Gly Asp Ile  
 485 490 495  
 40 Arg Leu Arg Leu Asn Asp Leu Leu Gly Ala Phe Leu Phe Gly Gly Glu  
 500 505 510  
 Ala Ser Glu Lys Lys Val Ser Val Leu Ser Gly Gly Glu Arg Ala Arg  
 515 520 525  
 45 Leu Ala Ile Ile Arg Leu Leu Gln Pro Ala Asn Phe Leu Ile Leu  
 530 535 540  
 Asp Glu Pro Thr Asn His Leu Asp Met Arg Ser Lys Asp Val Leu Lys  
 545 550 555 560  
 Glu Ala Ile Lys Asn Phe Asp Gly Thr Val Ile Val Val Ser His Asp  
 565 570 575  
 50 Arg Glu Phe Leu Asp Gly Leu Val Ser Lys Val Tyr Glu Phe Ala Asp  
 580 585 590  
 Gly Gln Val Asn Glu His Leu Gly Gly Ile Tyr Asp Tyr Leu Arg Thr  
 595 600 605  
 55 Arg Arg Met Gln Thr Leu Thr Glu Leu Glu Arg Thr Thr Thr Ile Glu  
 610 615 620  
 Thr Lys Thr Thr Arg Glu Ala Ile Pro Glu Thr Glu Ala Lys Ala Asp  
 625 630 635 640  
 Tyr Arg Arg Gln Lys Glu Val Ala Lys Gln Leu Arg Thr Leu Glu Arg  
 645 650 655  
 60 Thr Val Ala Thr Cys Glu Glu Arg Ile Gly Lys Leu Glu Ser Glu Leu  
 660 665 670  
 Gln Ala Ile Glu Met Leu Leu Gln Asp Pro Lys His Ala Thr Asp Ala  
 675 680 685  
 65 Asn Leu Phe Glu Arg Tyr Ala Gly Met Lys Gln Glu Leu Glu Lys Ala  
 690 695 700  
 Met Glu Asp Trp Glu Gln Ala Ser Glu Ala Leu Ser Glu Ala Gln Gly  
 705 710 715 720

(2) INFORMATION FOR SEQ ID NO:279

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 386 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

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(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

5 (vi) ORIGINAL SOURCE:  
(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:  
(A) NAME/KEY: misc\_feature  
10 (B) LOCATION 1...386

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:279

15 Tyr Leu Lys Leu Ile Leu Gln Ile Ala Leu Met Asn Phe Leu Lys  
1 5 10 15  
Lys Glu Pro Phe Lys Ile Phe Ser Met Ile Tyr Leu Leu Leu Asp Thr  
20 25 30  
Ile Thr Asn Arg Ala Gly Thr Glu Arg Ala Val Ile Asn Leu Ala Asn  
35 40 45

20 Asn Leu His Ala Asn Gly His Arg Val Ser Leu Val Ser Val Cys Thr  
50 55 60  
Lys Glu Gly Glu Pro Ser Phe Gln Val Glu Lys Gly Ile Glu Val His  
65 70 75 80  
His Leu Gly Ile Arg Leu Tyr Gly Asn Ala Leu Ala Arg Lys Thr Val  
25 85 90 95

Tyr Phe Lys Ala Tyr Arg Arg Ile Lys Ala Leu Tyr Lys Lys Arg Glu  
100 105 110  
Pro Val Leu Leu Ile Gly Thr Asn Ile Phe Ile Asn Thr Ile Leu Ser  
115 120 125

30 Gln Ile Ser Asn Arg Gly Arg Ile Phe Thr Ile Gly Cys Glu His Ile  
130 135 140  
Ser Tyr Asp Ile Ala Arg Pro Ile Thr Lys Arg Ile Arg Gly Phe Leu  
145 150 155 160  
Tyr Ser Gly Leu Asp Ala Val Val Ala Leu Thr Lys Arg Asp Gln Gln  
35 165 170 175

Ser Phe Glu Ala Ile Leu Arg Gly Arg Ser Lys Ala Tyr Val Ile Pro  
180 185 190  
Asn Gln Val Ser Phe Thr Thr Val Gln Arg Asp Ala Thr Thr His Lys  
195 200 205

40 Gln Met Leu Ala Ile Gly Arg Leu Thr Tyr Gln Lys Gly Phe Glu Phe  
210 215 220  
Met Ile Glu Asp Ala Ser Arg Val Leu Arg Glu Arg Pro Asp Trp Lys  
225 230 235 240  
Leu Ile Ile Val Gly Asp Gly Glu Asn Glu Ser Met Leu Arg Lys Glu  
45 245 250 255

Ile Ala Ser Arg Asn Met Glu Ser Gln Ile Glu Ile His Pro Ser Thr  
260 265 270  
Pro Glu Ile Arg Lys Tyr Tyr Glu Ser Ser Ala Ile Tyr Leu Met Thr  
275 280 285

50 Ser Arg Phe Glu Gly Leu Pro Met Val Leu Leu Glu Ala Glu Ala Tyr  
290 295 300  
Ala Leu Pro Ile Ile Ser Tyr Asp Cys Pro Thr Gly Pro Arg Glu Leu  
305 310 315 320  
Ile Glu Asn Gly Arg Asn Gly Phe Leu Val Pro Met Glu Ala His Glu  
55 325 330 335

Asp Phe Ala Asp Lys Leu Arg Leu Leu Met Asp Asp Glu Thr Leu Arg  
340 345 350  
Lys Lys Met Gly Gln Glu Ser Glu Leu Met Val Lys Ser Tyr Ser Pro  
355 360 365

60 Ala Asn Ile Tyr Glu Cys Trp Lys Lys Leu Phe Val Glu Ile Gly Tyr  
370 375 380  
Met Asn  
385

65 (2) INFORMATION FOR SEQ ID NO:280

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 655 amino acids  
70 (B) TYPE: amino acid  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

75 (iii) HYPOTHETICAL: YES

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(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Porphyromonas gingivalis*

(ix) FEATURE:

(A) NAME/KEY: misc\_feature

(B) LOCATION 1...655

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:280

10 Thr Thr Lys Glu Asn Glu Thr Thr Thr Lys Asn Glu Tyr Arg Ile Met  
 1 5 10 15  
 Gly Lys Ile Ile Gly Ile Asp Leu Gly Thr Thr Asn Ser Cys Val Ser  
 20 25 30  
 15 Val Leu Glu Gly Asn Glu Pro Ile Val Ile Thr Asn Ser Glu Gly Lys  
 35 40 45  
 Arg Thr Thr Pro Ser Val Val Ala Phe Val Asp Gly Gly Glu Arg Lys  
 50 55 60  
 Val Gly Asp Pro Ala Lys Arg Gln Ala Ile Thr Asn Pro Thr Lys Thr  
 65 70 75 80  
 20 Ile Tyr Ser Ile Lys Arg Phe Met Gly Glu Thr Tyr Asp Gln Val Ser  
 85 90 95  
 Arg Glu Val Glu Arg Val Pro Phe Lys Val Val Arg Gly Asp Asn Asn  
 100 105 110  
 25 Thr Pro Arg Val Asp Ile Asp Gly Arg Leu Tyr Thr Pro Gln Glu Ile  
 115 120 125  
 Ser Ala Met Ile Leu Gln Lys Met Lys Lys Thr Ala Glu Asp Tyr Leu  
 130 135 140  
 Gly Gln Glu Val Thr Glu Ala Val Ile Thr Val Pro Ala Tyr Phe Asn  
 145 150 155 160  
 30 Asp Ala Gln Arg Gln Ala Thr Lys Glu Ala Gly Glu Ile Ala Gly Leu  
 165 170 175  
 Lys Val Arg Arg Ile Val Asn Glu Pro Thr Ala Ala Ser Leu Ala Tyr  
 180 185 190  
 35 Gly Leu Asp Lys Ser Asn Lys Asp Met Lys Ile Ala Val Phe Asp Leu  
 195 200 205  
 Gly Gly Gly Thr Phe Asp Ile Ser Ile Leu Glu Leu Gly Asp Gly Val  
 210 215 220  
 Phe Glu Val Lys Ser Thr Asn Gly Asp Thr His Leu Gly Gly Asp Asp  
 225 230 235 240  
 40 Phe Asp His Val Ile Ile Asp Trp Leu Ala Glu Glu Phe Lys Ser Gln  
 245 250 255  
 Glu Gly Val Asp Leu Arg Gln Asp Pro Met Ala Met Gln Arg Leu Lys  
 260 265 270  
 45 Glu Ala Ala Glu Lys Ala Lys Ile Glu Leu Ser Ser Thr Ser Ser Thr  
 275 280 285  
 Glu Ile Asn Leu Pro Tyr Ile Met Pro Val Asn Gly Ile Pro Lys His  
 290 295 300  
 Leu Val Met Thr Leu Thr Arg Ala Lys Phe Glu Gln Leu Ala Asp Arg  
 305 310 315 320  
 50 Leu Ile Gln Ala Cys Val Ala Pro Cys Glu Thr Ala Leu Lys Asp Ala  
 325 330 335  
 Gly Met Ser Arg Gly Asp Ile Asp Glu Val Ile Leu Val Gly Gly Ser  
 340 345 350  
 55 Thr Arg Ile Pro Ala Ile Gln Glu Ile Val Glu Lys Ile Phe Gly Lys  
 355 360 365  
 Ala Pro Ser Lys Gly Val Asn Pro Asp Glu Val Val Ala Val Gly Ala  
 370 375 380  
 Ala Ile Gln Gly Gly Val Leu Thr Gly Glu Val Lys Asp Val Leu Leu  
 385 390 395 400  
 60 Leu Asp Val Thr Pro Leu Ser Leu Gly Ile Glu Thr Met Gly Gly Val  
 405 410 415  
 Met Thr Arg Leu Ile Asp Ala Asn Thr Thr Ile Pro Thr Lys Lys Ser  
 420 425 430  
 65 Glu Ile Phe Thr Thr Ala Val Asp Asn Gln Pro Ser Val Glu Ile His  
 435 440 445  
 Val Leu Gln Gly Glu Arg Ser Leu Ala Lys Asp Asn Lys Ser Ile Gly  
 450 455 460  
 Arg Phe Asn Leu Asp Gly Ile Ala Pro Ala Pro Arg Gln Thr Pro Gln  
 465 470 475 480  
 70 Ile Glu Val Thr Phe Asp Ile Asp Ala Asn Gly Ile Leu Asn Val Thr  
 485 490 495  
 Ala His Asp Lys Ala Thr Gly Lys Lys Gln Asn Ile Arg Ile Glu Ala  
 500 505 510  
 75 Ser Ser Gly Leu Ser Asp Asp Glu Ile Lys Arg Met Lys Glu Glu Ala  
 515 520 525



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Gln Ala Asn Ala Glu Ala Asp Lys Lys Glu Lys Glu Arg Ile Asp Lys  
 530 535 540  
 Ile Asn Gln Ala Asp Ser Met Ile Phe Gln Thr Glu Lys Gln Leu Lys  
 545 550 555 560  
 5 Glu Leu Gly Asp Lys Phe Pro Ala Asp Lys Lys Ala Pro Ile Asp Thr  
 565 570 575  
 Ala Leu Asp Lys Leu Lys Glu Ala His Lys Ala Gln Asp Val Ala Ala  
 580 585 590  
 10 Ile Asp Thr Ala Met Ala Glu Leu Gln Thr Ala Leu Ser Ala Ala Gly  
 595 600 605  
 Glu Glu Leu Tyr Lys Asn Ala Gly Ala Ala Gln Gly Gly Ala Gln Pro  
 610 615 620  
 Gly Pro Asp Phe Gly Gly Ala Gln Gly Pro Ser Ala Gly Asp Gln Pro  
 625 630 635 640  
 15 Ser Asp Asp Lys Asn Val Thr Asp Val Asp Phe Glu Glu Val Lys  
 645 650 655

(2) INFORMATION FOR SEQ ID NO:281

- 20 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 467 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
 25 (ii) MOLECULE TYPE: protein  
 (iii) HYPOTHETICAL: YES  
 (vi) ORIGINAL SOURCE:  
 30 (A) ORGANISM: Porphyromonas gingivalis  
 (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...467  
 35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:281

Lys Trp Ala Arg Thr Thr Thr Leu Arg Ile Ser Asn Ala Thr Ile Tyr  
 1 5 10 15  
 40 Lys Thr Met Arg Tyr Asp Leu Ala Ile Ile Gly Gly Gly Pro Ala Gly  
 20 25 30  
 Tyr Thr Ala Ala Glu Arg Ala Ala Lys Gly Gly Leu Lys Thr Leu Leu  
 35 40 45  
 Ile Glu Lys Asn Ala Leu Gly Gly Val Cys Leu Asn Glu Gly Cys Ile  
 50 55 60  
 45 Pro Thr Lys Thr Leu Leu Tyr Ser Ala Lys Val Leu His Gln Ile Ala  
 65 70 75 80  
 Thr Ala Ser Lys Tyr Ala Val Ser Gly Thr Ala Asp Gly Leu Asp Leu  
 85 90 95  
 50 Gly Lys Val Ile Ala Arg Lys Gly Lys Ile Ile Arg Lys Leu Thr Ala  
 100 105 110  
 Gly Ile Arg Ser Arg Leu Thr Glu Ala Gly Val Glu Met Val Thr Ala  
 115 120 125  
 55 Glu Ala Thr Val Thr Gly Cys Asp Ala Asp Gly Ile Ile Gly Ile Thr  
 130 135 140  
 Ala Gly Glu Ala Gln Tyr Lys Ala Ala Asn Leu Leu Cys Thr Gly  
 145 150 155 160  
 Ser Glu Thr Phe Ile Pro Pro Ile Pro Gly Val Glu Gln Thr Glu Tyr  
 165 170 175  
 60 Trp Thr Asn Arg Glu Ala Leu Gln Asn Lys Glu Ile Pro Thr Ser Leu  
 180 185 190  
 Val Ile Ile Gly Gly Gly Val Ile Gly Met Glu Phe Ala Ser Phe Phe  
 195 200 205  
 65 Asn Gly Ile Gly Thr Gln Val His Val Val Glu Met Leu Pro Glu Ile  
 210 215 220  
 Leu Asn Gly Ile Asp Pro Glu His Ala Ala Met Leu Arg Ala His Tyr  
 225 230 235 240  
 Glu Lys Glu Gly Ile Lys Phe Tyr Leu Gly His Lys Val Thr Ser Val  
 245 250 255  
 70 Arg Asn Gly Ala Val Thr Val Glu Tyr Glu Gly Glu Ser Lys Glu Ile  
 260 265 270  
 Glu Gly Glu Arg Ile Leu Met Ser Val Gly Arg Arg Pro Val Leu Gln  
 275 280 285  
 75 Gly Phe Glu Ser Leu Gly Leu Val Leu Ala Gly Lys Gly Val Lys Thr  
 290 295 300

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Asn Glu Arg Met Gln Thr Ser Leu Pro Asn Val Tyr Ala Ala Gly Asp  
 305 310 315 320  
 Ile Thr Gly Phe Ser Leu Leu Ala His Thr Ala Val Arg Glu Ala Glu  
 325 330 335  
 5 Val Ala Val Asp Gln Ile Leu Gly Lys Thr Asp Glu Thr Met Ser Tyr  
 340 345 350  
 Arg Ala Val Pro Gly Val Val Tyr Thr Asn Pro Glu Val Ala Gly Val  
 355 360 365  
 10 Gly Glu Thr Glu Glu Ser Leu Arg Lys Ala Gly Arg Ala Tyr Thr Val  
 370 375 380  
 Arg Arg Leu Pro Met Ala Phe Ser Gly Arg Phe Val Ala Glu Asn Glu  
 385 390 395 400  
 Gln Gly Asn Gly Glu Cys Lys Leu Leu Leu Asp Glu Glu Asn Arg Leu  
 405 410 415  
 15 Ile Gly Ala His Leu Ile Gly Asn Pro Ala Gly Glu Leu Ile Val Thr  
 420 425 430  
 Ala Ala Met Ala Ile Glu Thr Gly Met Thr Asp Arg Gln Ile Glu Arg  
 435 440 445  
 20 Ile Ile Phe Pro His Pro Thr Val Gly Glu Ile Leu Lys Glu Thr Leu  
 450 455 460  
 Ala Gly Gly  
 465

25 (2) INFORMATION FOR SEQ ID NO:282

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 945 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
 30  
 (ii) MOLECULE TYPE: protein  
 (iii) HYPOTHETICAL: YES  
 35 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Porphyromonas gingivalis  
 (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...945  
 40  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:282

45 Pro Lys Ile Leu Met Glu Leu Lys Arg Phe Leu Ser Leu Gly Leu Leu  
 1 5 10 15  
 Leu Val Gly Phe Ile Pro Met Lys Leu Ser Ala Gln Gln Ala Gln Pro  
 20 25 30  
 Leu Pro Thr Asp Pro Ala Val Arg Val Gly Lys Leu Asp Asn Gly Leu  
 35 40 45  
 50 Thr Tyr Phe Ile Arg His Asn Glu Asn Pro Lys Asp Arg Ala Asp Phe  
 50 55 60  
 Phe Ile Ala Gln Lys Val Gly Ser Ile Leu Glu Asp Ser Gln Ser  
 65 70 75 80  
 55 Gly Leu Ala His Phe Leu Glu His Met Ala Phe Asn Gly Thr Lys Asn  
 85 90 95  
 Phe Pro Gly Lys Asn Leu Ile Asn Tyr Leu Glu Thr Ile Gly Val Arg  
 100 105 110  
 Phe Gly Gln Asn Leu Asn Ala Ser Thr Gly Phe Asp Lys Thr Glu Tyr  
 115 120 125  
 60 Thr Ile Met Asp Val Pro Thr Thr Arg Gln Gly Ile Ile Asp Ser Cys  
 130 135 140  
 Leu Leu Ile Leu His Asp Trp Ser Asn Asn Ile Thr Leu Asp Gly His  
 145 150 155 160  
 65 Glu Ile Asp Glu Glu Arg Gly Val Ile Gln Glu Glu Trp Arg Ala Arg  
 165 170 175  
 Arg Asp Ala Asn Leu Arg Met Phe Glu Ala Ile Leu Ala Lys Ala Met  
 180 185 190  
 Pro Gly Asn Lys Tyr Ala Glu Arg Met Pro Ile Gly Leu Met Asp Val  
 195 200 205  
 70 Val Leu Asn Phe Lys His Asp Glu Leu Arg Asn Tyr Tyr Lys Lys Trp  
 210 215 220  
 Tyr Arg Pro Asp Leu Gln Gly Leu Val Ile Val Gly Asp Ile Asp Val  
 225 230 235 240  
 75 Asp Tyr Val Glu Asn Lys Ile Lys Glu Leu Phe Lys Asp Val Pro Ala  
 245 250 255

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	Pro	Val	Asn	Pro	Ala	Glu	Arg	Ile	Tyr	Thr	Pro	Val	Glu	Asp	Asn	Asp
				260					265					270		
	Glu	Pro	Ile	Val	Ala	Ile	Ala	Thr	Asp	Ala	Glu	Ala	Thr	Thr	Thr	Gln
			275					280					285			
5	Leu	Ser	Ile	Ser	Phe	Lys	Ser	Asp	Pro	Thr	Pro	Gln	Glu	Val	Arg	Gly
		290					295					300				
	Ser	Ile	Phe	Gly	Leu	Val	Glu	Asp	Tyr	Met	Lys	Gln	Val	Ile	Thr	Thr
	305				310					315						320
10	Ala	Val	Asn	Glu	Arg	Leu	Ser	Glu	Ile	Thr	His	Lys	Pro	Asn	Ala	Pro
				325						330					335	
	Phe	Leu	Ser	Ala	Gly	Ala	Phe	Phe	Ser	Asn	Phe	Met	Tyr	Ile	Thr	Gln
				340					345					350		
	Thr	Lys	Asp	Ala	Phe	Asn	Phe	Val	Ala	Thr	Val	Arg	Glu	Gly	Glu	Ala
			355					360					365			
15	Glu	Lys	Ala	Met	Asn	Ala	Leu	Val	Ala	Glu	Ile	Glu	Ser	Leu	Arg	Gln
		370					375					380				
	Phe	Gly	Ile	Thr	Lys	Gly	Glu	Tyr	Asp	Arg	Ala	Arg	Thr	Asn	Val	Leu
	385					390					395					400
20	Lys	Arg	Tyr	Glu	Asn	Gln	Tyr	Asn	Glu	Arg	Asp	Lys	Arg	Lys	Asn	Asn
				405						410					415	
	Ala	Tyr	Ala	Asn	Glu	Tyr	Ser	Thr	Tyr	Phe	Thr	Asp	Gly	Gly	Tyr	Ile
				420					425					430		
	Pro	Gly	Ile	Glu	Val	Glu	Tyr	Gln	Thr	Val	Asn	Ala	Phe	Ala	Pro	Gln
			435					440					445			
25	Val	Pro	Leu	Glu	Ala	Phe	Asn	Gln	Ala	Ile	Ala	Gln	Met	Ile	Asp	Pro
		450					455					460				
	Val	Lys	Asn	Ala	Val	Val	Thr	Leu	Thr	Gly	Pro	Ser	Lys	Ala	Glu	Ala
	465					470				475						480
30	Lys	Ile	Pro	Ser	Glu	Ala	Asp	Phe	Leu	Ala	Ala	Phe	Lys	Ala	Ala	Arg
					485					490					495	
	Gln	Gln	Lys	Val	Glu	Ala	Lys	Lys	Asp	Glu	Val	Ser	Asp	Gln	Lys	Leu
				500					505					510		
	Met	Glu	Lys	Ala	Pro	Lys	Ala	Gly	Lys	Ile	Val	Ser	Glu	Lys	Lys	Asp
			515					520					525			
35	Gln	Lys	Phe	Gly	Thr	Thr	Glu	Leu	Thr	Leu	Ser	Asn	Gly	Ile	Lys	Val
		530					535					540				
	Tyr	Leu	Lys	Lys	Thr	Asp	Phe	Lys	Ser	Asn	Glu	Ile	Leu	Met	Ser	Ala
	545					550					555					560
40	Leu	Ser	Pro	Gly	Gly	Ile	Leu	Ser	Gly	Lys	His	Ala	Pro	Asn	Gln	Ser
					565					570					575	
	Val	Met	Asn	Ser	Phe	Met	Asn	Val	Gly	Gly	Leu	Gly	Asn	Phe	Asp	Ala
					580				585					590		
	Ile	Gln	Leu	Asp	Lys	Val	Leu	Thr	Gly	Arg	Ser	Ala	Ser	Val	Ser	Pro
			595					600					605			
45	Ser	Leu	Ser	Leu	Leu	Ser	Glu	Gly	Leu	Ser	Gly	Lys	Thr	Thr	Val	Glu
		610					615					620				
	Asp	Met	Glu	Thr	Phe	Phe	Gln	Leu	Ile	Tyr	Leu	Gln	Met	Thr	Ala	Asn
	625					630					635					640
50	Arg	Lys	Asp	Pro	Glu	Ala	Phe	Lys	Ala	Thr	Gln	Glu	Lys	Leu	Tyr	Asn
					645						650				655	
	Asn	Leu	Lys	Asn	Gln	Glu	Ala	Asn	Pro	Met	Ala	Ala	Leu	Met	Asp	Ser
				660					665					670		
	Ile	Arg	His	Thr	Met	Tyr	Gly	Asp	Asn	Pro	Met	Met	Lys	Pro	Met	Lys
			675					680					685			
55	Ala	Ala	Asp	Val	Glu	Lys	Val	Asn	Tyr	Asp	Gln	Val	Met	Ala	Phe	Tyr
		690					695					700				
	Asn	Glu	Arg	Phe	Ala	Asp	Ala	Gly	Asp	Phe	Met	Phe	Phe	Phe	Ile	Gly
	705					710					715					720
60	Asn	Leu	Asp	Glu	Ala	Lys	Met	Lys	Pro	Leu	Ile	Glu	Thr	Tyr	Leu	Ala
					725					730					735	
	Ser	Leu	Pro	Asn	Leu	Lys	Arg	Gly	Asp	Lys	Met	Asn	Lys	Ala	Gln	Val
				740					745					750		
	Pro	Ala	Ala	Arg	Ser	Gly	Lys	Ile	Asp	Cys	Lys	Phe	Glu	Lys	Glu	Met
				755				760					765			
65	Asp	Thr	Pro	Ser	Thr	Thr	Ile	Phe	Asp	Val	Val	Ser	Gly	Asn	Val	Glu
		770					775						780			
	Tyr	Thr	Leu	Lys	Asn	Ser	Leu	Leu	Leu	Glu	Val	Phe	Ser	Ala	Val	Met
		785				790					795					800
70	Asp	Gln	Val	Tyr	Thr	Ala	Thr	Val	Arg	Glu	Lys	Glu	Gly	Gly	Ala	Tyr
					805						810				815	
	Ser	Val	Ala	Ala	Phe	Gly	Gly	Leu	Glu	Gln	Tyr	Pro	Gln	Pro	Lys	Ala
				820					825					830		
	Leu	Met	Gln	Ile	Tyr	Phe	Pro	Thr	Asp	Pro	Ala	Arg	Ala	Glu	Glu	Met
				835				840					845			
75	Asn	Ala	Ile	Val	Phe	Ala	Glu	Leu	Glu	Lys	Leu	Ala	Lys	Glu	Gly	Pro

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5                   850                   855                   860  
 Asn Val Glu Tyr Phe Lys Lys Thr Ile Glu Asn Leu Asn Lys Gln His  
 865                   870                   875                   880  
 Lys Glu Ser Leu Arg Glu Asn Arg Phe Trp Leu Glu Ala Met Lys Ala  
 885                   890                   895  
 Ser Phe Phe Glu Gly Asn Asp Phe Ile Thr Asp Tyr Glu Ser Val Leu  
 900                   905                   910  
 Asn Gly Leu Thr Pro Ala Glu Leu Gln Lys Phe Ala Ala Asp Leu Leu  
 915                   920                   925  
 10 Lys Gln Gln Asn Arg Val Val Val Met Met Ala Pro Val Ala Lys Ala  
 930                   935                   940  
 Gln  
 945

15 (2) INFORMATION FOR SEQ ID NO:283

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 686 amino acids  
 (B) TYPE: amino acid  
 20 (D) TOPOLOGY: linear  
  
 (ii) MOLECULE TYPE: protein  
  
 (iii) HYPOTHETICAL: YES  
  
 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Porphyromonas gingivalis  
  
 (ix) FEATURE:  
 (A) NAME/KEY: misc feature  
 (B) LOCATION 1...686  
 30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:283

35 Tyr Thr Met Ser Lys Lys Gly Thr Ile Gly Val Thr Ser Asp Asn Ile  
 1                   5                   10                   15  
 Phe Pro Val Ile Lys Lys Phe Leu Tyr Ser Asp His Glu Ile Phe Leu  
 20                   25                   30  
 40 Arg Glu Ile Val Ser Asn Ala Val Asp Ala Thr Gln Lys Leu Lys Thr  
 35                   40                   45  
 Leu Thr Ser Val Gly Glu Phe Lys Gly Glu Thr Gly Asp Leu Arg Val  
 50                   55                   60  
 Thr Val Ser Val Asp Glu Val Ala Arg Thr Ile Thr Val Ser Asp Arg  
 65                   70                   75                   80  
 45 Gly Val Gly Met Thr Glu Glu Glu Val Glu Lys Tyr Ile Asn Gln Ile  
 85                   90                   95  
 Ala Phe Ser Ser Ala Glu Glu Phe Leu Glu Lys Tyr Lys Asp Asp Lys  
 100                   105                   110  
 50 Ala Ala Ile Ile Gly His Phe Gly Leu Gly Phe Tyr Ser Ala Phe Met  
 115                   120                   125  
 Val Ser Glu Arg Val Asp Val Ile Thr Arg Ser Phe Arg Glu Asp Ala  
 130                   135                   140  
 Thr Ala Val Lys Trp Ser Cys Asp Gly Ser Pro Glu Tyr Thr Leu Glu  
 145                   150                   155                   160  
 55 Pro Ala Asp Lys Ala Asp Arg Gly Thr Asp Ile Val Met His Ile Asp  
 165                   170                   175  
 Glu Glu Asn Ser Glu Phe Leu Lys Lys Glu Lys Ile Glu Gly Leu Leu  
 180                   185                   190  
 60 Gly Lys Tyr Cys Lys Phe Leu Thr Val Pro Ile Ile Phe Gly Lys Lys  
 195                   200                   205  
 Gln Glu Trp Lys Asp Gly Lys Met Gln Asp Thr Asp Glu Asp Asn Gln  
 210                   215                   220  
 Ile Asn Asp Thr His Pro Ala Trp Thr Lys Lys Pro Ala Asp Leu Lys  
 225                   230                   235                   240  
 65 Asp Glu Asp Tyr Lys Glu Phe Tyr Arg Ser Leu Tyr Pro Met Ser Glu  
 245                   250                   255  
 Glu Pro Leu Phe Trp Ile His Leu Asn Val Asp Tyr Pro Phe Asn Leu  
 260                   265                   270  
 70 Thr Gly Ile Leu Tyr Phe Pro Lys Ile Lys Asn Asn Leu Asp Leu Gln  
 275                   280                   285  
 Arg Asn Lys Ile Gln Leu Tyr Cys Asn Gln Val Tyr Val Thr Asp Glu  
 290                   295                   300  
 Val Gln Gly Ile Val Pro Asp Phe Leu Thr Leu His Gly Val Ile  
 305                   310                   315                   320  
 75 Asp Ser Pro Asp Ile Pro Leu Asn Val Ser Arg Ser Tyr Leu Gln Ser

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					325					330					335				
	Asp	Ala	Asn	Val	Lys	Lys	Ile	Ser	Ser	His	Ile	Thr	Lys	Lys	Val	Ala			
				340	Glu				345	Asn				350	Phe	Glu	Glu		
5	Asp	Arg	Leu	355				Lys	360	Asp	Arg	Pro	Thr	365					
	Lys	Trp	Asp	Ser	Leu	Lys	Leu	Phe	Val	Glu	Tyr	Gly	Met	Leu	Thr	Asp			
		370				375						380							
	Glu	Lys	Phe	Tyr	Glu	Arg	Ala	Ala	Lys	Phe	Phe	Leu	Phe	Thr	Asp	Net			
10	Asp	Gly	His	Lys	Tyr	Thr	Phe	Asp	Glu	Tyr	Arg	Thr	Leu	Val	Glu	Gly			
				405						410					415				
	Val	Gln	Thr	Asp	Lys	Asp	Gly	Gln	Val	Val	Tyr	Leu	Tyr	Ala	Thr	Asp			
				420					425						430				
15	Lys	His	Gly	Gln	Tyr	Ser	His	Val	Lys	Arg	Ala	Ser	Asp	Lys	Gly	Tyr			
			435					440					445						
	Ser	Val	Met	Leu	Leu	Asp	Gly	Gln	Leu	Asp	Pro	His	Ile	Val	Ser	Leu			
		450				455						460							
	Leu	Glu	Gln	Lys	Leu	Glu	Lys	Thr	His	Phe	Val	Arg	Val	Asp	Ser	Asp			
20	Thr	Ile	Asn	Asn	Leu	Ile	Arg	Lys	Glu	Glu	Arg	Ala	Glu	Val	Lys	Leu			
				485						490					495				
	Ser	Asp	Thr	Glu	Arg	Ala	Thr	Leu	Val	Lys	Leu	Phe	Glu	Ala	Arg	Leu			
				500					505					510					
25	Pro	Arg	Asp	Glu	Lys	Lys	His	Phe	Asn	Val	Ala	Phe	Glu	Ser	Leu	Gly			
			515					520					525						
	Ala	Glu	Gly	Glu	Ala	Ile	Leu	Ile	Thr	Gln	Ala	Glu	Phe	Met	Arg	Arg			
		530				535						540							
	Met	Arg	Asp	Met	Ala	Gln	Leu	Gln	Pro	Gly	Met	Ser	Phe	Tyr	Gly	Glu			
30					550						555				560				
	Leu	Pro	Asp	Ser	Tyr	Asn	Leu	Val	Leu	Asn	Thr	Asp	His	Pro	Leu	Ile			
				565						570					575				
	Asp	Arg	Val	Leu	Ser	Gly	Glu	Lys	Glu	Ser	Val	Glu	Pro	Ser	Leu	Thr			
				580					585					590					
35	Glu	Leu	Arg	Ala	Lys	Ile	Ala	Glu	Leu	Lys	Ala	Glu	Glu	Ala	Lys	Leu			
			595					600					605						
	Leu	Asp	Glu	Glu	Lys	Gly	Lys	Lys	Pro	Glu	Glu	Ile	Pro	Val	Ala	Thr			
		610				615						620							
	Lys	Glu	Ala	Lys	Glu	Asn	Asn	Ala	Val	Glu	Gln	Ala	Lys	Thr	Glu	Gly			
40					630						635				640				

## (2) INFORMATION FOR SEQ ID NO:284

```

50      (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 482 amino acids
          (B) TYPE: amino acid
          (D) TOPOLOGY: linear

55      (ii) MOLECULE TYPE: protein

      (iii) HYPOTHETICAL: YES

60      (vi) ORIGINAL SOURCE:
          (A) ORGANISM: Porphyromonas gingivalis

      (ix) FEATURE:
          (A) NAME/KEY: misc_feature
          (B) LOCATION 1...482

65      (xi) SEQUENCE DESCRIPTION: SEQ ID NO:284

```

	Asp	Ile	Arg	Gln	Lys	Arg	Pro	Cys	Phe	Asn	Ala	Asn	Leu	Tyr	Phe	Tyr
	1				5					10					15	
70	Arg	Ala	Met	Glu	Lys	Leu	Ile	Asp	Ile	Leu	Val	Val	Asp	Asp	Asp	Val
				20					25					30		
	Ala	Val	Cys	Ala	Ala	Leu	Arg	Leu	Val	Leu	Lys	Arg	Ala	Gly	Tyr	Asn
			35					40					45			
	Pro	Val	Ile	Ala	Asn	Ser	Pro	Asp	Glu	Ala	Leu	Ser	Ile	Met	Arg	Asn
			50				55					60				
75	Pro	Asp	Gly	Gly	Cys	Lys	Pro	Ala	Val	Ile	Leu	Met	Asp	Met	Asn	Phe

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	65				70					75						80
	Ser	Leu	Ser	Thr	Ser	Gly	Arg	Glu	Gly	Leu	Glu	Leu	Leu	Glu	Lys	Met
					85					90					95	
5	Gln	Ile	Phe	Thr	Ser	Cys	Pro	Val	Ile	Leu	Met	Thr	Ala	Trp	Ala	Ser
				100					105					110		
	Ile	Pro	Leu	Ala	Val	Glu	Gly	Met	Arg	Leu	Gly	Ala	Phe	Asp	Phe	Ile
				115				120					125			
10	Gly	Lys	Pro	Trp	Asp	Asn	Asp	Arg	Leu	Leu	Arg	Thr	Ile	Asp	Thr	Ala
				130			135					140				
	Leu	His	Leu	Ala	Ala	Pro	Ser	Ala	Val	Ala	Asn	Pro	Ser	Glu	Gln	Ser
					150						155					160
	Asp	Arg	Asp	Thr	Ala	Arg	Gln	Pro	Lys	Ala	Thr	Val	Gln	Glu	Asn	Asp
					165					170					175	
15	Pro	Cys	Ala	His	Ile	Ile	Gly	Arg	Ser	Asp	Ala	Ile	Cys	Lys	Ile	Lys
				180					185					190		
	Glu	Arg	Ile	Arg	Arg	Ile	Ala	Pro	Thr	His	Ala	Ser	Val	Leu	Ile	Thr
				195				200					205			
20	Gly	Glu	Ser	Gly	Thr	Gly	Lys	Glu	Leu	Ile	Ala	Glu	Ala	Leu	His	Arg
				210			215					220				
	Gly	Ser	Lys	Arg	Ala	Ser	Ala	Pro	Phe	Val	Lys	Val	Asn	Leu	Gly	Gly
					230						235				240	
	Ile	Pro	Glu	Ser	Leu	Phe	Glu	Ser	Glu	Leu	Phe	Gly	His	Lys	Lys	Gly
					245					250				255		
25	Ala	Phe	Thr	Asn	Ala	Phe	Ser	Asp	Arg	Lys	Gly	Arg	Phe	Glu	Leu	Ala
				260					265					270		
	Asp	Gly	Gly	Thr	Ile	Phe	Leu	Asp	Glu	Ile	Gly	Glu	Leu	Pro	Val	Gly
				275				280					285			
	Asn	Gln	Val	Lys	Leu	Leu	Arg	Val	Leu	Gln	Glu	Gln	Thr	Phe	Glu	Pro
				290			295					300				
30	Leu	Gly	Glu	Ser	Val	Ser	His	Arg	Val	Asp	Ile	Arg	Val	Val	Ser	Ala
					310						315					320
	Thr	Asn	Ala	Ser	Leu	Glu	Arg	Met	Val	Ala	Glu	Gly	Arg	Phe	Arg	Glu
					325					330				335		
35	Asp	Leu	Tyr	Tyr	Arg	Ile	Asn	Leu	Ile	His	Leu	His	Leu	Pro	Pro	Leu
				340					345					350		
	Arg	Glu	Arg	Gln	Glu	Asp	Ile	Gln	Leu	Leu	Val	Glu	Ala	Phe	Ser	Glu
				355				360					365			
40	Ala	Phe	Ala	Gln	Ser	Asn	Gly	Leu	Pro	His	Ala	Val	Trp	Ser	Ala	Glu
					375						380					
	Ala	Met	Arg	Arg	Ile	Cys	Ala	Met	Pro	Leu	Pro	Gly	Asn	Val	Arg	Glu
					390						395				400	
	Leu	Lys	Asn	Val	Val	Glu	Arg									

```

55      (2) INFORMATION FOR SEQ ID NO:285

          (i) SEQUENCE CHARACTERISTICS:
              (A) LENGTH: 263 amino acids
              (B) TYPE: amino acid
              (D) TOPOLOGY: linear

60      (ii) MOLECULE TYPE: protein

          (iii) HYPOTHETICAL: YES

65      (vi) ORIGINAL SOURCE:
              (A) ORGANISM: Porphyromonas gingivalis

          (ix) FEATURE:
              (A) NAME/KEY: misc_feature
              (B) LOCATION 1...263

70      (xi) SEQUENCE DESCRIPTION: SEQ ID NO:285

```

75 Arg Ser Leu Gln Ser Phe Gln Asn Lys Lys His Ser Ser Met Leu Lys

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```

1       5       10       15
Ile Lys Asn Leu His Ala Thr Val Gln Gly Lys Glu Ile Leu Lys Gly
20       25       30
Ile Asn Leu Glu Ile Asn Ala Gly Glu Ile His Ala Ile Met Gly Pro
35       40       45
Asn Gly Ser Gly Lys Ser Thr Leu Ser Ser Val Leu Val Gly His Pro
50       55       60
Ser Phe Glu Val Thr Glu Gly Glu Val Thr Phe Asn Gly Ile Asp Leu
65       70       75       80
Leu Glu Leu Glu Pro Glu Glu Arg Ala His Leu Gly Leu Phe Leu Ser
85       90       95
Phe Gln Tyr Pro Val Glu Ile Pro Gly Val Ser Met Val Asn Phe Met
100      105      110
Arg Ala Ala Val Asn Glu His Arg Lys Ala Ile Gly Ala Glu Pro Val
115      120      125
Ser Ala Ser Asp Phe Leu Lys Met Met Arg Glu Lys Arg Ala Ile Val
130      135      140
Glu Leu Asp Asn Lys Leu Ala Ser Arg Ser Val Asn Glu Gly Phe Ser
145      150      155      160
Gly Gly Glu Lys Lys Arg Asn Glu Ile Phe Gln Met Ala Met Leu Glu
165      170      175
Pro Lys Leu Ala Ile Leu Asp Glu Thr Asp Ser Gly Leu Asp Ile Asp
180      185      190
Ala Leu Arg Ile Val Ala Gly Gly Val Asn Arg Leu Arg Ser Pro Glu
195      200      205
Asn Ala Ala Ile Val Ile Thr His Tyr Gln Arg Leu Leu Glu Tyr Ile
210      215      220
Lys Pro Asp Phe Val His Val Leu Tyr Lys Gly Arg Ile Val Lys Ser
225      230      235      240
Gly Gly Ala Glu Leu Ala Leu Thr Leu Glu Glu Lys Gly Tyr Asp Trp
245      250      255
Ile Lys Glu Glu Ile Gly Glu
260

```

## 35 (2) INFORMATION FOR SEQ ID NO:286

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 462 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Porphyromonas gingivalis
- (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...462
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:286

```

55 Ser Met Ala Lys Glu Lys Thr Ile Tyr Val Cys Arg Ser Cys Gly Thr
1       5       10       15
Lys Tyr Ala Lys Trp Gln Gly Asn Cys Asn Ala Cys Gly Glu Trp Asn
20       25       30
Cys Ile Asp Glu Glu Lys Val Pro Ala Pro Ala Ser Gly Lys His Ala
35       40       45
Ala Lys Ser Phe Met Pro Arg Glu Gln Asp Asn Arg Pro Arg Leu Leu
50       55       60
Gln Asp Val Glu Ser Gly Asp Glu Glu Arg Ile Arg Leu Gly Asp Glu
65       70       75       80
Glu Phe Asp Arg Val Leu Gly Gly Gly Ile Val Lys Gly Ala Phe Val
85       90       95
Leu Leu Gly Gly Glu Pro Gly Ile Gly Lys Ser Thr Leu Ile Leu Gln
100      105      110
Thr Val Leu Arg Leu Pro Gln Leu Arg Thr Leu Tyr Val Ser Gly Glu
115      120      125
Glu Ser Ala Arg Gln Leu Lys Met Arg Ala Glu Arg Leu Gly Gln Ala
130      135      140
Met Asn Gly Cys Tyr Val Tyr Cys Glu Thr Asn Ile Glu Arg Ile Leu
145      150      155      160
Ser Arg Ala Glu Glu Leu Thr Pro Asp Leu Leu Val Ile Asp Ser Ile
165      170      175

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165 170 175  
 Gln Thr Val Tyr Thr Glu Glu Met Glu Ser Ser Ala Gly Ser Val Gly  
 180 185 190  
 Gln Ile Arg Glu Cys Ala Ala Leu Leu Lys Tyr Cys Lys Thr Thr  
 195 200 205  
 Gly Ile Pro Val Ile Val Ile Gly His Ile Thr Lys Glu Gly Ser Ile  
 210 215 220  
 Ala Gly Pro Lys Val Leu Glu His Ile Val Asp Thr Val Leu Leu Phe  
 225 230 235 240  
 Asp Gly Asp Lys His His Leu Tyr Arg Ile Leu Arg Gly Gln Lys Asn  
 245 250 255  
 Arg Tyr Gly Ser Thr Ser Glu Leu Gly Ile Tyr Glu Met Arg Gln Asp  
 260 265 270  
 Gly Leu Arg Gly Val Glu Asn Pro Ser Glu His Leu Ile Thr Arg Asn  
 275 280 285  
 Arg Glu Asp Leu Ser Gly Ile Ala Ile Ala Val Ala Met Glu Gly Ile  
 290 295 300  
 Arg Pro Ile Leu Ile Glu Ala Gln Ala Leu Val Ser Ser Ala Ile Tyr  
 305 310 315 320  
 Ala Asn Pro Gln Arg Ser Ala Thr Gly Phe Asp Ile Arg Arg Met Asn  
 325 330 335  
 Met Leu Leu Ala Val Leu Glu Lys Arg Ala Gly Phe Lys Leu Ile Gln  
 340 345 350  
 Lys Asp Val Phe Leu Asn Ile Ala Gly Gly Ile Lys Ile Ala Asp Pro  
 355 360 365  
 Ala Thr Asp Leu Ala Val Ile Ser Ala Val Leu Ala Ser Ser Leu Asp  
 370 375 380  
 Ile Val Ile Pro Pro Ala Val Cys Met Thr Gly Glu Val Gly Leu Ser  
 385 390 395 400  
 Gly Glu Ile Arg Pro Val Ser Arg Ile Glu Gln Arg Ile Thr Glu Ala  
 405 410 415  
 Arg Arg Ile Gly Phe Lys Glu Ile Leu Val Pro Ala Asp Asn Phe Arg  
 420 425 430  
 Gln Glu Asp Ala Gly Arg Phe Gly Ile Arg Leu Val Pro Val Arg Lys  
 435 440 445  
 Val Glu Glu Ala Phe Arg His Leu Phe Ser Lys Gly Arg Glu  
 450 455 460

## (2) INFORMATION FOR SEQ ID NO:287

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 373 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
 (ii) MOLECULE TYPE: protein  
 (iii) HYPOTHETICAL: YES  
 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Porphyromonas gingivalis  
 (ix) FEATURE:  
 (A) NAME/KEY: misc feature  
 (B) LOCATION 1...373

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:287

Gly Ser Cys Gly Ser Ser Pro Ala Ile Gly Arg Ser Gly Cys Ser Arg  
 1 5 10 15  
 Cys Asp Arg Arg Ile Gly His Gly Leu Ser Thr Ser Ala Phe Arg Thr  
 20 25 30  
 Tyr Ala Gly Leu Val Cys His Ser Arg Leu Arg Asp Gln Ser Ser Cys  
 35 40 45  
 Arg Val Cys Gly Met Arg Pro Ile Gly Gln Leu Phe Phe Pro Ser Cys  
 50 55 60  
 Pro Arg Arg Ser Ala Ser Asp Ala Gly Arg Thr Glu Arg Ile Gln Ser  
 65 70 75 80  
 Pro Leu Gln Asn Leu Leu Gln Glu Met Gln Phe Ser Pro Thr Asn Arg  
 85 90 95  
 Arg Asn Pro Phe Asp Asn Met Asn Ser Arg His Leu Thr Ile Thr Ile  
 100 105 110  
 Ile Ala Gly Leu Ser Leu Phe Val Leu Thr Leu Gly Gly Cys Ser Val  
 115 120 125  
 Ala Gln Gln Asp Thr Gln Trp Thr Leu Gly Gly Lys Leu Phe Thr Ser



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130 135 140  
 Ala Trp Ile Gln Arg Ser Ala Glu Tyr Gln Ala Leu Cys Ile Gln Ala  
 145 150 155 160  
 Tyr Asn Ile Ala Thr Glu Arg Val Asp Ala Leu Pro Ala Glu Arg Lys  
 165 170 175  
 5 Gln Gly Asp Arg Pro Tyr Ala Ile Val Thr Asp Ile Asp Glu Thr Ile  
 180 185 190  
 Leu Asp Asn Thr Pro Asn Ser Val Tyr Gln Ala Leu Arg Gly Lys Asp  
 195 200 205  
 10 Tyr Asp Glu Glu Thr Trp Gly Lys Trp Cys Ala Gln Ala Asp Ala Asp  
 210 215 220  
 Thr Leu Ala Gly Ala Leu Ser Phe Phe Leu His Ala Ala Asn Lys Gly  
 225 230 235 240  
 15 Ile Glu Val Phe Tyr Val Thr Asn Arg Arg Asp Asn Leu Arg Glu Ala  
 245 250 255  
 Thr Leu Gln Asn Leu Gln Arg Tyr Gly Phe Pro Phe Ala Asp Glu Glu  
 260 265 270  
 His Leu Leu Thr Thr His Gly Pro Ser Asp Lys Glu Pro Arg Arg Leu  
 275 280 285  
 20 Lys Ile Gln Glu Gln Tyr Glu Ile Val Leu Leu Ile Gly Asp Asn Leu  
 290 295 300  
 Gly Asp Phe His His Phe Phe Asn Thr Lys Glu Glu Ser Gly Arg Lys  
 305 310 315 320  
 25 Gln Ala Leu Gly Leu Thr Ala Gly Glu Phe Gly Arg His Phe Ile Met  
 325 330 335  
 Leu Pro Asn Pro Asn Tyr Gly Ser Trp Glu Pro Ala Trp Tyr Gly Gly  
 340 345 350  
 Lys Tyr Pro Pro Leu Pro Glu Arg Asp Lys Ala Leu Lys Gln Leu His  
 355 360 365  
 30 Ser Gln Asn Ser Arg  
 370

## (2) INFORMATION FOR SEQ ID NO:288

- 35 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 426 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
 40 (ii) MOLECULE TYPE: protein  
 (iii) HYPOTHETICAL: YES  
 45 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Porphyromonas gingivalis  
 (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...426  
 50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:288

Arg Trp Gly Phe Ser Asn Phe Val Ala Met Ser Thr Asn Ile Asp Val  
 1 5 10 15  
 55 Gln Gln Ile Lys Gln Arg Phe Gly Ile Gly Ser Ser Pro Leu Met  
 20 25 30  
 Glu His Ala Ile Arg Val Ala Ala Gln Val Ala Pro Thr Asp Met Ser  
 35 40 45  
 60 Val Leu Val Thr Gly Glu Ser Gly Ser Gly Lys Glu Phe Phe Pro Gln  
 50 55 60  
 Ile Ile His Tyr Tyr Ser Ala Arg Lys His His Ser Tyr Ile Ala Val  
 65 70 75 80  
 Asn Cys Gly Ala Ile Pro Glu Gly Thr Ile Asp Ser Glu Leu Phe Gly  
 85 90 95  
 65 His Arg Lys Gly Ser Phe Thr Gly Ala Val Ser Asp Arg Lys Gly Tyr  
 100 105 110  
 Phe Glu Glu Ala Ser Gly Gly Thr Ile Phe Leu Asp Glu Val Gly Glu  
 115 120 125  
 70 Leu Pro Leu Pro Thr Gln Ala Arg Leu Leu Arg Val Leu Glu Thr Gly  
 130 135 140  
 Glu Phe Ile Pro Val Gly Ala Ser Gln Ser Gln Lys Thr Asp Val Arg  
 145 150 155 160  
 Ile Val Ala Ala Thr Asn Val Asn Leu Lys Glu Ala Val Ala Asn Gly  
 165 170 175  
 75 Lys Phe Arg Glu Asp Leu Phe Phe Arg Leu Asn Thr Val Pro Ile Glu

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180 185 190  
 Val Pro Ala Leu Arg Met Arg Pro Asp Asp Val Pro Leu Leu Phe Arg  
 195 200 205  
 5 Arg Phe Ala Ala Asp Ser Ala Glu Lys Tyr Arg Met Pro Pro Leu Arg  
 210 215 220  
 Leu Ser Asp Glu Ala Arg Thr Ile Leu Met Arg Tyr Arg Trp Pro Gly  
 225 230 235 240  
 Asn Val Arg Glu Leu Arg Asn Ile Thr Asp Arg Leu Ser Ile Leu Glu  
 245 250 255  
 10 Glu Glu Arg Thr Val Ser Ala Glu Thr Ile Thr Arg Tyr Leu Asp Ala  
 260 265 270  
 Glu Gly Met Gln Asp Leu His Pro Val Val Ile Arg Arg Asn Glu Thr  
 275 280 285  
 15 Thr Glu Ala Asp Lys Gln Ile Pro His Tyr Glu Arg Glu Ile Ile Tyr  
 290 295 300  
 Gln Val Leu Tyr Asp Met Lys Lys Glu Ile Ala Asp Leu Lys Gly Met  
 305 310 315 320  
 Met Asn Arg Leu Ala His His Glu Gln Pro Ser Trp Pro Val Gly Ser  
 325 330 335  
 20 Asp Val Trp Gly Asn Asp Asp Lys Arg Thr Ala Asp Pro Lys Trp Gly  
 340 345 350  
 Val Ser Thr His Lys Ala Pro Ile Ala Asn Ala Ala Glu Pro Val Glu  
 355 360 365  
 25 Pro Ile Gln Glu Ala Ser Glu Tyr Thr Glu Asp Pro Val Ser Leu Glu  
 370 375 380  
 Glu Val Glu Lys Lys Met Ile Ser Leu Ala Leu Glu Arg His Gly Gly  
 385 390 395 400  
 Arg Arg Lys Gln Thr Ala Glu Glu Leu Lys Ile Ser Glu Arg Thr Leu  
 405 410 415  
 30 Tyr Arg Lys Ile Lys Glu Tyr Gly Leu Glu  
 420 425

(2) INFORMATION FOR SEQ ID NO:289

- 35 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 653 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
 40 (ii) MOLECULE TYPE: protein  
 (iii) HYPOTHETICAL: YES  
 45 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Porphyromonas gingivalis  
 (ix) FEATURE:  
 (A) NAME/KEY: misc feature  
 (B) LOCATION 1...653  
 50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:289

55 Lys Asn Leu Pro Arg Tyr Ala Pro Ala Phe Gly Arg Asn Arg Lys Arg  
 1 5 10 15  
 Glu Gln Pro Asp Pro Asp Asn Asp Asp Ser Arg Gly Arg Ser His Arg  
 20 25 30  
 Gln Ser Gly Arg Ala Val Thr Val Val Cys Arg Arg Ile Gln Thr Pro  
 35 40 45  
 60 Leu Pro His Met Ile Leu Leu Phe Gly Gly Thr Thr Glu Gly Arg Ala  
 50 55 60  
 Ala Ala Arg Val Leu Asp Glu Ala Gly Ser Pro Phe Phe Tyr Ser Thr  
 65 70 75 80  
 Lys Gly Asn Leu Gln Glu Ile Gln Ser Ser His Gly His Arg Leu Thr  
 85 90 95  
 65 Gly Ala Met Thr Val Ala Asp Met Val Ser Phe Cys Arg Lys Glu Glu  
 100 105 110  
 Ile Arg Leu Ile Val Asp Ala Ala His Pro Phe Ala Glu Glu Leu His  
 115 120 125  
 70 Ala Ser Val Ala Glu Ala Ser Glu Gln Thr Gly Ile Pro Val Val Arg  
 130 135 140  
 Tyr Glu Arg Gln Tyr Pro Pro Arg Glu Glu Gly Ile Val Trp Cys Ala  
 145 150 155 160  
 Asn Tyr Asp Thr Ala Ala Glu Arg Met Leu Gly Asp Gly Val Gln Arg  
 165 170 175  
 75 Leu Leu Met Leu Thr Gly Val Asn Thr Ile Pro Lys Leu Ala Ala Phe

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180 185 190  
 Trp Lys Glu Arg Thr Thr Phe Cys Arg Ile Leu Lys Arg Asp Glu Ser  
 195 200 205  
 Val Ala Leu Ala Glu Lys Asn Gly Phe Pro Ala Glu Arg Ile Val Phe  
 210 215 220  
 Phe Glu Pro His Ala Asp Glu Glu Leu Met Gln Ala Val Arg Pro Asp  
 225 230 235 240  
 Ala Ile Ile Thr Lys Glu Ser Gly Glu Ser Gly Tyr Phe Arg Glu Lys  
 245 250 255  
 10 Ile Glu Ala Ala Arg Arg Met Gly Ile Arg Ile Tyr Ala Val Val Arg  
 260 265 270  
 Pro Pro Leu Pro Pro Ser Phe Ile Pro Val Gly Gly Pro Val Gly Leu  
 275 280 285  
 15 Arg Arg Ala Val Glu Arg Leu Val Pro Gly Phe Phe Ser Leu Arg Ser  
 290 295 300  
 Gly Phe Thr Thr Gly Thr Ala Thr Ala Ala Val Val Ala Ala Met  
 305 310 315 320  
 Tyr Arg Leu Met Gly Leu Gly Ser Leu Ala Glu Ala Pro Val Glu Leu  
 325 330 335  
 20 Pro Ser Gly Glu Ile Val Ser Leu Pro Ile Ala Glu Ile Arg Glu Glu  
 340 345 350  
 Glu Asp Ala Val Val Ser Ala Val Leu Lys Asp Ala Gly Asp Asp Pro  
 355 360 365  
 25 Asp Val Thr Asn Gly Met Ala Val Cys Ala Thr Ile Arg Leu Asn Pro  
 370 375 380  
 Glu His Glu Glu Val Arg Phe Leu Gln Gly Glu Gly Val Gly Val Val  
 385 390 395 400  
 Thr Leu Pro Gly Leu Gly Leu Glu Val Gly Gly Pro Ala Ile Asn Leu  
 405 410 415  
 30 Val Pro Arg Arg Met Met Thr Ala Glu Val Arg Arg Leu Tyr Ala Gln  
 420 425 430  
 Gly Gly Val Asp Ile Thr Ile Ser Val Pro Glu Gly Arg Glu Ala Ala  
 435 440 445  
 35 Thr Gln Thr Phe Asn Pro Arg Leu Gly Ile Arg Asp Gly Ile Ser Ile  
 450 455 460  
 Ile Gly Thr Ser Gly Val Val Lys Pro Phe Ser Ala Glu Ala Phe Val  
 465 470 475 480  
 Gly Ala Ile Arg Lys Gln Val Gly Ile Ala Thr Ala Leu Gly Ala Asn  
 485 490 495  
 40 His Ile Val Leu Asn Ser Gly Ala Lys Ser Glu Arg Tyr Val Lys Gly  
 500 505 510  
 Ala Tyr Pro Ala Leu Ile Pro Gln Ala Phe Val Gln Tyr Gly Asn Phe  
 515 520 525  
 45 Val Gly Glu Ser Leu Ser Cys Val Ala Ser Phe Pro Ser Val Arg Ser  
 530 535 540  
 Val Thr Val Gly Ile Met Leu Gly Lys Ala Val Lys Leu Ala Glu Gly  
 545 550 555 560  
 Tyr Leu Asp Thr His Ser Lys Lys Val Val Met Asn Arg Asp Phe Leu  
 565 570 575  
 50 His Glu Leu Ala Arg Gln Ala Gly Cys Ser Glu Asp Ile His Ala Ile  
 580 585 590  
 Ile Asp Ser Leu Asn Leu Ala Arg Glu Leu Trp Thr Met Pro Ser Ala  
 595 600 605  
 55 Glu Asp Ser Asp Arg Leu Leu Arg Lys Ile Ala Glu Arg Ser Trp Glu  
 610 615 620  
 Thr Cys Arg Pro Ser Val Pro Ser Ala Glu Leu Glu Leu Leu Ile  
 625 630 635 640  
 Asp Glu Ser Gly Ala Ile Arg Phe Arg Ile Gly Gly Glu  
 645 650

(2) INFORMATION FOR SEQ ID NO:290

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 451 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

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(A) NAME/KEY: misc\_feature  
(B) LOCATION: 1...451

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:290

5  
Gln Gln Arg Pro His Arg Ile Ile Met Leu Arg Thr Phe Arg Ile Gly  
1 5 10 15  
Gly Ile His Pro Pro Glu Asn Lys Leu Ser Ala Gly Lys Pro Val Glu  
20 25 30  
10 Val Leu Pro Ile Pro Ser Gln Val Val Ile Pro Leu Gly Gln His Ile  
35 40 45  
Gly Ala Pro Ala Thr Ala Thr Val Lys Lys Gly Asp Glu Val Lys Val  
50 55 60  
15 Gly Thr Ile Ile Ala Gln Ala Gly Gly Phe Val Ser Ala Asn Ile His  
65 70 75 80  
Ser Ser Val Ser Gly Lys Val Leu Lys Ile Asp Asn Val Tyr Asp Ser  
85 90 95  
Ser Gly Tyr Pro Lys Pro Ala Val Phe Ile Ser Val Glu Gly Asp Glu  
100 105 110  
20 Trp Glu Glu Gly Ile Asp Arg Ser Pro Ala Ile Val Lys Glu Cys Asn  
115 120 125  
Leu Asp Ala Lys Glu Ile Val Ala Lys Ile Ser Ala Ala Gly Ile Val  
130 135 140  
25 Gly Leu Gly Gly Ala Thr Phe Pro Thr His Val Lys Leu Ser Pro Pro  
145 150 155 160  
Pro Gly Asn Lys Ala Glu Ile Leu Ile Ile Asn Ala Val Glu Cys Glu  
165 170 175  
Pro Tyr Leu Thr Ser Asp His Val Leu Met Leu Glu His Gly Glu Glu  
180 185 190  
30 Ile Met Ile Gly Val Ser Ile Leu Met Lys Ala Ile Gln Val Asn Lys  
195 200 205  
Ala Val Ile Gly Val Glu Asn Asn Lys Lys Asp Ala Ile Ala His Leu  
210 215 220  
35 Thr Lys Leu Ala Thr Ala Tyr Pro Gly Ile Glu Val Met Pro Leu Lys  
225 230 235 240  
Val Gln Tyr Pro Gln Gly Gly Glu Lys Gln Leu Ile Asp Ala Val Ile  
245 250 255  
Arg Lys Gln Val Lys Ser Gly Ala Leu Pro Ile Ser Thr Gly Ala Val  
260 265 270  
40 Val Gln Asn Val Gly Thr Val Phe Ala Val Tyr Glu Ala Val Gln Lys  
275 280 285  
Asn Lys Pro Leu Val Glu Arg Ile Val Thr Val Thr Gly Lys Lys Leu  
290 295 300  
45 Ser Arg Pro Ser Asn Leu Leu Val Arg Ile Gly Thr Pro Ile Ala Ala  
305 310 315 320  
Leu Ile Glu Ala Ala Gly Gly Leu Pro Glu Asn Thr Gly Lys Ile Ile  
325 330 335  
Gly Gly Gly Pro Met Met Gly Arg Ala Leu Leu Ser Pro Asp Val Pro  
340 345 350  
50 Val Thr Lys Gly Ser Ser Gly Val Leu Ile Leu Asp Arg Glu Glu Ala  
355 360 365  
Val Arg Lys Pro Met Arg Asp Cys Ile Arg Cys Ala Lys Cys Val Gly  
370 375 380  
55 Val Cys Pro Met Gly Leu Asn Pro Ala Phe Leu Met Arg Asp Thr Leu  
385 390 395 400  
Tyr Lys Ser Trp Glu Thr Ala Glu Lys Gly Asn Val Val Asp Cys Ile  
405 410 415  
Glu Cys Gly Ser Cys Ser Phe Thr Cys Pro Ala Asn Arg Pro Leu Leu  
420 425 430  
60 Asp Tyr Ile Arg Gln Ala Lys Lys Thr Val Met Gly Ile Gln Arg Ala  
435 440 445  
Arg Lys Gln  
450

65 (2) INFORMATION FOR SEQ ID NO:291

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 489 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

70

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

75

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(vi) ORIGINAL SOURCE:  
(A) ORGANISM: Porphyromonas gingivalis

5 (ix) FEATURE:  
(A) NAME/KEY: misc\_feature  
(B) LOCATION 1...489

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:291

10 Met Asn Ser Gln Lys Lys Glu Ala Phe Asn Met Lys Arg Ile Gln Leu  
1 5 10 15  
Thr Leu Ile Ala Leu Phe Ala Ala Val Ala Gly Leu Val Ala Gln Asn  
20 25 30  
Ala Tyr Glu Gly Val Ile Ser Tyr Lys Ile Ser Leu Asp Lys Thr Gly  
15 35 40 45  
Asn Lys Val Val Leu Asn Gly Ala Ala Asp Met Ser Asn Leu Lys Leu  
50 55 60  
Lys Ser Thr Gln Met Ile Ile Val Thr Pro Ile Leu Arg Ser Glu Asp  
65 70 75 80  
20 Gly Thr Ser Arg Val Glu Phe Pro Ser Val Val Ile Thr Gly Arg Asn  
85 90 95  
Arg Thr Lys Ala Leu Lys Arg Glu Ile Ala Phe Ser Ser Ala Leu Pro  
100 105 110  
Gln Ala Lys His Ala Ala Gln Tyr Ile Arg Arg His Asn Gly Lys Ser  
115 120 125  
25 Glu Gln Phe Ala Phe Thr Gly Glu His Ala Tyr Ala Ser Trp Met Met  
130 135 140  
Asp Ala Lys Phe Val Val Arg Glu Glu Val Arg Gly Cys Ala Lys Cys  
145 150 155 160  
30 Pro Val Gly Leu Ser Ser Asn Ile Val Pro Phe Asp Pro Leu Phe Asn  
165 170 175  
Pro Ala Glu Ala Pro Tyr Leu Leu Ala His Ile Thr Pro Ala Glu Glu  
180 185 190  
Val Glu Lys Gln Arg Glu Ser Ser Phe Asp Ala Tyr Ile Asn Phe Lys  
195 200 205  
35 Val Asn Lys Ala Asp Val Leu Pro Glu Tyr Arg Asn Asn Lys Ala Glu  
210 215 220  
Leu Glu Lys Ile Lys Glu Phe Val Ser Thr Val Lys Ala Asn Pro Asn  
225 230 235 240  
40 Tyr Ser Val Asn Lys Met Ile Ile Glu Gly Phe Ala Ser Pro Glu Ala  
245 250 255  
Ser Ile Ala His Asn Lys Ala Leu Ser Glu Arg Arg Ala Lys Arg Leu  
260 265 270  
45 Ala Glu Glu Leu Val Arg Lys Tyr Gly Lys Thr Leu Pro Asn Ile Thr  
275 280 285  
Thr Glu Phe Gly Gly Glu Asp Trp Lys Gly Leu Lys Leu Ala Ile Glu  
290 295 300  
Lys Ser Asp Ile Ala Asp Arg Asp Arg Val Leu Glu Ile Ile Asn Ser  
305 310 315 320  
50 Asp Lys Tyr Ala Asp Asp Asp Ala Arg Glu Gln Ala Leu Lys Gln Leu  
325 330 335  
Ser Ser Tyr Arg Tyr Ile Leu Asp Gln Ile Tyr Pro Asn Leu Arg Arg  
340 345 350  
55 Asn Thr Ile Thr Met Gly Tyr Ile Val Arg Asp Tyr Thr Leu Glu Glu  
355 360 365  
Ala Arg Glu Ile Ile Lys Thr Ala Pro Lys Glu Leu Ser Glu Ala Glu  
370 375 380  
Met Tyr Arg Val Ala Met Ser Tyr Pro Glu Gly His Gln Glu Arg Leu  
385 390 395 400  
60 Phe Ala Leu Asn Thr Thr Leu Lys Tyr Phe Pro Glu Ser Val Thr Gly  
405 410 415  
Arg Ile Asn Leu Ala Val Ala Ala Phe Asn Gly Gly Asp Val Gln Gln  
420 425 430  
Ala Ile Ala Leu Leu Ser Pro Ile Gln Thr Glu Lys Gly Val Ser Asn  
435 440 445  
65 Ile Leu Gly Ala Ala Tyr Ala Arg Thr Gly Asp Phe Ala Arg Ala Glu  
450 455 460  
Thr Phe Phe Arg Lys Ala Val Ala Glu Gly Asp Ala Asn Ala Gln Arg  
465 470 475 480  
70 Asn Leu Asp Met Leu Leu Gly Lys Lys  
485

(2) INFORMATION FOR SEQ ID NO:292

75 (i) SEQUENCE CHARACTERISTICS:

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(A) LENGTH: 384 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

5 (ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

10 (A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

(A) NAME/KEY: misc\_feature  
 (B) LOCATION: 1...384

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:292

```

Asp Met Ala Glu Lys Arg Asp Tyr Tyr Glu Val Leu Gly Val Ser Lys
1      5      10      15
20 Asn Ala Thr Asp Asp Glu Leu Lys Lys Ala Tyr Arg Lys Lys Ala Ile
    20      25      30
    Gln Tyr His Pro Asp Lys Asn Pro Gly Asp Lys Glu Ala Glu Glu His
    35      40      45
25 Phe Lys Glu Val Ala Glu Ala Tyr Asp Val Leu Ser Asp Pro Gln Lys
    50      55      60
    Arg Ser Gln Tyr Asp Gln Phe Gly His Ala Gly Leu Gly Gly Ala Ala
    65      70      75      80
    Gly Gly Gly Phe Ser Gly Gly Gly Met Ser Met Glu Asp Ile Phe Ser
    85      90      95
30 Arg Phe Gly Asp Leu Phe Gly Gly Phe Gly Gly Phe Gly Gly Phe Ser
    100      105      110
    Asp Met Gly Gly Gly Ser Arg Arg Arg Val Arg Arg Gly Ser Asp Leu
    115      120      125
35 Arg Val Arg Val Lys Leu Ser Leu Ala Asp Ile Ser Lys Gly Val Glu
    130      135      140
    Lys Lys Val Lys Val Lys Lys Gln Val Val Cys Ser Lys Cys Arg Gly
    145      150      155      160
    Asp Gly Thr Glu Glu Ala Asn Gly Lys Thr Thr Cys Gln Thr Cys His
    165      170      175
40 Gly Thr Gly Val Val Thr Arg Val Ser Asn Thr Phe Leu Gly Ala Met
    180      185      190
    Gln Thr Gln Ser Thr Cys Pro Thr Cys His Gly Glu Gly Glu Ile Ile
    195      200      205
45 Thr Lys Pro Cys Ser Lys Cys Lys Gly Glu Gly Val Glu Ile Gly Glu
    210      215      220
    Glu Val Ile Ser Phe His Ile Pro Ala Gly Val Ala Glu Gly Met Gln
    225      230      235      240
    Met Ser Val Asn Gly Lys Gly Asn Ala Ala Pro Arg Gly Gly Val Asn
    245      250      255
50 Gly Asp Leu Ile Val Val Ile Ala Glu Glu Pro Asp Pro Asn Leu Ile
    260      265      270
    Arg Asn Gly Asn Asp Leu Ile Tyr Asn Leu Leu Ile Ser Val Pro Leu
    275      280      285
55 Ala Ile Lys Gly Gly Ser Val Glu Val Pro Thr Ile Asp Gly Arg Ala
    290      295      300
    Lys Ile Arg Ile Glu Ala Gly Thr Gln Pro Gly Lys Met Leu Arg Leu
    305      310      315      320
    Arg Asn Lys Gly Leu Pro Ser Val Asn Gly Tyr Gly Met Gly Asp Gln
    325      330      335
60 Leu Val Asn Val Asn Val Tyr Ile Pro Glu Ser Ile Asp Ala Lys Asp
    340      345      350
    Glu Gln Ala Ile Ala Ala Met Glu Asn Ser Asp Ser Phe Lys Pro Thr
    355      360      365
65 Asp Ala Ala Arg Lys Asp Ile Asp Lys Lys Tyr Arg Glu Met Leu Asp
    370      375      380
  
```

(2) INFORMATION FOR SEQ ID NO:293

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 309 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

75 (ii) MOLECULE TYPE: protein

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(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Porphyromonas gingivalis

5

(ix) FEATURE:

(A) NAME/KEY: misc\_feature

(B) LOCATION 1...309

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:293

```

Arg Phe Asp Ser Thr Thr Asn Val Ser Gln Ile Asn Leu Arg Thr Glu
1      5      10      15
Met Lys Lys Leu Ile Leu Ala Thr Leu Gly Leu Met Ala Ile Ala Met
15      20      25      30
Leu Ser Cys Ser Ser Asn Asn Lys Asp Leu Glu Asn Lys Gly Glu Ala
35      40      45
Thr Leu Leu Val Thr Phe Gly Ser Ser Tyr Lys Ala Pro Arg Glu Thr
50      55      60
Tyr Ala Lys Ile Glu Lys Thr Phe Ala Ala Ala Tyr Pro Asp Gln Arg
20      65      70      75      80
Ile Ser Trp Thr Tyr Thr Ser Ser Ile Ile Arg Lys Lys Leu Ala Gln
85      90      95
Gln Gly Ile Tyr Ile Asp Ala Pro Asp Glu Ala Leu Glu Lys Leu Ala
25      100      105      110
Arg Leu Gly Tyr Lys Lys Ile Asn Val Gln Ser Leu His Val Ile Pro
115      120      125
Gly Arg Glu Tyr Asp Glu Met Ile Asp Phe Val Asn Lys Phe Lys Ala
130      135      140
Ala His Ser Asp Ile Thr Val Lys Val Gly Ala Pro Leu Phe Asp Thr
30      145      150      155      160
Asp Glu Asp Met Arg Glu Val Ala Glu Ile Leu His Lys Arg Phe Gln
165      170      175
Gln Thr Ile Glu Lys Gly Glu Ala Ile Val Phe Met Gly His Gly Thr
35      180      185      190
Glu His Ala Ala Asn Asp Arg Tyr Ala Arg Ile Asn Lys Ile Met Lys
195      200      205
Asn Tyr Ser Lys Phe Met Ile Val Gly Thr Val Glu Ser Asp Pro Ser
210      215      220
Ile Asn Asp Val Ile Ala Glu Leu Lys Glu Thr Gly Ala Thr Ala Val
40      225      230      235      240
Thr Met Met Pro Leu Met Ser Val Ala Gly Asp His Ala Thr Asn Asp
245      250      255
Met Ala Gly Asp Glu Asp Asp Ser Trp Lys Thr Leu Leu Thr Asn Ala
45      260      265      270
Gly Tyr Thr Val Ser Ile Asp Lys Leu Asp Asn Gly Asn Phe Ser Ala
275      280      285
Leu Gly Asp Ile Glu Glu Ile Arg Asn Ile Trp Leu Lys His Met Lys
290      295      300
Ala Thr Ser Ala Arg
50      305

```

(2) INFORMATION FOR SEQ ID NO:294

55

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 491 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

60

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Porphyromonas gingivalis

65

(ix) FEATURE:

(A) NAME/KEY: misc\_feature

(B) LOCATION 1...491

70

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:294

```

Arg Arg Asp Ala Arg Arg Gln Leu Val Arg Arg Arg Lys Glu Leu
1      5      10      15
Ser Gly Thr Ala Asn Thr Arg Cys Arg Arg Arg Val Phe Pro Glu Arg
75

```

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5                   20                   25                   30  
 Arg Ser Ala Ile Arg Trp Cys Phe Pro Arg Leu Arg Asp Gly Leu Gln  
                   35                   40                   45  
 Pro Ile Arg Phe Gly Ser Leu Leu Ala Asn Pro Gln Gln Leu Ser Arg  
                   50                   55                   60  
 Gly Val Arg Leu Arg Ser Phe Glu Ser Arg Arg Gln Pro Ile Cys Arg  
 65                   70                   75                   80  
 Phe Gln Gly Ile Gln Gly Lys Arg Arg Asp Ile Leu Gln Pro Glu Gly  
                   85                   90                   95  
 10 Asn Ser Leu Leu Arg Thr His Ala His Ser Arg Leu Gly Ala Gly  
                   100                   105                   110  
 Arg Ser Tyr Arg Tyr Leu Ala Pro Arg Thr Thr Ser Arg Pro Pro Thr  
                   115                   120                   125  
 15 Ala Phe Leu Leu Phe Ala Pro Met Thr Ser Val Ser His Leu Arg Thr  
                   130                   135                   140  
 Ile Ser Val Ala Gly Ile Leu Ala Ala Leu Gly Gly Ala Val Leu Ile  
 145                   150                   155                   160  
 Leu Phe Gly Val Asn Leu Phe Leu Gly Ser Val Ala Ile Pro Met Ser  
                   165                   170                   175  
 20 Glu Ile Phe Arg His Leu Phe Ser Asp Arg Pro Glu Gly Gly Glu Ala  
                   180                   185                   190  
 Leu Val His Tyr Asn Ile Leu Trp Lys Ser Arg Leu Pro Glu Ala Leu  
                   195                   200                   205  
 25 Thr Ala Ala Phe Ala Gly Ala Gly Leu Ser Val Ser Gly Leu Gln Met  
                   210                   215                   220  
 Gln Thr Val Phe Arg Asn Pro Leu Ala Gly Pro Ser Val Leu Gly Ile  
 225                   230                   235                   240  
 Ser Ser Gly Ala Ser Leu Gly Val Ala Leu Val Val Leu Leu Ser Gly  
                   245                   250                   255  
 30 Ser Leu Gly Gly Val Ala Leu Ser Ser Leu Gly Tyr Met Gly Glu Val  
                   260                   265                   270  
 Ala Met Asn Ile Ala Ala Ala Val Gly Ser Leu Ala Val Met Gly Leu  
                   275                   280                   285  
 35 Ile Val Phe Val Ser Thr Lys Val Arg Ser His Val Thr Leu Leu Ile  
                   290                   295                   300  
 Ile Gly Val Met Ile Gly Tyr Val Ala Thr Ala Val Ile Gly Val Phe  
 305                   310                   315                   320  
 Lys Phe Phe Ser Ile Glu Glu Asp Ile Arg Ala Tyr Val Ile Trp Gly  
                   325                   330                   335  
 40 Leu Gly Ser Phe Ser Arg Ala Thr Asp Ser Gln Leu Ser Phe Phe Ala  
                   340                   345                   350  
 Ile Leu Met Leu Ile Phe Ile Pro Ala Gly Met Leu Leu Val Lys Gln  
                   355                   360                   365  
 45 Leu Asn Leu Leu Leu Leu Gly Glu Ser Tyr Ala Arg Asn Leu Gly Leu  
                   370                   375                   380  
 Asn Thr Arg Arg Ala Arg Leu Leu Val Ile Ser Ser Ala Gly Leu Leu  
 385                   390                   395                   400  
 Ile Ala Thr Val Thr Ala Tyr Cys Gly Pro Ile Gly Phe Leu Gly Met  
                   405                   410                   415  
 50 Ala Val Pro His Leu Ala Arg Val Ile Phe His Thr Ser Asp His Arg  
                   420                   425                   430  
 Ile Leu Met Pro Ala Thr Cys Leu Ile Gly Ser Ala Leu Ala Leu Phe  
                   435                   440                   445  
 55 Cys Asn Ile Ile Ala Arg Met Pro Gly Phe Glu Gly Ala Leu Pro Val  
                   450                   455                   460  
 Asn Ser Val Thr Ala Leu Val Gly Ala Pro Ile Ile Val Thr Val Leu  
 465                   470                   475                   480  
 Phe Arg Arg Arg Arg Phe Lys Glu Glu Thr Asp  
                   485                   490

(2) INFORMATION FOR SEQ ID NO:295

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 763 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

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(A) NAME/KEY: misc\_feature  
(B) LOCATION 1...763

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:295

5 His Phe Leu Val Thr Ile Met Arg Thr Lys Thr Ile Phe Phe Ala Ile  
1 5 10 15  
Ile Ser Phe Ile Ala Leu Leu Ser Ser Ser Leu Ser Ala Gln Ser Lys  
20 25 30  
10 Ala Val Leu Thr Gly Ser Val Ser Asp Ala Glu Thr Gly Glu Pro Leu  
35 40 45  
Ala Gly Ala Arg Ile Glu Val Lys His Thr Asn Ile Val Ala Gly Ala  
50 55 60  
15 Asp Ala Gly Gly His Phe Glu Ile Lys Asn Leu Pro Ala Gly Gln His  
65 70 75 80  
Thr Ile Ile Cys Ser Leu Gly Gly Tyr Gly Gln Lys Glu Glu Val Val  
85 90 95  
Ala Ile Glu Ala Gly Gln Thr Lys Thr Ile Ser Phe Ala Leu Arg Leu  
100 105 110  
20 Arg Thr Asn Asn Leu Glu Glu Val Val Val Thr Gly Thr Gly Thr Arg  
115 120 125  
Tyr Arg Leu Val Asp Ala Pro Val Ala Thr Glu Val Leu Thr Ala Lys  
130 135 140  
25 Asp Ile Ala Ser Phe Ser Ala Pro Thr Ser Glu Ala Leu Leu Gln Gly  
145 150 155 160  
Leu Ser Pro Ser Phe Asp Phe Gly Pro Asn Leu Met Gly Ser Phe Met  
165 170 175  
Gln Leu Asn Gly Leu Ser Ser Lys Tyr Ile Leu Ile Leu Ile Asp Gly  
180 185 190  
30 Lys Arg Val Tyr Gly Asp Val Gly Gly Gln Ala Asp Leu Ser Arg Ile  
195 200 205  
Ser Pro Asp Gln Ile Glu Arg Ile Glu Leu Val Lys Gly Ala Ser Ser  
210 215 220  
35 Ser Leu Tyr Gly Ser Asp Ala Ile Ala Gly Val Ile Asn Val Ile Thr  
225 230 235 240  
Lys Lys Asn Thr Asn Arg Leu Ser Ala Tyr Thr Ser His Arg Ile Ser  
245 250 255  
Lys Tyr Asn Asp Arg Gln Thr Asn Thr Ser Leu Asp Ile Asn Ile Gly  
260 265 270  
40 Lys Phe Ser Ser Asn Thr Asn Tyr Phe Phe Tyr His Thr Asp Gly Trp  
275 280 285  
Gln Asn Ser Pro Phe Glu Ile Lys Lys Lys Lys Gly Ser Gly Glu Pro  
290 295 300  
45 Val Leu Glu Glu Thr Tyr Lys Lys Thr Phe Arg Ala Gln Glu Asn Gln  
305 310 315 320  
Gly Val Ser Gln Ser Leu Ser Tyr Tyr Ala Thr Asn Asn Leu Ser Phe  
325 330 335  
Ser Gly Asn Val Gln Tyr Asn Lys Arg Gln Ile Phe Thr Pro Thr Phe  
340 345 350  
50 Ser Glu Lys Lys Ala Tyr Asp Met Asp Tyr Arg Ala Leu Thr Ala Ser  
355 360 365  
Leu Gly Thr Asn Tyr Leu Phe Pro Asn Gly Leu His Thr Leu Ser Phe  
370 375 380  
55 Asp Ala Val Tyr Asp Arg Phe Arg Phe Gly Tyr Leu Tyr His Asp Lys  
385 390 395 400  
Asp Ser Ser Glu Ser Leu Ile Asn Asn Gln Gly Gln Thr Glu Gln Pro  
405 410 415  
Thr Phe Phe Pro Gly Gln Leu Arg Asn Lys Asn Asp Gln Ile Arg Tyr  
420 425 430  
60 Thr Ala Glu Ala Arg Gly Val Phe Thr Leu Pro Tyr Ala Gln Lys Leu  
435 440 445  
Thr Gly Gly Leu Glu Tyr Phe Arg Glu Glu Leu Ile Ser Pro Tyr Asn  
450 455 460  
65 Leu Ile Thr Asp Lys Ala Asp Ala Ser Thr Leu Ser Ala Tyr Val Gln  
465 470 475 480  
Asp Glu Trp Lys Pro Leu Asp Trp Phe Asn Met Thr Ala Gly Phe Arg  
485 490 495  
Leu Val His His Gln Glu Phe Gly Thr Arg Met Thr Pro Lys Val Ser  
500 505 510  
70 Ile Leu Ala Lys Tyr Gly Pro Leu Asn Phe Arg Ala Thr Tyr Ala Asn  
515 520 525  
Gly Tyr Lys Thr Pro Thr Leu Lys Glu Leu Phe Ala Arg Asn Glu Leu  
530 535 540  
75 Thr Thr Met Gly Ser His Asn Leu Tyr Leu Gly Asn Ala Asp Leu Lys  
545 550 555 560

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Pro Gln Met Ser Asp Tyr Tyr Ala Leu Gly Leu Glu Tyr Asn Gln Gly  
 565 570 575  
 Pro Ile Ser Phe Ser Ala Thr Val Tyr Asp Asn Glu Leu Arg Asn Leu  
 580 585 590  
 5 Ile Ser Phe Met Asp Ile Pro Thr Ser Pro Glu His Glu Ala Gln Gly  
 595 600 605  
 Ile Lys Thr Tyr Lys Gln Tyr Ala Asn Ile Gly Lys Ala Arg Ser Arg  
 610 615 620  
 10 Gly Leu Asp Val Leu Cys Asp Ala Ser Ile Gly Trp Gly Ile Lys Leu  
 625 630 635 640  
 Gly Ala Gly Tyr Ser Leu Val Glu Ala Lys Asn Leu Gln Thr Asp Glu  
 645 650 655  
 Trp Leu Glu Gly Ala Ala Arg His Arg Ala Asn Val His Ala Asp Trp  
 660 665 670  
 15 Val His Tyr Trp Gly Gln Tyr Arg Leu Gly Val Ser Leu Phe Gly Arg  
 675 680 685  
 Ile Gln Ser Glu Arg Tyr Tyr Lys Asp Gly Asn Ala Pro Asp Tyr Thr  
 690 695 700  
 20 Leu Trp Arg Leu Ala Thr Ser His Arg Phe Ala His Phe Arg His Ile  
 705 710 715 720  
 Ile Leu Asp Gly Thr Leu Gly Ile Asp Asn Leu Phe Asp Tyr Val Asp  
 725 730 735  
 Asp Arg Pro Met Gly Val Asn Tyr Ala Thr Val Thr Pro Gly Arg Thr  
 740 745 750  
 25 Phe Phe Ala Gln Ile Ala Ile Arg Phe Asn Asn  
 755 760

## (2) INFORMATION FOR SEQ ID NO:296

- 30 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 365 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear
- 35 (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- 40 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Porphyromonas gingivalis
- (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...365
- 45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:296

Cys Cys Ala Arg Leu Arg Asp Thr Ser Pro Arg Lys Lys Ser Phe Arg  
 1 5 10 15  
 50 Asn Asp Thr Val Phe Pro Tyr Phe Val Ile His Leu Ile Lys His Ile  
 20 25 30  
 Ile Ile Met Thr Asp Asn Lys Gln Arg Asn Ile Val Phe Pro Ala Phe  
 35 40 45  
 55 Leu Leu Leu Leu Gly Val Ile Ala Val Val Thr Ile Val Gly Phe Phe  
 50 55 60  
 Met Leu Arg Pro Ala Glu Glu Ile Ile Gln Gly Gln Ile Glu Val Thr  
 65 70 75 80  
 Glu Tyr Arg Val Ser Ser Lys Val Pro Gly Arg Ile Lys Glu Leu Arg  
 85 90 95  
 60 Val Ser Glu Gly Gln Gln Val Gln Ala Gly Asp Thr Leu Ala Val Ile  
 100 105 110  
 Glu Ala Pro Asp Val Ala Ala Lys Met Glu Gln Ala Lys Ala Ala Glu  
 115 120 125  
 65 Ala Ala Ala Gln Ala Gln Asn Ala Lys Ala Leu Lys Gly Ala Arg Ser  
 130 135 140  
 Glu Gln Ile Gln Ala Ala Tyr Glu Met Trp Gln Lys Ala Gln Ala Gly  
 145 150 155 160  
 Val Ala Ile Ala Thr Lys Thr His Gln Arg Val Gln Asn Leu Tyr Asp  
 165 170 175  
 70 Gln Gly Val Val Pro Ala Gln Lys Leu Asp Glu Ala Thr Ala Gln Arg  
 180 185 190  
 Asp Ala Ala Ile Ala Thr Gln Lys Ala Ala Glu Ala Gln Tyr Asn Met  
 195 200 205  
 75 Ala Arg Asn Gly Ala Glu Arg Glu Asp Lys Leu Ala Ala Ser Ala Leu  
 210 215 220

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Val Asp Arg Ala Arg Gly Ala Val Ala Glu Val Glu Ser Tyr Ile Asn  
 225 230 235 240  
 Glu Thr Tyr Leu Ile Ala Pro Arg Ala Gly Glu Val Ser Glu Ile Phe  
 245 250 255  
 5 Pro Lys Ala Gly Glu Leu Val Gly Thr Gly Ala Pro Ile Met Asn Ile  
 260 265 270  
 Ala Glu Met Gly Asp Met Trp Ala Ser Phe Ala Val Arg Glu Asp Phe  
 275 280 285  
 10 Leu Ser Ser Met Thr Met Gly Ala Val Leu Glu Thr Val Val Pro Ala  
 290 295 300  
 Leu Asn Glu Glu Lys Val Arg Phe Lys Ile Thr Phe Ile Lys Asn Met  
 305 310 315 320  
 Gly Thr Tyr Ala Ala Trp Lys Ala Thr Lys Thr Thr Gly Gln Tyr Asp  
 325 330 335  
 15 Leu Lys Thr Phe Glu Val Lys Ala Thr Leu Ala Asp Lys Asp Lys Ala  
 340 345 350  
 Gln Lys Leu Arg Pro Gly Met Ser Val Ile Ile Arg Lys  
 355 360 365

20 (2) INFORMATION FOR SEQ ID NO:297

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 320 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

25 (ii) MOLECULE TYPE: protein

30 (iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Porphyromonas gingivalis

35 (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...320

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:297

40 Pro Gln Ser Ser Pro Asp Arg Arg Ser Phe Gln Asn Val Met Asn Lys  
 1 5 10 15  
 Tyr His Ser Gln Ser Val Leu Glu Val Gly Lys Ile Gly Ile Val Ile  
 20 25 30  
 45 Ile Phe Ala Pro Ile Val Arg Asn Val His Gln Gln Pro Pro Phe Leu  
 35 40 45  
 Ser His Lys Ser Ile Met Arg Ile Val Ser Asn Phe Leu Phe Val Ser  
 50 55 60  
 Phe Ser Val Leu Leu Phe Ala Ser Cys Arg Ser Gln Arg Glu Lys Val  
 65 70 75 80  
 50 Val Tyr Leu Gln Asp Ile Gln Thr Phe Asn Arg Glu Ile Ile Ala Lys  
 85 90 95  
 Pro Tyr Asp Val Lys Ile Glu Lys Asp Asp Val Leu Asn Ile Leu Val  
 100 105 110  
 55 Ser Ser Arg Asp Pro Glu Leu Ser Thr Pro Tyr Asn Gln Val Leu Thr  
 115 120 125  
 Thr Arg Ala Leu Ala Arg Asn Gly Tyr Gly Thr Asn Ser Asn Glu Gly  
 130 135 140  
 Phe Leu Val Asp Ser Lys Gly Tyr Ile Asn Tyr Pro Ile Leu Gly Gln  
 145 150 155 160  
 60 Ile Tyr Val Glu Gly Leu Thr Arg Thr Glu Leu Glu Lys Glu Ile Gln  
 165 170 175  
 Lys Arg Ile Ile Ser Ser Gly Phe Ile Lys Asp Pro Thr Val Thr Val  
 180 185 190  
 Gln Leu Gln Asn Phe Lys Val Ser Val Leu Gly Glu Val Asn His Pro  
 195 200 205  
 65 Gly Ser Met Ser Val Lys Gly Glu Arg Ile Thr Leu Leu Glu Ala Ile  
 210 215 220  
 Gly Met Ala Gly Asp Leu Thr Ile Tyr Gly Arg Arg Asp Arg Val Phe  
 225 230 235 240  
 70 Val Ile Arg Glu Thr Asp Gly His Arg Glu Val Phe Gln Thr Asp Leu  
 245 250 255  
 Arg Lys Ala Asp Leu Leu Ala Ser Pro Val Tyr Tyr Leu His Gln Asn  
 260 265 270  
 75 Asp Val Ile Tyr Val Glu Pro Asn Asp Lys Lys Thr Gln Met Ser Glu  
 275 280 285

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Ile Asn Gln Asn Asn Asn Val Asn Val Trp Leu Ser Val Thr Ser Thr  
 290 295 300  
 Leu Val Ser Ile Ser Thr Leu Thr Ile Thr Ile Ile Asp Lys Thr Lys  
 305 310 315 320

5

(2) INFORMATION FOR SEQ ID NO:298

(i) SEQUENCE CHARACTERISTICS:

10

(A) LENGTH: 582 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

15

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Porphyromonas gingivalis

20

(ix) FEATURE:

(A) NAME/KEY: misc feature

(B) LOCATION 1...582

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:298

25

Ser Lys Ile Val Leu Arg Lys Phe Cys Thr Leu Ala Arg Met Lys Lys  
 1 5 10 15  
 Thr Asn Leu Phe Leu Ser Leu Leu Val Ile Phe Ile Thr Gly Ser Phe  
 20 25 30  
 Met Thr Ala Cys Ala Gln Lys Ser Lys Thr Asn Lys Leu Thr Glu Glu  
 35 40 45  
 Asp Arg Ser Arg Asn Glu Tyr Val Gln Ser Met Asp Val Leu Ser Asn  
 50 55 60  
 Ile Ile Gly Asn Val Arg Leu Tyr Phe Val Asp Thr Ile Ser Ile Lys  
 65 70 75 80  
 His Met Thr Arg Arg Gly Ile Asp Ala Met Leu Gly Gly Leu Asp Pro  
 85 90 95  
 Tyr Thr Glu Tyr Ile Pro Tyr Glu Glu Met Asp Glu Leu Lys Leu Met  
 100 105 110  
 Thr Thr Gly Glu Tyr Ala Gly Val Gly Ala Ile Ile Ser Gln Arg Pro  
 115 120 125  
 Asp Ser Ala Val Ile Ile Gln Arg Pro Met Glu Gly Met Pro Ala Asp  
 130 135 140  
 Glu Ala Gly Leu Ile Ala Gly Asp Arg Ile Leu Thr Ile Asp Gly Lys  
 145 150 155 160  
 Asp Phe Arg Lys Ser Thr Thr Pro Lys Val Ser Gln Ala Leu Lys Gly  
 165 170 175  
 Ile Ala Gly Thr Val Ala Lys Val Thr Val Met Arg Tyr Gly Glu Thr  
 180 185 190  
 Lys Pro Arg Thr Phe Ser Val Lys Arg Gln Lys Val Ile Met Asn Ser  
 195 200 205  
 Val Thr Tyr Ser Gly Met Leu Asp Gly Ser Ile Gly Tyr Ile Arg Leu  
 210 215 220  
 Asn Asn Phe Thr Asp Lys Ser Ala Glu Glu Val Arg Thr Ala Leu Leu  
 225 230 235 240  
 Asp Leu Arg Asp Lys Gln Gly Ala Lys Gly Leu Ile Leu Asp Leu Arg  
 245 250 255  
 Gly Asn Gly Gly Gly Leu Met Gln Ala Ala Ile Glu Ile Val Asn Leu  
 260 265 270  
 Phe Val Pro Lys Gly Lys Glu Val Val Thr Thr Lys Gly Arg Ile Ala  
 275 280 285  
 Glu Ser Ala Ser Val Phe Arg Thr Leu Thr Glu Pro Ile Asp Thr Lys  
 290 295 300  
 Leu Pro Ile Val Val Leu Ile Asp Gly Gln Ser Ala Ser Ser Ser Glu  
 305 310 315 320  
 Ile Val Ala Gly Ala Leu Gln Asp Met Asp Arg Ala Val Leu Met Gly  
 325 330 335  
 Gln Lys Ser Tyr Gly Lys Gly Leu Val Gln Thr Thr Arg Gln Leu Pro  
 340 345 350  
 Tyr Asn Gly Val Ile Lys Leu Thr Thr Ala Lys Tyr Tyr Ile Pro Ser  
 355 360 365  
 Gly Arg Cys Ile Gln Arg Leu Asp Tyr Ser Arg Thr Asn Arg Thr Gly  
 370 375 380  
 Met Ala Thr Ala Ile Pro Asp Ser Leu His Lys Ile Phe Tyr Thr Ala  
 385 390 395 400

75

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Ala Gly Arg Arg Val Glu Asp Ala Gly Gly Ile Leu Pro Asp Ile Glu  
 405 410 415  
 Val Lys Gln Asp Thr Ala Ala Thr Leu Leu Tyr Tyr Met Ala Ile Asn  
 420 425 430  
 5 Asn Asp Val Phe Asp Phe Val Thr Gly Tyr Val Leu Lys His Lys Thr  
 435 440 445  
 Ile Ala Lys Pro Glu Asp Phe Ser Ile Thr Asn Glu Asp Tyr Ala Ala  
 450 455 460  
 10 Phe Cys Lys Met Met Glu Glu Lys Lys Phe Asp Tyr Asp Arg Gln Ser  
 465 470 475 480  
 Gly Lys Met Leu Asp Lys Leu Glu Glu Leu Ala Lys Ile Glu Gly Tyr  
 485 490 495  
 Leu Pro Glu Ala Asn Ser Glu Leu Lys Ala Leu Arg Glu Lys Leu Lys  
 500 505 510  
 15 Pro Asn Leu Ser Arg Asp Leu Leu Arg Phe Lys Lys Glu Ile Thr Asn  
 515 520 525  
 Tyr Leu Asn Asn Glu Ile Val Thr Arg Tyr Tyr Tyr Glu Arg Gly Ser  
 530 535 540  
 20 Ile Arg Gln Ser Leu Pro Glu Asp Lys Val Val Lys Glu Ala Ile Lys  
 545 550 555 560  
 Leu Leu Lys Asp His Pro Glu Gln Ile Arg Gln Ile Leu Ala Ala Pro  
 565 570 575  
 Lys Ala Glu Asn Lys Gly  
 580

25

(2) INFORMATION FOR SEQ ID NO:299

30

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 985 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

35

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Porphyromonas gingivalis

40

(ix) FEATURE:

(A) NAME/KEY: misc\_feature

(B) LOCATION 1...985

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:299

50

Val Thr Asp Lys Met Gln Asn Lys Gly Phe Val Ile Val Ile Thr Ser  
 1 5 10 15  
 Ala Leu Ala Ile Ile Cys Ala Phe Tyr Leu Ser Phe Ser Phe Val Thr  
 20 25 30  
 55 Asn Arg Tyr Glu Lys Lys Ala Lys Ala Met Gly Asp Val Ala Gly Met  
 35 40 45  
 Ala Tyr Leu Asp Ser Met Ser Asn Glu Lys Val Trp Phe Gly Tyr Thr  
 50 55 60  
 55 Leu Lys Glu Ala Gln Ala Gln Gln Ile Gly Leu Gly Leu Asp Leu Lys  
 65 70 75 80  
 Gly Gly Met Asn Val Ile Leu Lys Leu Asn Ala Ser Asp Leu Leu Arg  
 85 90 95  
 Asn Leu Ser Asn Lys Ser Leu Asp Pro Asn Phe Asn Lys Ala Leu Glu  
 100 105 110  
 60 Asn Ala Ala Lys Ser Thr Glu Gln Ser Asp Phe Ile Asp Ile Phe Val  
 115 120 125  
 Lys Glu Tyr Arg Lys Leu Asp Pro Asn Gly Arg Leu Ala Val Ile Phe  
 130 135 140  
 65 Gly Ser Gly Asp Leu Arg Asp Gln Ile Thr Ala Lys Ser Thr Asp Ala  
 145 150 155 160  
 Asp Val Val Arg Leu Leu Lys Glu Lys Tyr Asn Ser Ala Val Glu Ala  
 165 170 175  
 Ser Phe Asn Val Leu Arg Ala Arg Ile Asp Ala Phe Gly Val Val Ala  
 180 185 190  
 70 Pro Asn Leu Gln Arg Leu Glu Gly Gln Gly Arg Ile Leu Val Glu Leu  
 195 200 205  
 Pro Gly Val Lys Asp Pro Glu Arg Val Arg Thr Leu Leu Gln Arg Ser  
 210 215 220  
 75 Ala Asn Leu Gln Phe Trp Arg Thr Tyr Lys Phe Glu Glu Val Ser Gly  
 225 230 235 240

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Asp Leu Ile Ala Ala Asn Asp Arg Leu Ser Glu Leu Ala Met Asn Asn  
 Thr Asp Ala Thr 245 Pro Glu Thr Glu Pro Ala Thr Thr Asp Ser Val Ala  
 Ala Thr Ala Asp Ser Ala Ala Val Gln Ala Val Ala Asp Ser Ala Thr  
 Val Ala Gln Lys Glu Ala Lys Asp Ala Thr Arg Lys Asp Ala Leu Phe  
 Ser Leu Leu Thr Pro Val Asn Arg Gly Gly Ala Val Val Gly Val Ala  
 Arg Arg Ala Asn Met Ala Gln Ile Ser Glu Met Leu Gln Gln Ala His  
 Asp Leu Lys Val Thr Arg Glu Asp Val Leu Phe Leu Trp Gly Ala Lys  
 Ala Ile Glu Asp Pro Glu Thr Lys Glu Thr Asp Leu Tyr Glu Leu  
 Tyr Ala Ile Arg Thr Asn Arg Thr Gly Asp Pro Asp Leu Gly Gly Asp  
 Val Val Thr Ser Ala Lys Ser Asp Ile Gln Asn Asp Phe Gly Arg Ser  
 Glu Pro Ile Val Ser Met Thr Met Asn Glu Gly Ala Arg Lys Trp  
 Ala Arg Ile Thr Lys Asp Asn Val Gly Arg Ala Ile Ala Ile Val Leu  
 Asp Gly Val Val Tyr Ser Ala Pro Asn Val Asn Asp Glu Ile Thr Gly  
 Gly Arg Ser Gln Ile Ser Gly His Phe Thr Val Glu Glu Ala Gly Asp  
 Leu Ala Asn Val Leu Asn Ser Gly Lys Met Asp Ala Thr Val Ser Ile  
 Glu Gln Glu Asn Val Ile Gly Pro Thr Leu Gly Ala Glu Ser Ile Lys  
 Ala Gly Phe Leu Ser Phe Leu Leu Ala Leu Val Ile Leu Met Cys Tyr  
 Met Cys Leu Ala Tyr Gly Phe Leu Pro Gly Leu Ile Ala Asn Gly Ala  
 Leu Ile Val Asn Ser Phe Phe Thr Leu Gly Val Leu Ala Ser Phe His  
 Ala Val Leu Thr Leu Ser Gly Ile Ala Gly Leu Val Leu Thr Leu Gly  
 Met Ala Val Asp Ala Asn Val Leu Ile Phe Glu Arg Ile Lys Glu Glu  
 Leu Arg Ala Gly Lys Thr Pro Ile Arg Ala Val Thr Asp Gly Tyr Gly  
 Asn Ala Phe Ser Ala Ile Phe Asp Ser Asn Val Thr Thr Ile Ile Thr  
 Gly Ile Ile Leu Phe Leu Tyr Gly Thr Gly Pro Ile Arg Gly Phe Ala  
 Thr Thr Leu Ile Ile Gly Leu Ile Ala Ser Phe Ile Thr Ala Val Phe  
 Leu Thr Arg Ile Val Phe Glu Lys Leu Ala Lys Lys Gly Arg Leu Asp  
 Lys Ile Thr Phe Thr Thr Ser Ile Thr Arg Asn Leu Leu Val Asn Pro  
 Ser Tyr Asn Ile Leu Gly Lys Arg Lys Thr Gly Phe Ile Ile Pro Val  
 Ile Ile Ile Val Leu Gly Leu Ile Ala Ser Phe Thr Ile Gly Leu Asn  
 Arg Gly Ile Glu Phe Ser Gly Arg Asn Tyr Val Val Lys Phe Asp  
 Gln Pro Val Ser Ser Glu Ala Val Arg Ser Ala Leu Ser Ser Pro Leu  
 Gln Glu Lys Val Leu Val Thr Ser Ile Gly Thr Glu Gly Thr Glu Val  
 Arg Ile Ser Thr Asn Tyr Lys Ile Gln Glu Glu Ser Glu Glu Thr Glu  
 Ala Glu Ile Thr Asp Lys Leu Tyr Gln Ser Leu Lys Gly Phe Tyr Thr  
 Gln Gln Pro Thr Ala Asp Gln Phe Leu Asp Asn Ile Ile Ser Ser Gln  
 Lys Val Ser Pro Ser Met Ser Ser Asp Ile Thr Arg Gly Ala Ile Trp  
 Ala Val Leu Leu Ser Met Ile Phe Met Ala Ile Tyr Ile Leu Ile Arg  
 Phe Arg Asp Ile Ser Phe Ser Ala Gly Val Phe Val Ser Val Ala Ala

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5                   835                   840                   845  
 Thr Thr Phe Cys Ile Ile Ala Leu Tyr Ala Leu Leu Trp Lys Ile Leu  
       850                   855                   860  
 Pro Phe Thr Met Glu Ile Asp Gln Asn Phe Ile Ala Ala Ile Leu Ala  
       865                   870                   875                   880  
 Ile Ile Gly Tyr Ser Leu Asn Asp Thr Val Val Val Phe Asp Arg Ile  
       885                   890                   895  
 Arg Glu Thr Met Lys Leu Tyr Pro Asn Arg Asp Arg Tyr Gln Val Ile  
       900                   905                   910  
 10 Asn Asp Ala Leu Asn Ser Thr Leu Gly Arg Thr Leu Asn Thr Ser Leu  
       915                   920                   925  
 Thr Thr Phe Ile Val Met Leu Val Ile Phe Ile Phe Gly Gly Ala Thr  
       930                   935                   940  
 15 Met Arg Ser Phe Thr Phe Ser Ile Leu Leu Gly Ile Val Ile Gly Thr  
       945                   950                   955                   960  
 Tyr Ser Thr Leu Phe Val Ala Thr Pro Leu Ala Tyr Glu Ile Gln Lys  
       965                   970                   975  
 Arg Lys Leu Asn Lys Ala Ala Lys Lys  
       980                   985  
 20  
 (2) INFORMATION FOR SEQ ID NO:300  
  
 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1046 amino acids  
 25 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
  
 (ii) MOLECULE TYPE: protein  
 30 (iii) HYPOTHETICAL: YES  
  
 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Porphyromonas gingivalis  
 35 (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...1046  
  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:300  
 40 Asp Phe Pro Trp Val Arg Val Lys Pro Glu Lys Lys Arg Lys Gln His  
       1                   5                   10                   15  
 Asn Ser Asn Asn Phe Lys Phe Asn Ala Lys Glu Lys Ser Met Lys Arg  
       20                   25                   30  
 45 Met Thr Leu Phe Phe Leu Cys Leu Leu Thr Ser Ile Gly Trp Ala Met  
       35                   40                   45  
 Ala Gln Asn Arg Thr Val Lys Gly Thr Val Ile Ser Ser Glu Asp Asn  
       50                   55                   60  
 50 Glu Pro Leu Ile Gly Ala Asn Val Val Val Val Gly Asn Thr Thr Ile  
       65                   70                   75                   80  
 Gly Ala Ala Thr Asp Leu Asp Gly Asn Phe Thr Leu Ser Val Pro Ala  
       85                   90                   95  
 Asn Ala Lys Met Leu Arg Val Ser Tyr Ser Gly Met Thr Thr Lys Glu  
       100                   105                   110  
 55 Val Ala Ile Ala Asn Val Met Lys Ile Val Leu Asp Pro Asp Ser Lys  
       115                   120                   125  
 Val Leu Glu Gln Val Val Val Leu Gly Tyr Gly Thr Gly Gln Lys Leu  
       130                   135                   140  
 60 Ser Thr Val Ser Gly Ser Val Ala Lys Val Ser Ser Glu Lys Leu Ala  
       145                   150                   155                   160  
 Glu Lys Pro Val Ala Asn Ile Met Asp Ala Leu Gln Gly Gln Val Ala  
       165                   170                   175  
 Gly Met Gln Val Met Thr Thr Ser Gly Asp Pro Thr Ala Val Ala Ser  
       180                   185                   190  
 65 Val Glu Ile His Gly Thr Gly Ser Leu Gly Ala Ser Ser Ala Pro Leu  
       195                   200                   205  
 Tyr Ile Val Asp Gly Met Gln Thr Ser Leu Asp Val Val Ala Thr Met  
       210                   215                   220  
 70 Asn Pro Asn Asp Phe Glu Ser Met Ser Val Leu Lys Asp Ala Ser Ala  
       225                   230                   235                   240  
 Thr Ser Ile Tyr Gly Ala Arg Ala Ala Asn Gly Val Val Phe Ile Gln  
       245                   250                   255  
 Thr Lys Lys Gly Lys Met Ser Glu Arg Gly Arg Ile Thr Phe Asn Ala  
       260                   265                   270  
 75 Ser Tyr Gly Ile Ser Gln Ile Leu Asn Thr Lys Pro Leu Asp Asn Met

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5	Met	Thr	275	Asp	Glu	Leu	Leu	280	Phe	Gln	Val	Lys	285	Ala	Gly	Phe	Trp
	290	Asn	Asn	Gln	Thr	Val	Gln	295	Val	Lys	Asp	Met	Ile	Leu	Ala	Gly	
	305	Glu	Asp	Leu	Tyr	Gly	Asn	310	Asp	Ser	Leu	Lys	Asp	Glu	Tyr	320	
	Ala	Glu	Asp	Leu	Tyr	325	Gly	Asn	Tyr	Asp	330	Leu	Lys	Asp	Glu	Tyr	335
10	Lys	Thr	Leu	Phe	Pro	Val	Asp	Phe	Asn	His	Asp	Ala	Asp	Trp	Leu	Lys	
	340	Leu	Phe	Lys	Thr	Ala	Pro	Thr	Ser	Gln	Gly	Asp	Ile	Ser	Phe	Ser	
	355	Gly	Gly	Ser	Gln	Gly	Thr	Ser	Tyr	Tyr	Ala	Ser	Ile	Gly	Tyr	Phe	Asp
	370	Gln	Glu	Gly	Met	Ala	Arg	Glu	Pro	Ala	Asn	Phe	Lys	Arg	Tyr	Ser	Gly
15	385	Arg	Leu	Asn	Phe	Glu	Ser	Arg	Ile	Asn	Glu	Trp	Leu	Lys	Val	Gly	Ala
	405	Asn	Leu	Ser	Gly	Ala	Ile	Ala	Asn	Arg	Ser	Ala	Asp	Tyr	Phe	Gly	
	420	Lys	Tyr	Tyr	Met	Gly	Ser	Gly	Thr	Phe	Gly	Val	Leu	Thr	Met	Pro	Arg
	435	Tyr	Tyr	Asn	Pro	Phe	Asp	Val	Asn	Gly	Asp	Leu	Ala	Asp	Val	Tyr	Tyr
20	450	Met	Tyr	Gly	Ala	Thr	Arg	Pro	Ser	Met	Thr	Glu	Pro	Tyr	Phe	Ala	Lys
	465	Met	Arg	Pro	Phe	Ser	Ser	Glu	Ser	His	Gln	Ala	Asn	Val	Asn	Gly	Phe
	485	Ala	Gln	Ile	Thr	Pro	Ile	Lys	Gly	Leu	Thr	Leu	Lys	Ala	Gln	Ala	Gly
	500	Val	Asp	Ile	Thr	Asn	Thr	Arg	Thr	Ser	Ser	Lys	Arg	Met	Pro	Asn	Asn
25	515	Pro	Tyr	Asp	Ser	Thr	Pro	Leu	Gly	Glu	Arg	Arg	Glu	Arg	Ala	Tyr	Arg
	530	Asp	Val	Ser	Lys	Ser	Phe	Thr	Asn	Thr	Ala	Glu	Tyr	Lys	Phe	Ser	Ile
	545	Asp	Glu	Lys	His	Asp	Leu	Thr	Ala	Leu	Met	Gly	His	Glu	Tyr	Ile	Glu
	565	Tyr	Glu	Gly	Asp	Val	Ile	Gly	Ala	Ser	Ser	Lys	Gly	Phe	Glu	Ser	Asp
30	580	Lys	Leu	Met	Leu	Leu	Ser	Gln	Gly	Lys	Thr	Gly	Asn	Ser	Leu	Ser	Leu
	595	Pro	Glu	His	Arg	Val	Ala	Glu	Tyr	Ala	Tyr	Leu	Ser	Phe	Phe	Ser	Arg
	610	Phe	Asn	Tyr	Gly	Phe	Asp	Lys	Trp	Met	Tyr	Ile	Asp	Phe	Ser	Val	Arg
	625	Asn	Asp	Gln	Ser	Ser	Arg	Phe	Gly	Ser	Asn	Asn	Arg	Ser	Ala	Trp	Phe
35	645	Tyr	Ser	Val	Gly	Met	Phe	Asp	Ile	Tyr	Asn	Lys	Phe	Ile	Gln	Glu	
	660	Ser	Asn	Trp	Leu	Ser	Asp	Leu	Arg	Leu	Lys	Met	Ser	Tyr	Gly	Thr	Thr
	675	Gly	Asn	Ser	Glu	Ile	Gly	Asn	Tyr	Asn	His	Gln	Ala	Leu	Val	Thr	Val
	690	Asn	Asn	Tyr	Thr	Glu	Asp	Ala	Met	Gly	Leu	Ser	Ile	Ser	Thr	Ala	Gly
40	705	Asn	Pro	Asp	Leu	Ser	Trp	Glu	Lys	Gln	Ser	Gln	Phe	Asn	Phe	Gly	Leu
	725	Ala	Ala	Gly	Ala	Phe	Asn	Asn	Arg	Leu	Ser	Ala	Glu	Val	Asp	Phe	Tyr
	740	Val	Arg	Thr	Thr	Asn	Asp	Met	Leu	Ile	Asp	Val	Pro	Met	Pro	Tyr	Ile
	755	Ser	Gly	Phe	Phe	Ser	Gln	Tyr	Gln	Asn	Val	Gly	Ser	Met	Lys	Asn	Thr
45	770	Gly	Val	Asp	Leu	Ser	Leu	Lys	Gly	Thr	Ile	Tyr	Gln	Asn	Lys	Asp	Trp
	785	Asn	Val	Tyr	Ala	Ser	Ala	Asn	Phe	Asn	Tyr	Asn	Arg	Gln	Glu	Ile	Thr
	805	Lys	Leu	Phe	Phe	Gly	Leu	Asn	Lys	Tyr	Met	Leu	Pro	Asn	Thr	Gly	Thr
	820	Ile	Trp	Glu	Ile	Gly	Tyr	Pro	Asn	Ser	Phe	Tyr	Met	Ala	Glu	Tyr	Ala
50	835	Gly	Ile	Asp	Lys	Lys	Thr	Gly	Lys	Gln	Leu	Trp	Tyr	Val	Pro	Gly	Gln
	850	Val	Asp	Ala	Asp	Gly	Asn	Lys	Val	Thr	Thr	Ser	Gln	Tyr	Ser	Ala	Asp
	865																



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Leu Glu Thr Arg Ile Asp Lys Ser Val Thr Pro Pro Ile Thr Gly Gly  
 885 890 895  
 Phe Ser Leu Gly Ala Ser Trp Lys Gly Leu Ser Leu Asp Ala Asp Phe  
 900 905 910  
 5 Ala Tyr Ile Val Gly Lys Trp Met Ile Asn Asn Asp Arg Tyr Phe Thr  
 915 920 925  
 Glu Asn Ala Gly Gly Leu Met Gln Leu Asn Lys Asp Lys Met Leu Leu  
 930 935 940  
 10 Asn Ala Trp Thr Glu Asp Asn Lys Glu Thr Asp Val Pro Lys Leu Gly  
 945 950 955 960  
 Gln Ser Pro Gln Phe Asp Thr His Leu Leu Glu Asn Ala Ser Phe Leu  
 965 970 975  
 Arg Leu Lys Asn Leu Lys Leu Thr Tyr Val Leu Pro Asn Ser Leu Phe  
 980 985 990  
 15 Ala Gly Gln Asn Val Ile Gly Gly Ala Arg Val Tyr Leu Met Ala Arg  
 995 1000 1005  
 Asn Leu Leu Thr Val Thr Lys Tyr Lys Gly Phe Asp Pro Glu Ala Gly  
 1010 1015 1020  
 20 Gly Asn Val Gly Lys Asn Gln Tyr Pro Asn Ser Lys Gln Tyr Val Ala  
 1025 1030 1035 1040  
 Gly Ile Gln Leu Ser Phe  
 1045

(2) INFORMATION FOR SEQ ID NO:301

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 869 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...869

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:301

Trp His Arg Asn Ile Phe Ile Phe Ala Ser Thr Phe Ser Pro Lys Asn  
 1 5 10 15  
 Met Leu Pro Leu Pro Tyr Arg Tyr Ala Lys Thr Glu His Leu Phe Leu  
 20 25 30  
 Ala Lys Gly Tyr Cys Lys Asn Pro Ile Thr Asn Ile Ile Leu Phe  
 35 40 45  
 50 Met Lys Lys Lys Asn Phe Leu Leu Leu Gly Ile Phe Val Ala Leu Leu  
 50 55 60  
 Thr Phe Ile Gly Ser Met Gln Ala Gln Gln Ala Lys Asp Tyr Phe Asn  
 65 70 75 80  
 Phe Asp Glu Arg Gly Glu Ala Tyr Phe Ser Phe Lys Val Pro Asp Arg  
 85 90 95  
 55 Ala Val Leu Gln Glu Leu Ala Leu Ile Met Ser Ile Asp Glu Phe Asp  
 100 105 110  
 Pro Val Thr Asn Glu Ala Ile Ala Tyr Ala Ser Glu Glu Phe Glu  
 115 120 125  
 60 Ala Phe Leu Arg Tyr Gly Leu Lys Pro Thr Phe Leu Thr Pro Pro Ser  
 130 135 140  
 Met Gln Arg Ala Val Glu Met Phe Asp Tyr Arg Ser Gly Glu Lys Tyr  
 145 150 155 160  
 65 Glu Trp Asn Ala Tyr Pro Thr Tyr Glu Ala Tyr Ile Ser Met Met Glu  
 165 170 175  
 Glu Phe Gln Thr Lys Tyr Pro Ser Leu Cys Thr Thr Ser Val Ile Gly  
 180 185 190  
 Lys Ser Val Lys Asp Arg Lys Leu Met Ile Cys Lys Leu Ser Ser  
 195 200 205  
 70 Ala Asn Thr Gly Lys Lys Pro Arg Val Leu Tyr Thr Ser Thr Met His  
 210 215 220  
 Gly Asp Glu Thr Thr Gly Tyr Val Val Leu Leu Arg Leu Ile Asp His  
 225 230 235 240  
 75 Leu Leu Ser Asn Tyr Glu Ser Asp Pro Arg Ile Lys Asn Ile Leu Asp  
 245 250 255

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	Lys	Thr	Glu	Val	Trp	Ile	Cys	Pro	Leu	Thr	Asn	Pro	Asp	Gly	Ala	Tyr	
			260						265					270			
	Arg	Ala	Gly	Asn	His	Thr	Val	Gln	Gly	Ala	Thr	Arg	Tyr	Asn	Ala	Asn	
			275					280					285				
5	Asn	Val	Asp	Leu	Asn	Arg	Asn	Phe	Lys	Asp	Asp	Val	Ala	Gly	Asp	His	
			290				295					300					
	Pro	Asp	Gly	Lys	Pro	Trp	Gln	Pro	Glu	Ala	Thr	Ala	Phe	Met	Asp	Leu	
			305			310					315					320	
10	Glu	Gly	Asn	Thr	Ser	Phe	Val	Leu	Gly	Ala	Asn	Ile	His	Gly	Gly	Thr	
					325						330				335		
	Glu	Val	Val	Asn	Tyr	Pro	Trp	Asp	Asn	Lys	Lys	Glu	Arg	His	Ala	Asp	
				340					345					350			
	Asp	Glu	Trp	Tyr	Lys	Leu	Ile	Ser	Arg	Asn	Tyr	Ala	Ala	Ala	Cys	Gln	
			355					360					365				
15	Ser	Ile	Ser	Ala	Ser	Tyr	Met	Thr	Ser	Glu	Thr	Asn	Ser	Gly	Ile	Ile	
			370				375					380					
	Asn	Gly	Ser	Asp	Trp	Tyr	Val	Ile	Arg	Gly	Ser	Arg	Gln	Asp	Asn	Ala	
			385			390					395					400	
20	Asn	Tyr	Phe	His	Arg	Leu	Arg	Glu	Ile	Thr	Leu	Glu	Ile	Ser	Asn	Thr	
				405						410					415		
	Lys	Leu	Val	Pro	Ala	Ser	Gln	Leu	Pro	Lys	Tyr	Trp	Asn	Leu	Asn	Lys	
				420					425					430			
	Glu	Ser	Leu	Leu	Ala	Leu	Ile	Glu	Glu	Ser	Leu	Tyr	Gly	Ile	His	Gly	
			435					440					445				
25	Thr	Val	Thr	Ser	Ala	Ala	Asn	Gly	Gln	Pro	Leu	Lys	Cys	Gln	Ile	Leu	
			450				455					460					
	Ile	Glu	Asn	His	Asp	Lys	Arg	Asn	Ser	Asp	Val	Tyr	Ser	Asp	Ala	Thr	
			465			470					475					480	
30	Thr	Gly	Tyr	Tyr	Val	Arg	Pro	Ile	Lys	Ala	Gly	Thr	Tyr	Thr	Val	Lys	
				485						490					495		
	Tyr	Lys	Ala	Glu	Gly	Tyr	Pro	Glu	Ala	Thr	Arg	Thr	Ile	Thr	Ile	Lys	
				500					505					510			
	Asp	Lys	Glu	Thr	Val	Ile	Met	Asp	Ile	Ala	Leu	Gly	Asn	Ser	Val	Pro	
			515				520						525				
35	Leu	Pro	Val	Pro	Asp	Phe	Thr	Ala	Ser	Pro	Met	Thr	Ile	Ser	Val	Gly	
			530				535					540					
	Glu	Ser	Val	Gln	Phe	Gln	Asp	Gln	Thr	Thr	Asn	Asn	Pro	Thr	Asn	Trp	
			545			550					555					560	
40	Glu	Trp	Thr	Phe	Glu	Gly	Gly	Gln	Pro	Ala	Met	Ser	Thr	Glu	Gln	Asn	
				565						570					575		
	Pro	Leu	Val	Ser	Tyr	Ser	His	Pro	Gly	Gln	Tyr	Asp	Val	Thr	Leu	Lys	
				580					585					590			
	Val	Trp	Asn	Ala	Ser	Gly	Ser	Asn	Thr	Ile	Thr	Lys	Glu	Lys	Phe	Ile	
			595					600					605				
45	Thr	Val	Asn	Ala	Val	Met	Pro	Val	Ala	Glu	Phe	Val	Gly	Thr	Pro	Thr	
			610				615						620				
	Glu	Ile	Glu	Glu	Gly	Gln	Thr	Val	Ser	Phe	Gln	Asn	Gln	Ser	Thr	Asn	
			625			630					635					640	
50	Ala	Thr	Asn	Tyr	Val	Trp	Ile	Phe	Asp	Gly	Gly	Thr	Pro	Ala	Thr	Ser	
				645						650					655		
	Glu	Asp	Glu	Asn	Pro	Thr	Val	Leu	Tyr	Ser	Lys	Ala	Gly	Gln	Tyr	Asp	
				660					665					670			
	Val	Thr	Leu	Lys	Ala	Ile	Ser	Ala	Ser	Gly	Glu	Thr	Val	Lys	Thr	Lys	
			675					680					685				
55	Glu	Lys	Tyr	Ile	Thr	Val	Lys	Lys	Ala	Pro	Val	Pro	Ala	Pro	Val	Ala	
			690				695					700					
	Asp	Phe	Glu	Gly	Thr	Pro	Arg	Lys	Val	Lys	Lys	Gly	Glu	Thr	Val	Thr	
				705		710				715						720	
60	Phe	Lys	Asp	Leu	Ser	Thr	Asn	Asn	Pro	Thr	Ser	Trp	Leu	Trp	Val	Phe	
				725						730					735		
	Glu	Gly	Gly	Ser	Pro	Ala	Thr	Ser	Thr	Glu	Gln	Asn	Pro	Val	Val	Thr	
				740					745					750			
	Tyr	Asn	Glu	Thr	Gly	Lys	Tyr	Asp	Val	Gln	Leu	Thr	Ala	Thr	Asn	Glu	
				755			760						765				
65	Gly	Gly	Ser	Asn	Val	Lys	Lys	Ala	Glu	Asp	Tyr	Ile	Glu	Val	Ile	Leu	
			770				775					780					
	Asp	Asp	Ser	Val	Glu	Asp	Ile	Val	Ala	Gln	Thr	Gly	Ile	Val	Ile	Arg	
				785		790					795					800	
70	Pro	Gln	Asn	Gly	Thr	Lys	Gln	Ile	Leu	Ile	Glu	Ala	Asn	Ala	Ala	Ile	
				805						810					815		
	Lys	Ala	Ile	Val	Leu	Tyr	Asp	Ile	Asn	Gly	Arg	Val	Val	Leu	Lys	Thr	
				820					825					830			
	Thr	Pro	Asn	Gln	Leu	Arg	Ser	Thr	Val	Asp	Leu	Ser	Ile	Leu	Pro	Glu	
				835				840					845				
75	Gly	Ile	Tyr	Thr	Ile	Asn	Ile	Lys	Thr	Glu	Lys	Ser	Ala	Arg	Thr	Glu	

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850                      855                      860  
 Lys Ile His Ile Gly  
 865

## 5 (2) INFORMATION FOR SEQ ID NO:302

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 106 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Porphyromonas gingivalis
- (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...106
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:302

25 Leu Ser Tyr Ser Gly Glu Ser Asp Ala Lys Glu Ser Asp Gln Asn Cys  
 1                      5                      10                      15  
 Arg Lys Cys Thr Phe Ile Gly Phe Glu Lys Arg Val Asn Thr Met Arg  
                     20                      25                      30  
 Leu Ile Lys Ala Phe Leu Val Gln Leu Leu Leu Pro Ile Phe Phe  
 30                      35                      40                      45  
 Tyr Lys Arg Phe Ile Ser Pro Leu Thr Pro Pro Ser Cys Arg Phe Thr  
                     50                      55                      60  
 Pro Ser Cys Ser Ser Tyr Ala Ile Glu Ala Leu Arg Lys Tyr Gly Pro  
 65                      70                      75                      80  
 35 Gly Lys Gly Leu Leu Leu Ser Ile Lys Arg Ile Leu Arg Cys His Pro  
                     85                      90                      95  
 Trp Gly Gly Ser Gly Tyr Asp Pro Val Pro  
                     100                      105

## 40 (2) INFORMATION FOR SEQ ID NO:303

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 861 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Porphyromonas gingivalis
- (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...861
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:303

60 Leu Glu Met Ala Tyr Asp Phe Thr Gln Thr Phe Arg Asn Ser Leu Glu  
 1                      5                      10                      15  
 Tyr Ser Tyr Gln Glu Ala Thr Arg Leu Gly Val Val Ala Val Thr Gln  
                     20                      25                      30  
 Asp Met Leu Val Leu Gly Ile Ile Arg Asp Gly Asp Asn Gly Ala Ile  
 65                      35                      40                      45  
 Asp Ile Met Arg His Tyr Gly Ile Asn Leu Tyr Glu Leu Lys Arg Leu  
                     50                      55                      60  
 Ile Glu Leu Glu Ala Ile Ala Glu Ser Leu Pro Ala Ser Pro Glu Gly  
 65                      70                      75                      80  
 70 Ser Pro Ile Phe Thr Pro Ser Ala Arg Glu Ala Ile Asp Asp Ala Thr  
                     85                      90                      95  
 Asp Ile Cys Ala Asp Met Glu Asp Glu Ala Val Ser Pro Val His Leu  
                     100                      105                      110  
 75 Leu Leu Ser Ile Leu Asn Ser Thr Gln Glu Ser Leu Val Gln Lys Ile  
                     115                      120                      125

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	Phe	Met	Lys	Gln	Gly	Ile	Lys	Tyr	Asp	Thr	Ile	Leu	Ser	Asp	Tyr	Phe
	130						135					140				
	Gly	Gln	Arg	Asn	Pro	Ser	Glu	Gly	Lys	Ser	Pro	Ser	Glu	Met	Glu	Ile
	145					150					155					160
5	Leu	Asp	Gly	Tyr	Gln	Asp	Asn	Asp	Phe	Asp	Asp	Glu	Glu	Asp	Glu	Ser
					165					170					175	
	Ser	Pro	Pro	Ser	Gly	Asn	Ser	Gly	Thr	Gly	Gly	Gly	Ser	Gly	Asp	Ala
					180					185				190		
10	Pro	Glu	Gln	Asn	Thr	Gly	Gly	Gly	Asp	Thr	Thr	Thr	Thr	Thr	Arg	Ser
					195					200				205		
	Gly	Gly	Asp	Thr	Pro	Ala	Leu	Asp	Thr	Phe	Gly	Thr	Asp	Ile	Thr	Ala
					210							220				
	Met	Ala	Ala	Ala	Gly	Lys	Leu	Asp	Pro	Val	Val	Gly	Arg	Glu	Gln	Glu
	225					230						235				240
15	Ile	Glu	Arg	Val	Ile	Gln	Ile	Leu	Ser	Arg	Arg	Lys	Lys	Asn	Asn	Pro
					245						250				255	
	Val	Leu	Ile	Gly	Glu	Pro	Gly	Val	Gly	Lys	Ser	Ala	Ile	Val	Glu	Gly
					260					265				270		
20	Leu	Ala	Glu	Arg	Ile	Val	Asn	Arg	Lys	Val	Ser	Arg	Ile	Leu	Phe	Asp
					275					280				285		
	Lys	Arg	Ile	Ile	Ser	Leu	Asp	Leu	Ala	Gln	Met	Val	Ala	Gly	Thr	Lys
					290					295			300			
	Tyr	Arg	Gly	Gln	Phe	Glu	Glu	Arg	Leu	Lys	Ala	Val	Leu	Asp	Glu	Leu
	305					310					315					320
25	Lys	Lys	Asn	Pro	Gln	Ile	Ile	Leu	Phe	Ile	Asp	Glu	Ile	His	Thr	Ile
					325						330				335	
	Val	Gly	Ala	Gly	Ser	Ala	Ala	Gly	Ser	Met	Asp	Thr	Ala	Asn	Met	Leu
					340					345				350		
30	Lys	Pro	Ala	Leu	Ala	Arg	Gly	Gln	Val	Gln	Cys	Ile	Gly	Ala	Thr	Thr
					355					360				365		
	Leu	Asp	Glu	Tyr	Arg	Lys	Asn	Ile	Glu	Lys	Asp	Gly	Ala	Leu	Glu	Arg
					370					375			380			
	Arg	Phe	Gln	Lys	Val	Pro	Ile	Ala	Pro	Ser	Thr	Ala	Glu	Glu	Thr	Leu
	385					390					395					400
35	Thr	Ile	Leu	Gln	Asn	Ile	Lys	Glu	Lys	Tyr	Glu	Asp	Tyr	His	Gly	Val
					405						410				415	
	Arg	Tyr	Thr	Asp	Glu	Ala	Ile	Lys	Ala	Ala	Val	Glu	Leu	Thr	Asp	Arg
					420					425				430		
40	Tyr	Val	Ser	Asp	Arg	Phe	Phe	Pro	Asp	Lys	Ala	Ile	Asp	Ala	Met	Asp
					435					440				445		
	Glu	Ala	Gly	Ala	Ser	Val	His	Ile	Thr	Asn	Val	Val	Ala	Pro	Lys	Glu
					450					455			460			
	Ile	Glu	Ile	Leu	Glu	Ala	Glu	Leu	Ala	Ser	Val	Arg	Glu	Asn	Lys	Leu
	465					470					475					480
45	Ser	Ala	Val	Lys	Ala	Gln	Asn	Tyr	Glu	Leu	Ala	Ala	Ser	Phe	Arg	Asp
					485					490					495	
	Gln	Glu	Arg	Arg	Thr	Gln	Gln	Gln	Ile	Ala	Glu	Glu	Lys	Lys	Lys	Trp
					500					505				510		
50	Glu	Glu	Gln	Met	Ser	Lys	His	Arg	Glu	Thr	Val	Asp	Glu	Asn	Val	Val
					515					520				525		
	Ala	His	Val	Val	Ala	Leu	Met	Thr	Gly	Val	Pro	Ala	Glu	Arg	Leu	Ser
					530					535			540			
	Thr	Gly	Glu	Gly	Glu	Arg	Leu	Arg	Thr	Met	Ala	Asp	Asp	Leu	Lys	Thr
	545					550					555					560
55	Lys	Val	Val	Gly	Gln	Asp	Thr	Ala	Ile	Glu	Lys	Met	Val	His	Ala	Ile
					565					570				575		
	Gln	Arg	Asn	Arg	Leu	Gly	Leu	Arg	Asn	Glu	Lys	Lys	Pro	Ile	Gly	Ser
					580					585				590		
60	Phe	Leu	Phe	Leu	Gly	Pro	Thr	Gly	Val	Gly	Lys	Thr	Tyr	Leu	Ala	Lys
					595					600				605		
	Lys	Leu	Ala	Glu	Tyr	Leu	Phe	Glu	Asp	Glu	Asn	Ala	Met	Ile	Arg	Val
					610					615			620			
	Asp	Met	Ser	Glu	Tyr	Met	Glu	Lys	Phe	Ser	Val	Ser	Arg	Leu	Val	Gly
	625					630					635					640
65	Ala	Pro	Pro	Gly	Tyr	Val	Gly	Tyr	Glu	Glu	Gly	Gly	Gln	Leu	Thr	Glu
					645					650					655	
	Arg	Val	Arg	Arg	Lys	Pro	Tyr	Ser	Val	Val	Leu	Leu	Asp	Glu	Ile	Glu
					660					665				670		
70	Lys	Ala	His	Ala	Asp	Val	Phe	Asn	Leu	Leu	Leu	Gln	Val	Met	Asp	Glu
					675					680				685		
	Gly	Gln	Leu	Thr	Asp	Ser	Leu	Gly	Arg	Arg	Val	Asn	Phe	Lys	Asn	Thr
					690					695			700			
	Val	Ile	Ile	Ile	Thr	Ser	Asn	Val	Gly	Thr	Arg	Gln	Leu	Lys	Asp	Phe
	705					710					715					720
75	Gly	Gln	Gly	Ile	Gly	Phe	Arg	Ser	Glu	Lys	Asp	Glu	Glu	Ala	Asn	Lys

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5                               725                               730                               735  
       Glu His Ser Arg Ser Val Ile Gln Lys Ala Leu Asn Lys Thr Phe Ser  
           740                               745                               750  
 10   Pro Glu Phe Leu Asn Arg Leu Asp Asp Ile Ile Leu Phe Asp Gln Leu  
           755                               760                               765  
       Gly Lys Thr Glu Ile Arg Arg Met Val Asp Ile Glu Leu Lys Ala Val  
           770                               775                               780  
       Leu Ala Arg Ile His Arg Ala Gly Tyr Asp Leu Val Leu Thr Asp Glu  
           785                               790                               795                               800  
 15   Ala Lys Asp Val Ile Ala Thr Lys Gly Tyr Asp Leu Gln Tyr Gly Ala  
           805                               810                               815  
       Arg Pro Leu Lys Arg Thr Leu Gln Asn Glu Val Glu Asp Arg Leu Thr  
           820                               825                               830  
 20   Asp Leu Ile Leu Ser Gly Gln Ile Glu Lys Gly Gln Thr Leu Thr Leu  
           835                               840                               845  
       Ser Ala Arg Asp Gly Glu Ile Ile Val Gln Glu Gln Ala  
           850                               855                               860

20   (2) INFORMATION FOR SEQ ID NO:304  
       (i) SEQUENCE CHARACTERISTICS:  
           (A) LENGTH: 456 amino acids  
           (B) TYPE: amino acid  
           (D) TOPOLOGY: linear  
 25   (ii) MOLECULE TYPE: protein  
       (iii) HYPOTHETICAL: YES  
 30   (vi) ORIGINAL SOURCE:  
           (A) ORGANISM: Porphyromonas gingivalis  
       (ix) FEATURE:  
           (A) NAME/KEY: misc\_feature  
 35   (B) LOCATION 1...456  
       (xi) SEQUENCE DESCRIPTION: SEQ ID NO:304

40   Arg Gly Gly Gln Ile Arg Arg His His Thr Asp Ser Ser Arg Gly Ser  
       1                               5                               10                               15  
       Asp Ser Lys Ala Cys Arg Phe Ser Phe His Ala Glu Thr Ile Gly Phe  
           20                               25                               30  
       Ser Asn His Gln Arg Ala Lys Met Asn Tyr Leu Tyr Ile Leu Ile Thr  
           35                               40                               45  
 45   Leu Leu Leu Ser Gly Phe Phe Ser Gly Ala Glu Ile Ala Phe Leu Ser  
       50                               55                               60  
       Ser Asp Lys Leu Arg Leu Glu Leu Asp Arg Asn Arg Gly Asp Leu Thr  
           65                               70                               75                               80  
 50   Gly Arg Ala Leu Asn Leu Leu Tyr Arg His Pro Asp Gln Leu Val Thr  
           85                               90                               95  
       Thr Leu Leu Val Gly Asn Asn Ile Val Leu Val Val Tyr Gly Leu Leu  
           100                               105                               110  
       Met Ala Gly Leu Leu Ala Ala Pro Leu Ala Gln Trp Ile Asp Asn Asp  
           115                               120                               125  
 55   Ala Met Ile Val Val Leu Gln Ser Val Leu Ser Thr Ile Ile Ile Leu  
       130                               135                               140  
       Phe Thr Gly Glu Phe Leu Pro Lys Ala Ile Phe Lys Thr Asn Ala Asn  
           145                               150                               155                               160  
 60   Met Met Met Arg Val Phe Ala Leu Pro Ile Val Ala Ile Tyr Tyr Leu  
       165                               170                               175  
       Leu Tyr Pro Leu Ser Lys Leu Phe Thr Gly Leu Ser Arg Ser Phe Ile  
           180                               185                               190  
       Arg Leu Val Asp Lys Asn Tyr Val Pro Thr Thr Val Gly Leu Gly Arg  
           195                               200                               205  
 65   Val Asp Leu Asp His Tyr Leu Ala Glu Asn Met Ser Gly Glu Asn Glu  
       210                               215                               220  
       Gln Asn Asp Leu Thr Thr Glu Val Lys Ile Ile Gln Asn Ala Leu Asp  
           225                               230                               235                               240  
 70   Phe Ser Gly Ile Gln Val Arg Asp Cys Met Ile Pro Arg Asn Glu Met  
       245                               250                               255  
       Ile Ala Cys Glu Leu Gln Thr Asp Ile Glu Val Leu Lys Thr Thr Phe  
           260                               265                               270  
       Ile Asp Thr Gly Leu Ser Lys Ile Ile Ile Tyr Arg Gln Asn Ile Asp  
           275                               280                               285  
 75   Asp Val Val Gly Tyr Ile His Ser Ser Glu Met Phe Arg Gly Gln Asp

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290 295 300  
 Trp Gln Lys Arg Ile Asn Thr Thr Val Phe Val Pro Glu Ser Met Tyr  
 305 310 315 320  
 5 Ala Asn Lys Leu Met Arg Leu Leu Met Gln Arg Lys Lys Ser Ile Ala  
 325 330 335  
 Ile Val Ile Asp Glu Leu Gly Gly Thr Ala Gly Met Val Thr Leu Glu  
 340 345 350  
 Asp Leu Val Glu Glu Ile Phe Gly Asp Ile Glu Asp Glu His Asp Thr  
 355 360 365  
 10 Arg Lys Ile Ile Ala Lys Gln Leu Gly Pro His Thr Tyr Leu Val Ser  
 370 375 380  
 Gly Arg Met Glu Ile Asp Asp Val Asn Glu Arg Phe Gly Leu Ser Leu  
 385 390 395 400  
 15 Pro Glu Ser Asp Asp Tyr Leu Thr Val Ala Gly Phe Ile Leu Asn Ser  
 405 410 415  
 His Gln Asn Ile Pro Gln Ala Asn Glu Val Val Glu Ile Ala Pro Tyr  
 420 425 430  
 Thr Phe Thr Ile Leu Arg Ser Ser Ser Thr Lys Ile Glu Leu Val Lys  
 435 440 445  
 20 Met Ser Ile Asp Asp Gln Ser Asn  
 450 455

(2) INFORMATION FOR SEQ ID NO:305

- 25 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 299 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
 30 (ii) MOLECULE TYPE: protein  
 (iii) HYPOTHETICAL: YES  
 (vi) ORIGINAL SOURCE:  
 35 (A) ORGANISM: Porphyromonas gingivalis  
 (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...299  
 40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:305

Leu Lys Lys Glu Ile Thr Met Lys Gln Asn Tyr Phe Lys Arg Val Cys  
 1 5 10 15  
 45 Ser Leu Leu Trp Leu Val Leu Pro Met Leu Ile Met Pro Leu Glu Val  
 20 25 30  
 Ala Ala Gln Glu Ile Ile Pro Asn Glu Glu Val Leu Glu Ser Leu Thr  
 35 40 45  
 50 Phe Val Ala Pro Val Glu Glu Thr Asp Ala Ile Glu Ala Glu Val Glu  
 50 55 60  
 Ala Leu Gln Glu Ile Val Ala Thr Glu Glu Ile Ala Glu Gln Ala Val  
 65 70 75 80  
 Arg Ser Tyr Thr Tyr Thr Val Tyr Arg Asp Gly Val Lys Ile Ala Ser  
 85 90 95  
 55 Gly Leu Thr Glu Pro Thr Phe Leu Asp Glu Asp Val Pro Ala Gly Glu  
 100 105 110  
 His Thr Tyr Cys Val Glu Val Gln Tyr Gln Gly Gly Val Ser Asp Lys  
 115 120 125  
 60 Val Cys Val Asp Val Glu Val Lys Asp Phe Lys Pro Val Thr Asn Leu  
 130 135 140  
 Thr Gly Thr Ala Ser Asn Asp Glu Val Ser Leu Asp Trp Asp Gly Val  
 145 150 155 160  
 Glu Glu Lys Ala Glu Glu Pro Ala Ser Asp Lys Ala Val Ser Tyr Asn  
 165 170 175  
 65 Val Tyr Lys Asn Gly Thr Leu Ile Gly Asn Thr Ala Glu Thr His Tyr  
 180 185 190  
 Val Glu Thr Gly Val Ala Asn Gly Thr Tyr Ile Tyr Glu Val Glu Val  
 195 200 205  
 70 Lys Tyr Pro Asp Gly Val Ser Pro Lys Val Ala Val Thr Val Thr Val  
 210 215 220  
 Thr Asn Ser Ser Leu Ser Asn Val Asp Gly Gln Ala Pro Tyr Thr Leu  
 225 230 235 240  
 Arg Val Glu Gly Lys Lys Ile Ile Ala Glu Ala His Gly Met Ile Thr  
 245 250 255  
 75 Leu Tyr Asp Ile Asn Gly Arg Thr Val Ala Val Ala Pro Asn Arg Leu

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5                   260                   265                   270  
 Glu Tyr Met Ala Gln Thr Gly Phe Tyr Ala Val Arg Phe Asp Val Gly  
                   275                   280                   285  
 Asn Lys His His Val Ser Lys Ile Gln Val Arg  
                   290                   295

(2) INFORMATION FOR SEQ ID NO:306

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 377 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:  
 (A) NAME/KEY: misc feature  
 (B) LOCATION 1...377

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:306

1 Leu Phe Asn His Lys Lys Ser Trp Tyr Glu Thr Phe Gln Phe Tyr Leu  
 5                   5                   10                   15  
 30 Val Val Phe Arg Ser Gly Phe Ile Leu Leu Cys Glu Asn Thr Leu Ala  
                   20                   25                   30  
 Gln Gln Lys Thr Glu Glu Phe Ala Pro Val Ser Asp Leu Arg Ala Glu  
                   35                   40                   45  
 Ala Tyr Gly Ser Thr Val Phe Leu His Trp Thr Pro Pro Tyr Asp Asn  
                   50                   55                   60  
 35 Pro Met Ile Pro Leu Ser Glu Ser Phe Glu Ser Gly Ile Pro Ala Ile  
                   65                   70                   75                   80  
 Trp Lys Thr Ile Asp Ala Asp Gly Asp Gly Tyr Asn Trp Met His Leu  
                   85                   90                   95  
 40 Thr Asn Phe Thr Gly Gln Ser Gly Leu Cys Val Ser Ser Ala Ser Tyr  
                   100                   105                   110  
 Ile Gly Gly Val Gly Ala Leu Thr Pro Asp Asn Tyr Leu Ile Thr Pro  
                   115                   120                   125  
 Glu Leu Lys Leu Pro Thr Asp Ala Leu Val Glu Ile Ile Tyr Trp Val  
                   130                   135                   140  
 45 Cys Thr Gln Asp Leu Thr Ala Pro Ser Glu His Tyr Ala Val Tyr Ser  
                   145                   150                   155                   160  
 Ser Ser Thr Gly Asn Asn Ala Ala Asp Phe Val Asn Leu Leu Tyr Glu  
                   165                   170                   175  
 50 Glu Thr Leu Thr Ala Lys Arg Ile Gln Ser Pro Glu Leu Ile Arg Gly  
                   180                   185                   190  
 Asn Arg Thr Gln Gly Val Trp Tyr Gln Arg Lys Val Val Leu Pro Asn  
                   195                   200                   205  
 Asp Thr Lys Tyr Val Ala Phe Arg His Phe Asn Ser Thr Asp Asn Phe  
                   210                   215                   220  
 55 Trp Leu Asn Leu Asp Glu Val Ser Ile Leu Tyr Thr Pro Leu Pro Arg  
                   225                   230                   235                   240  
 Arg Ala Pro Cys Pro His Pro Gly Gly Tyr Thr Tyr Ser Val Phe Arg  
                   245                   250                   255  
 Asp Gly Gln Lys Ile Ala Ser Gly Leu Ser Ala Leu Ala Tyr Ile Asp  
                   260                   265                   270  
 60 Thr Asp Val Pro Tyr Gly Thr Gln Asp Tyr Cys Val Gln Val Asn Tyr  
                   275                   280                   285  
 Leu Gln Gly Asp Ser Tyr Lys Val Cys Lys Asn Ile Val Val Ala Asn  
                   290                   295                   300  
 65 Ser Ala Asn Ile Tyr Gly Ala Asp Lys Pro Phe Ala Leu Thr Val Val  
                   305                   310                   315                   320  
 Gly Lys Thr Ile Val Ala Ser Ala Phe Lys Gly Glu Ile Thr Leu Tyr  
                   325                   330                   335  
 70 Asp Ile Arg Gly Arg Leu Ile Ala Ser Gly Cys Asp Thr Leu Arg Tyr  
                   340                   345                   350  
 Lys Ala Glu Asn Gly Phe Tyr Leu Ile Lys Ile Gln Val Asn Gly Thr  
                   355                   360                   365  
 Val Tyr Thr Glu Lys Ile Gln Ile Gln  
                   370                   375

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## (2) INFORMATION FOR SEQ ID NO:307

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 849 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

(A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...849

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:307

5 Phe Gly Ile Ser Pro Ser Met Lys Lys Ser Phe Leu Leu Ala Ile Val  
 1 5 10 15  
 Met Leu Phe Gly Ile Ala Met Gln Gly His Ser Ala Pro Val Thr Lys  
 20 25 30  
 25 Glu Arg Ala Leu Ser Leu Ala Arg Leu Ala Leu Arg Gln Val Ser Leu  
 35 40 45  
 Arg Met Gly Gln Thr Ala Val Ser Asp Lys Ile Ser Ile Asp Tyr Val  
 50 55 60  
 30 Tyr Arg Gln Gly Asp Ala Glu Arg Gly Ile Thr Ser Gln Glu Glu Gly  
 65 70 75 80  
 Ser Pro Ala Tyr Phe Tyr Val Ala Asn Arg Gly Asn Asn Glu Gly Tyr  
 85 90 95  
 Ala Leu Val Ala Ala Asp Asp Arg Ile Pro Thr Ile Leu Ala Tyr Ser  
 100 105 110  
 35 Pro Ile Gly Arg Phe Asp Met Asp Ser Met Pro Asp Asn Leu Arg Met  
 115 120 125  
 Trp Leu Gln Ile Tyr Asp Gln Glu Ile Gly Leu Ile Leu Ser Gly Lys  
 130 135 140  
 40 Ala Gln Leu Asn Glu Glu Ile Leu Arg Thr Glu Gly Val Pro Ala Glu  
 145 150 155 160  
 Val His Ala Leu Met Asp Asn Gly His Phe Ala Asn Asp Pro Met Arg  
 165 170 175  
 Trp Asn Gln Gly Tyr Pro Trp Asn Asn Lys Glu Pro Leu Leu Pro Asn  
 180 185 190  
 45 Gly Asn His Ala Tyr Thr Gly Cys Val Ala Thr Ala Ala Ala Gln Ile  
 195 200 205  
 Met Arg Tyr His Ser Trp Pro Leu Gln Gly Glu Gly Ser Phe Asp Tyr  
 210 215 220  
 50 His Ala Gly Ser Leu Val Gly Asn Trp Ser Gly Thr Phe Gly Glu Met  
 225 230 235 240  
 Tyr Asp Trp Ile Asn Met Pro Gly Asn Pro Asp Leu Asp Asn Leu Thr  
 245 250 255  
 Gln Ser Gln Val Asp Ala Tyr Ala Thr Leu Met Arg Asp Val Ser Ala  
 260 265 270  
 55 Ser Val Ser Met Ser Phe Tyr Glu Asn Gly Ser Gly Thr Tyr Ser Val  
 275 280 285  
 Tyr Val Val Gly Ala Leu Arg Asn Asn Phe Arg Tyr Lys Arg Ser Leu  
 290 295 300  
 60 Gln Leu His Val Arg Ala Leu Tyr Thr Ser Gln Glu Trp His Asp Met  
 305 310 315 320  
 Ile Arg Gly Glu Leu Ala Ser Gly Arg Pro Val Tyr Tyr Ala Gly Asn  
 325 330 335  
 Asn Gln Ser Ile Gly His Ala Phe Val Cys Asp Gly Tyr Ala Ser Asp  
 340 345 350  
 65 Gly Thr Phe His Phe Asn Trp Gly Trp Gly Gly Val Ser Asn Gly Phe  
 355 360 365  
 Tyr Lys Leu Thr Leu Leu Ser Pro Thr Ser Leu Gly Ile Gly Gly Glu  
 370 375 380  
 70 Gly Ile Gly Phe Thr Ile Tyr Gln Glu Ile Ile Thr Gly Ile Glu Pro  
 385 390 395 400  
 Ala Lys Thr Pro Ala Glu Ala Gly Thr Asp Ala Leu Pro Ile Leu Ala  
 405 410 415  
 Leu Lys Asp Ile Glu Ala Glu Tyr Lys Ser Glu Ser Gly Leu Asn Val  
 420 425 430  
 75 Gly Tyr Ser Ile Tyr Asn Thr Gly Glu Glu Ser Asn Leu Asp Leu



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			435				440				445					
	Gly	Tyr	Arg	Leu	Asn	Lys	Ala	Asp	Gly	Glu	Val	Ile	Glu	Val	Lys	Thr
		450					455					460				
5	Ser	Ser	Ile	Asn	Ile	Ser	Trp	Tyr	Gly	Tyr	Gly	Glu	His	Pro	Glu	Ser
	465					470					475				480	
	Phe	Ser	Leu	Ala	Pro	Asn	Gln	Leu	Ser	Gln	Gly	Ile	Asn	Thr	Ile	Thr
				485					490						495	
	Leu	Leu	Tyr	Arg	Arg	Thr	Gly	Thr	Glu	Gln	Trp	Glu	Pro	Val	Arg	His
				500					505					510		
10	Ala	Gln	Gly	Gly	Tyr	Val	Asn	Ser	Ile	Lys	Val	Asn	Thr	Thr	Asp	Pro
		515					520					525				
	Asn	Asn	Val	Val	Val	Thr	Val	Asp	Asn	Asn	Glu	Gly	Lys	Leu	Ser	Ile
		530					535					540				
15	Val	Pro	Asn	Ser	Phe	Val	Ala	Asp	Leu	Asn	Ser	Tyr	Glu	His	Ser	Thr
	545				550						555				560	
	Ile	Thr	Val	Gln	Phe	Asn	Ser	Asp	Ser	Pro	Asp	Glu	Ile	Arg	Thr	Pro
				565					570						575	
	Val	Ala	Phe	Ala	Leu	Ser	Thr	Gly	Ala	Thr	Ala	Asp	Asp	Val	Ile	Ser
			580					585					590			
20	Leu	Gly	Trp	Val	Met	Ala	Glu	Val	Pro	Gly	Gly	Ser	Ser	Asn	Tyr	Pro
		595					600						605			
	Val	Val	Trp	Ser	Lys	Asp	Val	Leu	Thr	Leu	Ser	Glu	Gly	Asp	Tyr	Thr
		610				615						620				
25	Leu	Trp	Tyr	Arg	Phe	Ser	Ile	Asn	Asn	Gln	Lys	Asp	Glu	Trp	Lys	Lys
	625				630						635				640	
	Ile	Gly	Ser	Val	Ser	Val	Lys	Thr	Pro	Thr	Glu	Tyr	Thr	His	Pro	Leu
				645						650					655	
	Phe	Glu	Val	Gly	His	Asn	Gln	Thr	Ser	Thr	Tyr	Thr	Leu	Asp	Met	Ala
			660						665					670		
30	His	Asn	Arg	Val	Leu	Pro	Asp	Phe	Thr	Leu	Lys	Asn	Leu	Gly	Leu	Pro
		675					680						685			
	Phe	Asn	Gly	Glu	Leu	Val	Val	Val	Phe	Arg	Gln	Thr	Gln	Ser	Ser	Ser
		690				695						700				
35	Gly	Ser	Leu	Trp	Ala	Ala	Gln	Glu	Thr	Val	His	Ile	Lys	Gln	Gly	Glu
	705				710					715					720	
	Thr	Phe	Val	Tyr	Lys	Pro	Val	Val	Glu	Gly	Pro	Ile	Pro	Asp	Gly	Ser
				725						730					735	
	Tyr	Arg	Ala	Thr	Leu	His	Ala	Phe	Val	Asn	Gly	Gln	Gln	Gln	Leu	Tyr
		740						745						750		
40	Leu	Lys	Gly	Lys	Arg	Asn	Tyr	Thr	Val	Lys	Ile	Val	Asn	Gly	Thr	Ala
		755					760						765			
	Val	Glu	Ala	Ile	Glu	Ser	Ser	Glu	Glu	Ile	Arg	Val	Phe	Pro	Asn	Pro
		770				775						780				
45	Ala	Arg	Asp	Tyr	Val	Glu	Ile	Ser	Ala	Pro	Cys	Ile	Pro	Gln	Glu	Thr
	785				790					795					800	
	Ser	Ile	Ile	Leu	Phe	Asp	Leu	Ser	Gly	Lys	Ile	Val	Met	Lys	Asn	Ser
				805					810					815		
	Leu	Ser	Ala	Gly	His	Gly	Arg	Met	Asp	Val	Ser	Arg	Leu	Pro	Asn	Gly
		820						825					830			
50	Ala	Tyr	Ile	Leu	Lys	Val	Asp	Gly	Tyr	Thr	Thr	Lys	Ile	Asn	Ile	Val
		835					840						845			
	His															

55 (2) INFORMATION FOR SEQ ID NO:308

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 295 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

60

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

65

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

(A) NAME/KEY: misc\_feature

(B) LOCATION 1...295

70

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:308

75

Thr Lys Lys Thr Leu Met Lys Lys Leu Phe Leu Ser Leu Thr Ser Leu

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1      5      10      15
Val Met Val Phe Ala Val Ala Ser Cys Asp Ile Ile Asp Lys Asp Gln
20      25      30
5  Thr Leu Leu Pro Ala Pro Thr Asn Val Thr Pro Asp Asn Pro Asp Asp
35      40      45
Asn Pro Ser Glu Ile Asp Ile Thr Gln Thr His Thr Glu Lys Tyr Val
50      55      60
Leu Ala Glu Glu Phe Thr Gly Gln Lys Cys Leu Asn Cys Pro Lys Gly
65      70      75      80
10 His Arg Lys Leu Ala Ala Leu Lys Glu Gln Tyr Gly Lys Arg Leu Thr
85      90      95
Val Val Gly Ile His Ala Gly Pro Gly Ser Leu Val Pro Pro Leu Phe
100      105      110
15 Arg Thr Glu Ala Gly Asp Ala Tyr Tyr Ser Lys Phe Ala Asn Asn Thr
115      120      125
Pro Leu Pro Ala Leu Met Val Ser Arg Lys Lys Phe Gly Ser Ser Tyr
130      135      140
Val Tyr Asp Lys Ser Tyr Lys Thr Trp Asp Val Pro Ile Ala Glu Gln
145      150      155      160
20 Met Glu Gln Lys Ala Lys Ile Asn Ile Phe Ala Val Ala Glu Tyr Thr
165      170      175
Asp Thr Gln Lys Ile Lys Val Thr Val Lys Gly Lys Ile Leu Glu Gly
180      185      190
25 Asn Thr Leu Pro Lys Ser Met Val Gln Val Tyr Leu Leu Glu Asp Lys
195      200      205
Leu Ile Ala Pro Gln Val Asp Gly Asn Thr Thr Val Glu Asn Tyr Glu
210      215      220
His Asn His Val Leu Arg Gly Ala Val Asn Gly Ile Trp Gly Glu Glu
225      230      235      240
30 Phe Val Asn Leu Lys Asp Tyr Leu Tyr Thr Tyr Ala Val Glu Pro Leu
245      250      255
Ser Gly Met Ser Phe Val Ala Glu Asn Tyr Ser Ile Val Ala Phe Val
260      265      270
35 Tyr Asp Val Gln Thr Phe Glu Val Tyr Asp Val Val His Val Lys Ile
275      280      285
Asn Pro Gln Ser Asp Gly Lys
290      295

```

## (2) INFORMATION FOR SEQ ID NO:309

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 230 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Porphyromonas gingivalis
- (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...230
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:309

```

60 Thr Asn Lys Lys Glu Glu Thr Met Lys Lys Ser Ser Val Val Ala Ser
1      5      10      15
Val Leu Ala Val Ala Leu Val Phe Ala Gly Cys Gly Leu Asn Asn Met
20      25      30
Ala Lys Gly Gly Leu Ile Gly Ala Gly Val Gly Gly Ala Ile Gly Ala
35      40      45
65 Gly Val Gly Asn Val Ala Gly Asn Thr Ala Val Gly Ala Ile Val Gly
50      55      60
Thr Ala Val Gly Gly Ala Ala Gly Ala Leu Ile Gly Lys Lys Met Asp
65      70      75      80
Lys Gln Lys Lys Glu Leu Glu Ala Ala Val Pro Asp Ala Thr Ile Gln
85      90      95
70 Thr Val Asn Asp Gly Glu Ala Ile Leu Val Thr Phe Asp Ser Gly Ile
100      105      110
Leu Phe Ala Thr Asn Ser Ser Thr Leu Ser Pro Asn Ser Arg Thr Ala
115      120      125
75 Leu Thr Lys Phe Ala Ala Asn Met Asn Lys Asn Pro Asp Thr Asp Ile

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130 135 140  
 Arg Ile Val Gly His Thr Asp Asn Thr Gly Ser Asp Lys Ile Asn Asp  
 145 150 155 160  
 Pro Leu Ser Glu Arg Arg Ala Ala Ser Val Tyr Ser Phe Leu Asn Ser  
 165 170 175  
 5 Gln Gly Val Ser Met Ser Arg Met Ala Ala Glu Gly Arg Gly Ser His  
 180 185 190  
 Glu Pro Val Ala Asp Asn Ser Thr Val Ala Gly Arg Ser Ala Asn Arg  
 195 200 205  
 10 Arg Val Glu Val Tyr Ile Leu Pro Asn Ala Lys Met Ile Glu Gln Ala  
 210 215 220  
 Gln Gln Gly Thr Leu Lys  
 225 230  
 15 (2) INFORMATION FOR SEQ ID NO:310  
 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 342 amino acids  
 (B) TYPE: amino acid  
 20 (D) TOPOLOGY: linear  
 (ii) MOLECULE TYPE: protein  
 (iii) HYPOTHETICAL: YES  
 25 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Porphyromonas gingivalis  
 (ix) FEATURE:  
 30 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...342  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:310  
 35 Asn Arg Asn Arg Asn Met Ser Lys Lys Ser Ile Leu Leu Leu Cys Cys  
 1 5 10 15  
 Ser Leu Cys Phe Ile Ser Ala Thr Lys Ala Val Thr Pro Val Arg Asn  
 20 25 30  
 40 Val Arg Asn Ser Gln Val Asn Ser Lys Ala Lys Thr Glu Arg Thr Lys  
 35 40 45  
 Pro Ser Asp Ser Val Arg Tyr Ile Ser Asn Met Ile Ala Asp Arg Leu  
 50 55 60  
 Glu Phe Arg Asn Lys Ile Ser Ser Glu Lys Glu Val Arg Lys Ala Glu  
 65 70 75 80  
 45 Tyr Glu Asn Arg Leu Ala Met Glu Ala Leu Asn Tyr Pro Ala Ile Asp  
 85 90 95  
 Leu Tyr Gly Glu Asp Ser Trp Ser Glu Tyr Val Asn Pro Phe Val Gly  
 100 105 110  
 50 Ala Gly Thr Asp Val Glu Ile Pro Asn Ser Tyr Asp Ile Asp Cys Ser  
 115 120 125  
 Ser Phe Val Met Pro Val Glu Asp Lys Gln Val Thr Ser Gln Phe Gly  
 130 135 140  
 Tyr Arg Arg Arg Phe Gly Arg Met His Tyr Gly Ile Asp Leu Ser Val  
 145 150 155 160  
 55 Asn Arg Gly Asp Thr Ile Arg Ala Ala Phe Asp Gly Lys Val Arg Val  
 165 170 175  
 Arg Ser Tyr Glu Ala Arg Gly Tyr Gly Tyr Tyr Ile Val Leu Arg His  
 180 185 190  
 60 Pro Asn Gly Leu Glu Thr Val Tyr Gly His Met Ser Arg Gln Leu Val  
 195 200 205  
 Asp Glu Asn Gln Ile Val Arg Ala Gly Gln Pro Ile Gly Leu Gly Gly  
 210 215 220  
 Ser Thr Gly Arg Ser Thr Gly Pro His Leu His Phe Glu Thr Arg Phe  
 225 230 235 240  
 65 Met Gly Ile Pro Ile Asn Pro Ser Thr Ile Ile Asp Phe Asp Asn Gly  
 245 250 255  
 Val Pro Leu Arg Asp Ile Tyr Thr Phe Lys Arg Gly Ser Asn Ser Arg  
 260 265 270  
 70 Tyr Ala Lys Ala Ser Lys Thr Ser Ser Arg Tyr Ala Lys Lys Gly Lys  
 275 280 285  
 Lys Gly Arg Gln Ala Ser Ser Pro Met Thr Tyr Arg Ile Lys Lys Gly  
 290 295 300  
 Asp Thr Leu Glu Thr Ile Ala Lys Arg His Gly Thr Ser Val Gln Lys  
 305 310 315 320  
 75 Leu Cys Ala Thr Asn Gly Ile Gly Lys Ser Lys Ile Leu Thr Pro Gly

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	325	330	335
Lys Ala Leu Arg Ile Lys			
340			

5 (2) INFORMATION FOR SEQ ID NO:311

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 159 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

(A) NAME/KEY: misc feature

(B) LOCATION 1...159

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:311

25	Pro	Ser	Lys	Thr	Ile	Ile	Lys	Thr	Met	Ala	Lys	Ile	Asn	Phe	Tyr	Ala
	1				5					10					15	
30	Glu	Gly	Val	Ser	Leu	Pro	Arg	Ile	Arg	Arg	Arg	Ile	Val	Gly	Lys	Trp
				20					25					30		
	Ile	Ala	Glu	Val	Cys	Ser	Arg	Tyr	Gly	Lys	Ala	Val	Gly	Glu	Ile	Ser
35				35					40				45			
	Tyr	Leu	Phe	Cys	Asp	Asp	Glu	Tyr	Ile	Leu	Lys	Ala	Asn	Gln	Glu	Phe
		50					55					60				
40	Leu	Asp	His	Asp	Tyr	Tyr	Thr	Asp	Ile	Ile	Thr	Phe	Asp	Ser	Cys	Glu
						70					75				80	
	Ala	Asp	Thr	Val	Asn	Gly	Asp	Leu	Leu	Ile	Ser	Leu	Asp	Thr	Val	Arg
45					85					90					95	
	Ser	Asn	Ala	Arg	Ala	Leu	Asp	Leu	Arg	Tyr	Glu	Asp	Glu	Leu	His	Arg
				100					105					110		
	Val	Ile	Ile	His	Gly	Ile	Leu	His	Leu	Cys	Gly	Leu	Lys	Asp	Lys	Ser
50				115				120					125			
	Lys	Lys	Asp	Glu	Ala	Gln	Met	Arg	Ala	Ala	Glu	Glu	Lys	Ala	Leu	Val
							135					140				
55	Met	Leu	Arg	Glu	Thr	Ile	Gly	Ser	Glu	Leu	Ser	Leu	Leu	His	Thr	
						150					155					

45 (2) INFORMATION FOR SEQ ID NO:312

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 395 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Porphyromonas gingivalis*

(ix) FEATURE:

(A) NAME/KEY: misc feature

(B) LOCATION 1...395

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:312

(E1) SEQUENCE DESCRIPTION: SEQ ID NO:312																	
65	Lys	Ser	Lys	Thr	Met	Lys	Val	Lys	Tyr	Leu	Met	Leu	Thr	Leu	Val	Gly	
	1				5					10					15		
	Ala	Ile	Ala	Leu	Asn	Ala	Ser	Ala	Gln	Glu	Asn	Thr	Val	Pro	Ala	Thr	
				20					25					30			
70	Gly	Gln	Leu	Pro	Ala	Lys	Asn	Val	Ala	Phe	Ala	Arg	Asn	Lys	Ala	Gly	
			35					40					45				
	Ser	Asn	Trp	Phe	Val	Thr	Leu	Gln	Gly	Gly	Val	Ala	Ala	Gln	Phe	Leu	
		50					55					60					
	Asn	Asp	Asn	Asn	Asn	Lys	Asp	Leu	Met	Asp	Arg	Leu	Gly	Ala	Ile	Gly	
75	65					70					75					80	

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Ser Leu Ser Val Gly Lys Tyr His Ser Pro Phe Phe Ala Thr Arg Leu  
 85 90 95  
 Gln Ile Asn Gly Gly Gln Ala His Thr Phe Leu Gly Lys Asn Gly Glu  
 100 105 110  
 5 Gln Glu Ile Asn Thr Asn Phe Gly Ala Ala His Phe Asp Phe Met Phe  
 115 120 125  
 Asp Val Val Asn Tyr Phe Ala Pro Tyr Arg Glu Asn Arg Phe Phe His  
 130 135 140  
 10 Leu Ile Pro Trp Val Gly Val Gly Tyr Gln His Lys Phe Ile Gly Ser  
 145 150 155 160  
 Glu Trp Ser Lys Asp Asn Val Glu Ser Leu Thr Ala Asn Val Gly Val  
 165 170 175  
 Met Met Ala Phe Arg Leu Gly Lys Arg Val Asp Phe Val Ile Glu Ala  
 180 185 190  
 15 Gln Ala Ala His Ser Asn Leu Asn Leu Ser Arg Ala Tyr Asn Ala Lys  
 195 200 205  
 Lys Thr Pro Val Phe Glu Asp Pro Ala Gly Arg Tyr Tyr Asn Gly Phe  
 210 215 220  
 20 Gln Gly Met Ala Thr Ala Gly Leu Asn Phe Arg Leu Gly Ala Val Gly  
 225 230 235 240  
 Phe Asn Ala Ile Unk Pro Met Asp Tyr Ala Leu Ile Asn Asp Leu Asn  
 245 250 255  
 Gly Gln Ile Asn Arg Leu Arg Ser Glu Val Glu Glu Leu Ser Lys Arg  
 260 265 270  
 25 Pro Val Ser Cys Pro Glu Cys Pro Glu Val Thr Pro Val Thr Lys Thr  
 275 280 285  
 Glu Asn Ile Leu Thr Glu Lys Ala Val Leu Phe Arg Phe Asp Ser His  
 290 295 300  
 30 Val Val Asp Lys Asp Gln Leu Ile Asn Leu Tyr Asp Val Ala Gln Phe  
 305 310 315 320  
 Val Lys Glu Thr Asn Glu Pro Ile Thr Val Val Gly Tyr Ala Asp Pro  
 325 330 335  
 Thr Gly Asn Thr Gln Tyr Asn Glu Lys Leu Ser Glu Arg Arg Ala Lys  
 340 345 350  
 35 Ala Val Val Asp Val Leu Thr Gly Lys Tyr Gly Val Pro Ser Glu Leu  
 355 360 365  
 Ile Ser Val Glu Trp Lys Gly Asp Ser Thr Gln Pro Phe Ser Lys Lys  
 370 375 380  
 40 Ala Trp Asn Arg Val Val Ile Val Arg Ser Lys  
 385 390 395

## (2) INFORMATION FOR SEQ ID NO:313

- 45 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 387 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
 50 (ii) MOLECULE TYPE: protein  
 (iii) HYPOTHETICAL: YES  
 (vi) ORIGINAL SOURCE:  
 55 (A) ORGANISM: Porphyromonas gingivalis  
 (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...387  
 60 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:313

Tyr Lys Met Thr Tyr Arg Ile Met Lys Ala Lys Ser Leu Leu Leu Ala  
 1 5 10 15  
 65 Leu Ala Gly Leu Ala Cys Thr Phe Ser Ala Thr Ala Gln Glu Ala Thr  
 20 25 30  
 Thr Gln Asn Lys Ala Gly Met His Thr Ala Phe Gln Arg Asp Lys Ala  
 35 40 45  
 Ser Asp His Trp Phe Ile Asp Ile Ala Gly Gly Ala Gly Met Ala Leu  
 50 55 60  
 70 Ser Gly Trp Asn Asn Asp Val Asp Phe Val Asp Arg Leu Ser Ile Val  
 65 70 75 80  
 Pro Thr Phe Gly Ile Gly Lys Trp His Glu Pro Tyr Phe Gly Thr Arg  
 85 90 95  
 75 Leu Gln Phe Thr Gly Phe Asp Ile Tyr Gly Phe Pro Gln Gly Ser Lys  
 100 105 110

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5 Glu Arg Asn His Asn Tyr Phe Gly Asn Ala His Leu Asp Phe Met Phe  
 115 120 125  
 Asp Leu Thr Asn Tyr Phe Gly Val Tyr Arg Pro Asn Arg Val Phe His  
 130 135 140  
 Ile Ile Pro Trp Ala Gly Ile Gly Phe Gly Tyr Lys Phe His Ser Glu  
 145 150 155 160  
 Asn Ala Asn Gly Glu Lys Val Gly Ser Lys Asp Asp Met Thr Gly Thr  
 165 170 175  
 10 Val Asn Val Gly Leu Met Leu Lys Phe Arg Leu Ser Arg Val Val Asp  
 180 185 190  
 Phe Asn Ile Glu Gly Gln Ala Phe Ala Gly Lys Met Asn Phe Ile Gly  
 195 200 205  
 Thr Lys Arg Gly Lys Ala Asp Phe Pro Val Met Ala Thr Ala Gly Leu  
 210 215 220  
 15 Thr Phe Asn Leu Gly Lys Thr Glu Trp Thr Glu Ile Val Pro Met Asp  
 225 230 235 240  
 Tyr Ala Leu Val Asn Asp Leu Asn Asn Gln Ile Asn Ser Leu Arg Gly  
 245 250 255  
 20 Gln Val Glu Glu Leu Ser Arg Arg Pro Val Ser Cys Pro Glu Cys Pro  
 260 265 270  
 Glu Pro Thr Gln Pro Thr Val Thr Arg Val Val Val Asp Asn Val Val  
 275 280 285  
 Tyr Phe Arg Ile Asn Ser Ala Lys Ile Asp Arg Asn Gln Glu Ile Asn  
 290 295 300  
 25 Val Tyr Asn Thr Ala Glu Tyr Ala Lys Thr Asn Asn Ala Pro Ile Lys  
 305 310 315 320  
 Val Val Gly Tyr Ala Asp Glu Lys Thr Gly Thr Ala Ala Tyr Asn Met  
 325 330 335  
 30 Lys Leu Ser Glu Arg Arg Ala Lys Ala Val Ala Lys Met Leu Glu Lys  
 340 345 350  
 Tyr Gly Val Ser Ala Asp Arg Ile Thr Ile Glu Trp Lys Gly Ser Ser  
 355 360 365  
 Glu Gln Ile Tyr Glu Glu Asn Ala Trp Asn Arg Ile Val Val Met Thr  
 370 375 380  
 35 Ala Ala Glu  
 385

(2) INFORMATION FOR SEQ ID NO:314

- 40 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 195 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
 45 (ii) MOLECULE TYPE: protein  
 (iii) HYPOTHETICAL: YES  
 50 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Porphyromonas gingivalis  
 (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...195  
 55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:314

60 Val Ile Gly Ile Ile Met Glu Phe Phe Met Leu Phe Ile Ala Ala Val  
 1 5 10 15  
 Phe Val Asn Asn Val Val Leu Ser Gln Phe Leu Gly Ile Cys Pro Phe  
 20 25 30  
 Leu Gly Val Ser Lys Lys Val Asp Thr Ser Ile Gly Met Gly Ala Ala  
 35 40 45  
 65 Val Thr Phe Val Leu Ala Leu Ala Thr Leu Val Thr Phe Leu Ile Gln  
 50 55 60  
 Lys Phe Val Leu Asp Arg Phe Gly Leu Gly Phe Met Gln Thr Ile Ala  
 65 70 75 80  
 Phe Ile Leu Val Ile Ala Ala Leu Val Gln Met Val Glu Ile Ile Leu  
 85 90 95  
 70 Lys Lys Val Ser Pro Pro Leu Tyr Gln Ala Leu Gly Val Phe Leu Pro  
 100 105 110  
 Leu Ile Thr Thr Asn Cys Cys Val Leu Gly Val Ala Ile Leu Val Ile  
 115 120 125  
 75 Gln Lys Asp Tyr Thr Leu Leu Gln Ser Phe Val Tyr Ala Ile Ser Thr  
 130 135 140

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Ala Ile Gly Phe Thr Leu Ala Met Val Thr Phe Ala Gly Ile Arg Glu  
 145 150 155 160  
 Gln Leu Asp Met Thr Asn Leu Pro Lys Ala Met Lys Gly Ile Pro Ser  
 165 170 175  
 5 Ala Leu Leu Ala Ala Gly Ile Leu Ala Met Ala Phe Met Gly Phe Ser  
 180 185 190  
 Gly Ile Ala  
 195

10 (2) INFORMATION FOR SEQ ID NO:315

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 876 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

15 (ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

20 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:  
 (A) NAME/KEY: misc feature  
 (B) LOCATION: 1...876

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:315

30 Tyr Arg Ser Tyr Arg Gly Ile Gly Ser Gly Thr His Ser Pro Asn Leu  
 1 5 10 15  
 Lys Asn Arg Leu Lys Arg Ile Gly Ile Arg Ile Pro Asn Arg His Tyr  
 20 25 30  
 35 Ile His Ile Lys Pro Ile Lys Pro Lys Asn Lys Met Lys Gln Leu Asn  
 35 40 45  
 Ile Ile Ser Phe Ile Ile Ala Phe Leu Phe Leu Gly Thr Ser Ala Ser  
 50 55 60  
 Ala Gln Gln Ser Gly Gly Ser Val Thr Gly Thr Val Val Asp Lys Ser  
 65 70 75 80  
 40 Ser Lys Glu Pro Ile Ala Tyr Val Gln Val Phe Val Lys Gly Thr Thr  
 85 90 95  
 Leu Gly Thr Ser Thr Asp Ala Asn Gly Asn Tyr Ser Ile Lys Gly Ile  
 100 105 110  
 Pro Ser Gly Asn Gln Thr Ile Val Ala Arg Leu Met Gly Tyr Ser Thr  
 115 120 125  
 45 Cys Glu Glu Lys Val His Ile Glu Lys Gly Gly Ser Arg His Val Asp  
 130 135 140  
 Leu Tyr Leu Thr Glu Glu Ile Leu Ser Leu Asp Gly Val Val Val Ser  
 145 150 155 160  
 50 Ala Asn Arg Asn Glu Thr Phe Arg Arg Gln Ala Pro Ser Leu Val Thr  
 165 170 175  
 Val Leu Ser Pro Glu Leu Phe Leu Lys Thr Asn Ser Thr Asn Leu Ser  
 180 185 190  
 Gln Gly Leu Lys Phe Gln Pro Gly Leu Arg Val Glu Asp Asn Cys Gln  
 195 200 205  
 55 Asn Cys Gly Phe Asn Gln Val Arg Ile Asn Gly Leu Glu Gly Ala Tyr  
 210 215 220  
 Ser Gln Ile Leu Ile Asp Ser His Pro Ile Phe Ser Ser Leu Ala Gly  
 225 230 235 240  
 60 Val Tyr Gly Leu Glu Gln Met Pro Ala Asn Met Ile Glu Arg Val Glu  
 245 250 255  
 Val Ile Arg Gly Gly Ser Ala Leu Phe Gly Ser Asn Ala Val Gly  
 260 265 270  
 65 Gly Val Ile Asn Val Ile Thr Lys Glu Pro Leu Arg Asn Ser Ala Glu  
 275 280 285  
 Ile Ser His Ser Thr Met Thr Phe Asp His Ala Lys Gly Trp Gly Ser  
 290 295 300  
 Phe Gln Asn Thr Thr Gln Phe Asn Gly Ser Met Leu Thr Glu Asp Arg  
 305 310 315 320  
 70 Lys Ala Gly Val Met Val Phe Gly Gln His Asn Tyr Arg Pro Gly Gln  
 325 330 335  
 Asp Ile Asp Gly Asp Asn Phe Thr Glu Leu Pro Asn Leu Arg Asn Arg  
 340 345 350  
 75 Ser Leu Gly Phe Arg Ser Tyr Tyr Lys Thr Gly Leu Tyr Ser Lys Ala  
 355 360 365

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Thr Leu Glu Tyr His Ser Met Gln Glu Tyr Arg Arg Gly Gly Asp Arg  
 370 375 380  
 Leu Asp Asn Pro Pro Phe Glu Ala Gln Ile Ala Glu Tyr Leu Gln His  
 385 390 395 400  
 5 Tyr Ile Asn Gly Gly Ser Phe Lys Phe Asp Gln Gly Phe Ser Gly Gly  
 405 410 415  
 Lys Asp Phe Phe Ser Leu Tyr Ala Ser Ala Gln Asp Val Gln Arg Arg  
 420 425 430  
 10 Ser Tyr Tyr Gly Gly Asp Tyr Thr Glu Asn Leu Leu Asn Gly Ala  
 435 440 445  
 Val Gln Ser Gly Ser Thr Glu Ser Asp Glu Tyr Asn Asp Ala Phe Thr  
 450 455 460  
 Ala Leu Thr Ser Tyr Gly Thr Thr Lys Gly Phe Asp Leu Gln Gly Gly  
 465 470 475 480  
 15 Gly Met Tyr Arg His Thr Phe Gly Glu Asn Trp Asp Phe Thr Gly Gly  
 485 490 495  
 Leu Glu Tyr Ile Tyr Gly Gln Leu Asp Asp Arg Ser Gly Tyr Arg Pro  
 500 505 510  
 20 Ser Lys Ile Asp Gln Asn Thr Ser Thr Phe Ser Gln Tyr Asp Gln Leu  
 515 520 525  
 Glu Tyr Lys Thr Glu Lys Leu Ser Ala Leu Ile Gly Ala Arg Ile Asp  
 530 535 540  
 Tyr Val Leu Leu Asn Gln Asp Gly Lys Arg Tyr Ile Asp Pro Leu Phe  
 545 550 555 560  
 25 Ile Phe Ser Pro Arg Ala Asn Val Arg Tyr Asn Pro Asn Lys Asn Leu  
 565 570 575  
 Ser Phe Arg Leu Ser Tyr Ser Glu Gly Phe Arg Ala Pro Gln Tyr Phe  
 580 585 590  
 30 Asp Glu Asp Leu His Val Glu Leu Ala Gly Gly Thr Pro Ile Ser Arg  
 595 600 605  
 Val Leu Ser Pro Asn Leu Lys Glu Glu Arg Ser Arg Ser Ile Ser Ala  
 610 615 620  
 Ser Phe Asp Tyr Tyr His Arg Ala Asp Glu Trp Gln Phe Asn Ile Met  
 625 630 635 640  
 35 Gly Glu Ala Phe Ser Thr Phe Ile Ser Asn Gln Phe Lys Pro Ser Asp  
 645 650 655  
 Lys Val Glu Thr Thr Ser Asp Gly Lys Glu Trp Ile Ile Arg Thr Ile  
 660 665 670  
 40 Tyr Asn Asp Lys Asp Gly Val Ser Lys Val Tyr Gly Val Asn Leu Glu  
 675 680 685  
 Gly Arg Ile Ala Tyr Asn Lys Ser Phe Asp Leu Gln Leu Gly Gly Thr  
 690 695 700  
 Trp Gln Arg Ser Arg Tyr Gly Ser Ile Tyr Thr Ala Val Glu Ala Asp  
 705 710 715 720  
 45 Lys Thr Thr Gly Gln Ala Glu Ile Ser Val Lys Asp Tyr Val Arg Thr  
 725 730 735  
 Pro Asn Leu Tyr Gly Tyr Phe Val Ala Thr Val Arg Pro Thr Glu His  
 740 745 750  
 50 Phe Ala Ile Asn Leu Ser Gly Thr Phe Thr Gly Lys Met Asp Val Val  
 755 760 765  
 His Glu Ala Tyr Glu Gly Asp Ile Pro Ala Glu His Ile Ala Pro Asp  
 770 775 780  
 Gly Ser Phe Asp Phe Glu Met Asn Gly Gln Gln Phe Lys Gly Leu Ala  
 785 790 795 800  
 55 Glu Gly His Ala Lys Leu Val Lys Thr Pro Ala Phe Ala Asp Ile Asp  
 805 810 815  
 Leu Lys Leu Ser His Asp Phe His Leu Ala Ser Thr Met Thr Leu Glu  
 820 825 830  
 60 Leu Asn Ala Gly Ile Gln Asn Ile Phe Asn Ser Tyr Gln Lys Asp Thr  
 835 840 845  
 Asp Lys Gly Pro Gly Arg Ala Ser Thr Tyr Val Tyr Gly Pro Met Gln  
 850 855 860  
 Pro Arg Arg Ile Phe Val Gly Thr Lys Ile Asn Phe  
 865 870 875

(2) INFORMATION FOR SEQ ID NO:316

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 899 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES



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## (71) ORIGINAL SOURCE:

(A) ORGANISM: *Porphyromonas gingivalis*

5

## (15) FEATURE:

(A) NAME/KEY: misc\_feature

(B) LOCATION 1...899

## (31) SEQUENCE DESCRIPTION: SEQ ID NO:316

10

```

Ile Leu Asn His Leu Arg Lys Thr Met Tyr Lys Lys Ile Ile Ala Val
1      5      10      15
Ala Ala Leu Phe Cys Ala Ser Ile Gly Ile Leu Lys Gly Gln Ser Ser
20      25      30
15 Asp Leu Thr Pro Gln Asp Thr Ile Tyr Ser Pro Glu Ile Ser Tyr Ala
35      40      45
Lys Pro Ile His Lys Thr Ile Ala Ser Ile Glu Ile Glu Gly Met Arg
50      55      60
Ser Phe Asp Asp Phe Val Leu Arg Asn Leu Ser Gly Leu Ala Val Gly
65      70      75      80
20 Asp Glu Val Leu Ile Pro Gly Asp Ala Met Ser Ala Ala Val Asn Arg
85      90      95
Ile Met Arg Gln Gly Tyr Phe Ser Asn Val Arg Ile Ile Ala Asp Lys
100      105      110
25 Tyr Val Gly Asn Lys Val Tyr Leu Lys Ile Ile Val Thr Glu Arg Pro
115      120      125
Arg Ile Ser Lys Val Thr Phe Ser Gly Val Lys Lys Ser Glu Arg Glu
130      135      140
30 Asp Leu Glu Met Lys Ile Gly Leu Arg Glu Gly Ile Gln Met Thr Arg
145      150      155      160
Asn Asn Glu Asp Lys Val Arg Gln Ile Val Gln Lys Tyr Phe Ser Glu
165      170      175
Lys Gly Tyr Arg Asp Ala Ser Ile Arg Ile Thr Gln Glu Pro Asp Leu
180      185      190
35 Ser Lys Asp Gly Phe Val Asn Val Leu Ile Ser Ile Glu Lys Lys Ser
195      200      205
Lys Thr Lys Val Asn Glu Ile Tyr Phe Ser Gly Asn Lys Ala Leu Ser
210      215      220
40 Asn His Lys Leu Arg Met Ala Met Lys Asn Thr Asn Ala Lys Phe Ser
225      230      235      240
Leu Arg Lys His Ile Arg Ser Ser Phe Leu Lys Leu Phe Ser Thr His
245      250      255
Lys Phe Val Glu Glu Ser Tyr Arg Glu Asp Leu Val Arg Leu Ile Glu
260      265      270
45 Lys Tyr Gln Glu Tyr Gly Tyr Arg Asp Ala Glu Ile Leu Thr Asp Ser
275      280      285
Val Val Lys Ala Pro Asp Gly Lys Arg Val Asp Ile Tyr Leu Asn Ile
290      295      300
50 Glu Glu Gly Gln Lys Tyr Tyr Ile Lys Asp Val Asn Phe Val Gly Asn
305      310      315      320
Ser Gln Tyr Pro Ser Glu Tyr Leu Glu Arg Val Leu Gly Ile Lys Ser
325      330      335
Gly Asp Val Tyr Asn Gln Arg Arg Leu Ala Lys Arg Leu Asn Glu Asp
340      345      350
55 Glu Asp Ala Val Gly Asn Leu Tyr Tyr Asn Asn Gly Tyr Ile Phe Ala
355      360      365
Trp Val Asp Pro Val Glu Thr Asn Val Val Gly Asp Ser Val Ser Leu
370      375      380
60 Asp Ile Arg Ile Ala Glu Gly Lys Gln Ala Asn Ile Asn Lys Val Ile
385      390      395      400
Ile Lys Gly Asn Thr Val Val Tyr Glu Asp Val Val Arg Arg Glu Leu
405      410      415
Tyr Thr Lys Pro Gly Gln Leu Phe Ser Arg Glu Asp Ile Ile Asn Ser
420      425      430
65 Ile Arg Leu Ile Asn Gln Leu Gly His Phe Asp Ala Glu Lys Ser Ile
435      440      445
Pro Arg Pro Ile Pro Asn Pro Glu Thr Gly Thr Val Asp Ile Glu Tyr
450      455      460
70 Asp Leu Val Pro Arg Ser Ser Asp Gln Leu Glu Leu Ser Val Gly Trp
465      470      475      480
Ser Gln Ser Gly Leu Leu Phe Arg Gly Ala Ile Lys Phe Thr Asn Phe
485      490      495
Ser Val Gly Asn Leu Leu His Pro Ser Met Tyr Lys Lys Gly Ile Ile
500      505      510
75 Pro Gln Gly Asp Gly Gln Thr Leu Ser Leu Ser Ala Gln Thr Asn Gly

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515 520 525  
 Lys Tyr Tyr Gln Gln Tyr Ser Val Thr Phe Met Asp Pro Trp Phe Gly  
 530 535 540  
 Gly Lys Arg Pro Asp Met Phe Ser Phe Ser Ala Phe Tyr Ser Lys Thr  
 545 550 555 560  
 Thr Ala Ile Asp Ser Lys Phe Tyr Asn Ser Asn Ala Gly Asn Tyr Tyr  
 565 570 575  
 Asn Ala Tyr Tyr Asn Ser Tyr Tyr Asn Asn Tyr Asn Ser Tyr Tyr Asn  
 580 585 590  
 Gly Met Ser Asn Tyr Thr Gly Asp Leu Tyr Thr Gln Ala Ser Asp Pro  
 595 600 605  
 Asp Arg Ser Leu Gln Met Leu Gly Thr Ser Ile Gly Tyr Gly Lys Arg  
 610 615 620  
 Leu Thr Trp Pro Asp Asn Trp Phe Gln Ile Tyr Thr Ser Leu Asn Tyr  
 625 630 635 640  
 Thr Tyr Tyr Arg Leu Arg Asn Trp Ser Tyr Asn Thr Phe Gln Asn Phe  
 645 650 655  
 His His Gly Ser Ala Asn Asp Leu Asn Leu Glu Leu Arg Leu Ser Arg  
 660 665 670  
 Thr Ser Ile Asp Asn Pro Ile Tyr Thr Arg Ser Gly Ser Asp Phe Met  
 675 680 685  
 Val Ser Val Ala Ala Thr Leu Pro Tyr Ser Leu Trp Asp Asn His Asp  
 690 695 700  
 Tyr Ala Ser Gln Asn Leu Ser Val Ser Asp Arg Tyr Arg Phe Ile Glu  
 705 710 715 720  
 Tyr His Lys Trp Lys Phe Arg Gly Arg Val Phe Thr Pro Leu Leu Asn  
 725 730 735  
 Pro Ala Thr His Lys Tyr Thr Pro Val Leu Met Ser Arg Val Glu Gly  
 740 745 750  
 Ala Val Leu Gly Ser Tyr Asn Ser Asn Lys Lys Ser Pro Phe Gly Thr  
 755 760 765  
 Phe Tyr Met Gly Gly Asp Gly Met Ser Ser Tyr Tyr Gly Gly Tyr Met  
 770 775 780  
 Asn Glu Thr Ile Gly Leu Arg Gly Tyr Lys Asn Gly Ser Ile Ala Gly  
 785 790 795 800  
 Asn Asn Tyr Asp Tyr Ala Tyr Ala Tyr Met Arg Leu Thr Met Glu Leu  
 805 810 815  
 Arg Phe Pro Ile Leu Phe Glu Asn Ser Phe Asn Ala Trp Leu Leu Ala  
 820 825 830  
 Phe Ala Glu Ala Gly Asn Ala Trp Arg Ser Ile Asp Asn Tyr Asn Pro  
 835 840 845  
 Phe Asn Leu Lys Arg Ser Ala Gly Val Gly Leu Arg Val Thr Leu Pro  
 850 855 860  
 Met Val Gly Met Leu Gly Ile Asp Trp Gly Tyr Gly Phe Asp Arg Pro  
 865 870 875 880  
 Asp Asn Ser Leu Gln Arg Gly Gly Ser Asn Val His Phe Val Leu Gly  
 885 890 895  
 Gln Glu Phe

50

(2) INFORMATION FOR SEQ ID NO:317

55 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 177 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

60 (ii) MOLECULE TYPE: protein

60 (iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Porphyromonas gingivalis

65 (ix) FEATURE:  
 (A) NAME/KEY: misc feature  
 (B) LOCATION 1...177

70 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:317

75 Gln Ile Asn Met Asn Gly Asp Met Lys Arg Phe Leu Ile Leu Ile Gly  
 1 5 10 15  
 Phe Ala Leu Ala Val Ala Phe Ser Gly Phe Ser Gln Lys Phe Ala Leu  
 20 25 30  
 Val Asp Met Glu Tyr Ile Leu Arg Asn Ile Pro Asp Tyr Glu Met Met

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      35      40      45
Asn Glu Gln Leu Glu Gln Val Ser Lys Lys Trp Gln Asn Glu Ile Glu
  50      55      60
Ala Leu Glu Asn Glu Ala Gln Ser Met Tyr Lys Lys Tyr Gln Ser Asp
  65      70      75      80
Leu Val Phe Leu Ser Ala Ala Gln Lys Lys Thr Gln Glu Glu Ala Ile
      85
Val Lys Lys Glu Gln Gln Ala Ser Glu Leu Lys Arg Lys Tyr Phe Gly
      90      95
10  Pro Glu Gly Glu Leu Tyr Lys Lys Arg Ser Asp Leu Met Lys Pro Ile
      100      105      110
Gln Asp Glu Ile Trp Asn Ala Ile Lys Glu Ile Ala Lys Arg Asn Asn
      115      120      125
15  Tyr Gln Met Val Leu Asp Arg Gly Thr Ser Gly Ile Ile Phe Ala Ser
      130      135      140
145 Pro Ser Ile Asp Ile Ser Asp Leu Val Leu Ser Lys Met Gly Phe Ser
      145      150      155      160
      165      170      175
Lys

```

20

(2) INFORMATION FOR SEQ ID NO:318

```

      (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 170 amino acids
            (B) TYPE: amino acid
            (D) TOPOLOGY: linear
25

```

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

```

      (vi) ORIGINAL SOURCE:
            (A) ORGANISM: Porphyromonas gingivalis
30

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      (ix) FEATURE:
            (A) NAME/KEY: misc_feature
            (B) LOCATION 1...170
35

```

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:318

```

40  Arg Ile Asn Lys Gln His Glu Met Lys Lys Phe Phe Leu Met Leu Leu
      1      5      10      15
Met Ala Leu Pro Leu Ser Leu Leu Ala Gln Lys Val Ala Val Val Asn
      20      25      30
45  Thr Glu Glu Ile Ile Ser Lys Met Pro Glu Gln Val Ala Ala Thr Lys
      35      40      45
Gln Leu Asn Glu Leu Ala Glu Lys Tyr Arg Leu Asp Leu Lys Ser Met
      50      55      60
50  Asp Asp Glu Phe Ala Lys Lys Thr Glu Glu Phe Val Lys Glu Lys Asp
      65      70      75      80
Ser Leu Leu Glu Asn Ile Arg Asn Arg Arg Gln Gln Glu Leu Gln Asp
      85      90      95
Ile Gln Thr Arg Tyr Gln Gln Ser Tyr Gln Thr Met Gln Glu Asp Leu
      100      105      110
55  Gln Lys Arg Gln Gln Gln Leu Phe Ala Pro Ile Gln Gln Lys Val Ala
      115      120      125
Asp Ala Ile Lys Lys Val Gly Asp Glu Glu Asn Cys Ala Tyr Ile Met
      130      135      140
60  Glu Ala Gly Met Met Leu Tyr Thr Gly Ala Thr Ala Ile Asp Leu Thr
      145      150      155      160
Ala Lys Val Lys Ala Lys Leu Gly Ile Lys
      165      170

```

(2) INFORMATION FOR SEQ ID NO:319

```

      (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 828 amino acids
            (B) TYPE: amino acid
            (D) TOPOLOGY: linear
70

```

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

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(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

(A) NAME/KEY: misc\_feature

(B) LOCATION: 1...828

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:319

10 Ile Met Lys Glu Ala Ile Pro Arg Lys Asn Lys Tyr Ile Lys Leu Asn  
1 5 15  
Gly Ile Tyr Arg Leu Ser Phe Ile Leu Leu Cys Cys Leu Leu Cys Ser  
20 25 30  
Gln Ala Ala Met Ala Gln Gly Val Arg Val Ser Gly Tyr Val Leu Asp  
35 40 45  
15 Arg Gly Glu Lys Pro Ile Pro Phe Ala Gly Val Lys Val Arg Gly Thr  
50 55 60  
Gly Thr Gly Ala Thr Thr Asn Leu Lys Gly Tyr Tyr Glu Phe Arg Met  
65 70 75 80  
20 Lys Ala Thr Thr Asp Ser Ile Thr Ile Glu Phe Ser Ser Met Gly Tyr  
85 90 95  
Gln Gly Val Ser Arg Ser Phe Pro Ser Leu Thr Lys Asp Thr Arg Leu  
100 105 110  
Asn Val Arg Leu Ala Glu Ala Glu Met Glu Leu Ser Ser Val Thr Val  
115 120 125  
25 Gln Ala Thr Lys Arg Arg Leu Asn Thr Met Glu Arg Val Asn Thr Arg  
130 135 140  
Asp Leu Arg Val Asn Ala Gly Pro Thr Gly Gly Val Glu Ser Leu Ile  
145 150 155 160  
30 Ser Thr Tyr Ala Gly Val Thr Gln Asn Asn Glu Leu Ser Ser Gln Tyr  
165 170 175  
Ser Val Arg Gly Gly Ser Tyr Asp Glu Asn Met Val Tyr Val Asn Gly  
180 185 190  
Val Glu Val Tyr Arg Pro Leu Leu Val Arg Ser Ala Gln Gln Glu Gly  
195 200 205  
35 Leu Ser Phe Val Asn Pro Asp Leu Thr Gln Ser Val Gln Phe Ser Ala  
210 215 220  
Gly Gly Phe Thr Ala Asp Tyr Gly Asp Lys Met Ser Ser Val Leu Asp  
225 230 235 240  
40 Ile Arg Tyr Lys Gln Pro Gln Glu Lys Glu Gly Ala Val Leu Leu Gly  
245 250 255  
Met Leu Gln Ser Ser Ala Tyr Tyr Gly Ser Ser Ala Gly Ala Phe Ser  
260 265 270  
Gln Ile Thr Gly Val Arg Tyr Lys Ser Ala Lys Ser Leu Leu Gly Thr  
275 280 285  
45 Thr Asp Thr Lys Ala Glu Tyr Asp Pro Ile Tyr Ala Asp Gly Gln Thr  
290 295 300  
Phe Met Thr Tyr Arg Phe Ser Pro Lys Leu Ser Val Ser Phe Leu Gly  
305 310 315 320  
50 Asn Ile Ser Gln Thr Arg Tyr Lys Phe Val Pro Gln Thr Arg Glu Thr  
325 330 335  
Ser Phe Gly Thr Leu Ser Asp Ala Lys Lys Leu Lys Ile Phe Phe Asp  
340 345 350  
Gly Gln Glu Gln Asp Arg Phe Leu Thr Tyr Phe Gly Ala Phe Ser Met  
355 360 365  
55 Asn Phe Val Pro Asp Asp Lys Gln Arg His Thr Val Thr Leu Ser Ala  
370 375 380  
Phe Asn Ser Asn Glu Arg Glu Thr Tyr Asp Ile Gln Gly Glu Tyr Phe  
385 390 395 400  
60 Leu Asn Asp Val Gln Leu Gly Ala Asp Gly Thr Ala Ser Met Ala Ser  
405 410 415  
Gly Ser Glu Asn Ser Asn Gly Leu Gly Ile Gly Arg Asn His Glu His  
420 425 430  
Ala Arg Asn Arg Leu Ser Tyr Arg Val Leu Asn Met Gly Tyr Arg Gly  
435 440 445  
65 Glu Met Lys Leu Asn Glu Lys His Arg Leu Gln Ala Gly Val Ser Ala  
450 455 460  
Gln Met Glu Lys Ile Ala Asp His Ile Ser Glu Trp Glu Arg Arg Asp  
465 470 475 480  
70 Ser Val Gly Tyr Asn Leu Pro His Ser Glu Thr Val Leu Leu Met Tyr  
485 490 495  
Asn Asn Leu Tyr Ala Asp Thr Gln Met Arg Gly Thr Arg Leu Ser Ala  
500 505 510  
Phe Val Gln Asp Arg Phe Asn Phe Ser Met Gly Gly Thr Phe Ser  
515 520 525  
75 Leu Ile Pro Gly Ile Arg Ala Ser Trp Trp Ser Phe Asn Lys Glu Leu

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530 535 540  
 Leu Val Ser Pro Arg Ile Ser Val Gly Tyr Ser Pro Glu Ser Asn Pro  
 545 550 555 560  
 Ala Leu Val Leu Arg Ala Ala Ala Gly Leu Tyr Tyr Gln Ala Pro Phe  
 565 570 575  
 Tyr Lys Glu Leu Arg Gln Thr His Lys Asp Ala Glu Gly Asn Asn Val  
 580 585 590  
 Val Val Leu Asn Glu Lys Ile Arg Ser Gln Gly Ala Phe His Ile Leu  
 595 600 605  
 10 Ala Gly Ala Asp Tyr Thr Phe Glu Met Gly Gly Arg Lys Tyr Lys Phe  
 610 615 620  
 Thr Ala Glu Ala Tyr Tyr Lys Ser Leu Phe Asn Ile Asn Pro Tyr Ile  
 625 630 635 640  
 15 Ile Glu Asn Val Lys Ile Arg Tyr Leu Gly Glu Asn Ile Gly Ser Gly  
 645 650 655  
 Tyr Ala Ala Gly Ile Asp Leu Lys Leu Phe Gly Glu Leu Val Pro Gly  
 660 665 670  
 Val Asp Ser Trp Leu Thr Ala Ser Ile Ile Lys Ala Arg Gln Lys Leu  
 675 680 685  
 20 Asp Gly Tyr Gly Ser Leu Pro Leu Met Asn Ala Pro Thr Tyr Asn Phe  
 690 695 700  
 Ser Phe Phe Leu Gln Glu Tyr Val Pro Gly Asn Lys Arg Ile Thr Ala  
 705 710 715 720  
 25 Thr Leu Arg Ala Ala Leu Ser Gly Gly Leu Pro Gln Leu Asn Pro Ser  
 725 730 735  
 Lys Gly Leu Ser Ser Pro Ala Phe Thr Ala Pro Ala Tyr Lys Arg Val  
 740 745 750  
 Asp Leu Gly Val Met Tyr Lys Trp Leu Asp Pro Asp Asp Ser Phe Ala  
 755 760 765  
 30 Gly Arg Ser Lys Trp Leu Met Gly Val Lys Gly Ala Tyr Ile Gly Ala  
 770 775 780  
 Asp Leu Phe Asn Leu Phe Asp Met Thr Asn Val Asn Ser Tyr Tyr Trp  
 785 790 795 800  
 35 Val Ser Asp Ala Tyr Gln Gln Gln Tyr Ala Val Pro Asn Tyr Leu Thr  
 805 810 815  
 Arg Arg Gln Phe Asn Leu Arg Leu Leu Val Glu Phe  
 820 825

40 (2) INFORMATION FOR SEQ ID NO:320

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 679 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

45 (ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

50 (vi) ORIGINAL SOURCE:

(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

(A) NAME/KEY: misc feature

55 (B) LOCATION 1...679

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:320

60 Pro Ile Pro Phe Leu Leu Asn Met Tyr Ser Gly His His Lys Ile His  
 1 5 10 15  
 Tyr Pro Phe Leu Ile Leu Leu Val Cys Leu Ala Phe Ala Ala Cys Lys  
 20 25 30  
 Ser Val Lys Leu Lys Asp Ala Glu Lys Ala His Asp Arg Gln Glu Tyr  
 35 40 45  
 65 Thr Lys Ala Ala Asp Met Tyr Asn Thr Leu Tyr Arg Arg Thr Arg Arg  
 50 55 60  
 Lys Gln Val Glu Met Lys Ala Tyr Thr Ala Phe Arg Ser Gly Glu Asn  
 65 70 75 80  
 70 Tyr Arg Ala Ala Gly Arg Gln Ala Lys Ala Leu Arg Gly Tyr Leu Asn  
 85 90 95  
 Ala Arg Arg Tyr Gly Tyr Pro Asp Ser Val Val Leu Leu Arg Leu Ala  
 100 105 110  
 Gln Thr Tyr Gln Gln Gly Gly Asn Tyr Lys Glu Ala Glu Val Leu Phe  
 115 120 125  
 75 Arg Gly Tyr Leu Glu Ala Tyr Pro Lys Ser Tyr Phe Ala Ala Ile Gly

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	130		135		140
	Leu Glu Gly Cys Leu Phe Ala Arg Gln Gln Lys Glu Tyr Pro Thr Arg				
	145		150		155
5	Tyr Arg Ile Arg Arg Ala Ala Glu Trp Asn Ser Ala Arg Gly Asp Phe				160
		165		170	
	Gly Pro Ala Tyr Ala Pro Asp Ala Ser Ala Leu Tyr Phe Thr Ser Ser				175
		180		185	
	Arg Ser Lys Asp Asp Gly Leu Asp Asn Ser Ser Ile Thr Gly Leu Lys				190
		195		200	
10	Pro Asn Asp Ile Tyr Ile Ile Lys Arg Asp Ala Gln Gly Arg Trp Gly				205
		210		215	
	Arg Pro Asp Ser Val Ser Gly Gly Ile Asn Thr Thr Trp Asp Glu Gly				220
		225		230	
	Val Pro Thr Ile Thr Pro Asp Gly Ser Thr Ile Tyr Tyr Thr Leu Ala				235
15			245		250
	Gln Gln Gly Ala Asp Tyr Asp Arg Thr Val Gln Ile Tyr Ser Ala Ala				255
		260		265	
	Arg Ser Gly Glu Gly Gly Trp Ser Asn Gly Ser Leu Val Asp Ile Met				270
20		275		280	
	Arg Asp Ser Leu Arg Met Ala Ala His Pro Ser Met Ser Ala Ser Gly				285
		290		295	
	Asp Tyr Leu Tyr Phe Val Ser Asn Ile Gly Gly Ser Tyr Gly Gly Lys				300
		305		310	
25	Asp Ile Tyr Arg Val Lys Val Ser Asp Arg Ser Tyr Gly Ser Pro Glu				315
		325		330	
	Asn Leu Gly Pro Asp Ile Asn Thr Pro Gly Asp Glu Met Phe Pro Phe				335
		340		345	
	Ile Asp Gly Asp Ser Thr Leu Phe Phe Ala Ser Asp Gly His Ala Gly				350
30		355		360	
	Leu Gly Gly Leu Asp Ile Phe Lys Ala Thr Leu Asp Ser Thr Gly Gln				365
		370		375	
	Trp His Val Val Asn Met Gly Gln Pro Val Asn Ser Ser Ala Asp Asp				380
		385		390	
35	Phe Gly Leu Ala Val Glu Pro Lys Gly Lys Asn Lys Glu Glu Ala Leu				395
		405		410	
	Pro Asp Asn Gly Val Lys Gly Val Phe Cys Ser Asn Arg Gly Asp Ala				415
		420		425	
	Arg Gly Trp Pro His Leu Phe His Phe Glu Leu Pro Ala Ile Tyr Thr				430
40		435		440	
	Glu Ile Gln Gly Tyr Val Met Asp Arg Glu Glu Asn Pro Ile Ala Gly				445
		450		455	
	Ala Thr Val Arg Ile Val Gly Glu Arg Gly Pro Val Gly Gln Gly Phe				460
		465		470	
45	Val Thr Thr Arg Asp Asp Gly Ser Tyr Lys Met Ser Val Gln Gly Asp				475
		485		490	
	Thr Arg Tyr Val Met Leu Ala Gly Ala Ser Gly Tyr Leu Asn Gln Tyr				495
		500		505	
	Val Glu Leu Lys Thr Asp Thr Ala Lys Gln Ser Glu Thr Tyr Tyr Val				510
50		515		520	
	Asp Phe Phe Leu Ala Ser Arg Glu Lys Ala Glu Gly Leu Gln Asn Ile				525
		530		535	
	Phe Tyr Asp Phe Asp Lys Ala Thr Leu Arg Pro Glu Ser Met Lys Ser				540
		545		550	
55	Leu Asp Glu Leu Ile Arg Ile Leu Thr Asp Asn Pro Asp Ile Arg Ile				555
		565		570	
	Glu Leu Gly Ser His Ala Asp Arg Lys Gly Pro Asp Ala Tyr Asn Leu				575
		580		585	
	Gly Leu Ser Asp Arg Arg Ala Lys Ser Val Val Asp Tyr Leu Thr Ser				590
60		595		600	
	Arg Gly Ile Ala Ala Asp Arg Leu Thr Trp Lys Gly Tyr Gly Lys Ser				605
		610		615	
	Val Pro Lys Thr Val Thr Ala Lys Ile Ala Glu Arg His Asp Phe Leu				620
		625		630	
65	Lys Glu Gly Asp Val Leu Thr Glu Glu Phe Val Ala Pro Leu Thr Glu				635
		645		650	
	Glu Gln Gln Ser Val Cys Asp Gln Leu Asn Arg Arg Thr Glu Phe Arg				655
		660		665	
	Val Ile Glu Glu Glu Leu Arg				670
70		675			

(2) INFORMATION FOR SEQ ID NO:321

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 772 amino acids

(B) TYPE: amino acid

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(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

5 (iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Porphyromonas gingivalis*

10 (ix) FEATURE:

(A) NAME/KEY: misc\_feature

(B) LOCATION 1...772

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:321

15

Pro	Ala	Gln	Pro	Lys	Thr	Tyr	Cys	Ile	Arg	Tyr	Phe	Arg	Arg	Glu	Val
1				5					10					15	
Ser	Pro	Arg	Arg	Gln	Thr	Glu	Arg	Thr	Leu	Tyr	Ala	Asp	Lys	Met	Arg
			20					25					30		
20	Arg	His	Ile	Val	Lys	Cys	Cys	Pro	Ser	Ala	Ser	Ile	Leu	Leu	Gln
			35					40					45		
Tyr	Ser	Thr	Thr	Glu	Leu	Phe	Ile	His	His	Phe	Asn	Ile	Ser	Ile	Ile
			50			55					60				
25	Met	Lys	Lys	Phe	Phe	Phe	Ala	Leu	Leu	Ser	Ile	Gly	Ile	Ser	Ala
	65					70				75					80
Ala	Phe	Ala	Lys	Thr	Asp	Asn	Val	Pro	Thr	Asp	Ser	Leu	Arg	Val	His
				85					90					95	
Asn	Leu	Gln	Thr	Val	Thr	Val	Tyr	Ser	Thr	Arg	Thr	Ala	Val	Pro	Leu
			100					105					110		
30	Lys	Lys	Ile	Pro	Ala	Lys	Met	Glu	Leu	Ile	Ser	Ser	Arg	Asn	Ile
			115					120					125		
Gln	Ser	Gly	Phe	Asn	Asn	Met	Thr	Asp	Ile	Leu	Lys	Thr	Gln	Ser	Ser
			130			135					140				
35	Leu	Asp	Val	Ile	Gln	Tyr	Pro	Gly	Phe	Ser	Ser	Asn	Ile	Gly	Ile
	145					150				155					160
Gly	Phe	Lys	Pro	Ser	Gly	Lys	Tyr	Val	Thr	Val	Leu	Val	Asn	Gly	Ile
					165				170					175	
Pro	Ala	Gly	Thr	Asp	Asn	Ile	Ser	Thr	Leu	Asn	Thr	Ser	Asn	Ile	Glu
			180					185					190		
40	Gln	Ile	Glu	Ile	Leu	Lys	Gly	Pro	Phe	Ser	Ser	Ile	Tyr	Gly	Thr
			195					200					205		
Ala	Met	Gly	Gly	Val	Val	Asn	Ile	Ile	Thr	His	Lys	Ser	Lys	Asp	Lys
			210			215					220				
45	Ile	His	Gly	Asn	Val	Ser	Leu	Phe	Gly	Gly	Ser	Tyr	Gln	Thr	Met
	225					230					235				240
Gly	Ser	Phe	Asn	Leu	Gly	Gly	Arg	Phe	Glu	Asp	Ile	Phe	Ser	Phe	Asp
				245					250					255	
Leu	Ser	Leu	Gly	Leu	Asp	Lys	Gln	Asn	Lys	Asp	Tyr	Lys	Thr	Gly	Ser
			260					265					270		
50	Asn	Asn	Phe	Leu	Ser	Leu	Ser	Lys	Leu	Glu	Glu	Ala	Ile	Val	Asp
			275					280					285		
Asn	Ala	Thr	Lys	Asn	Lys	Lys	Met	Lys	Gly	Ser	Asp	Tyr	Thr	Val	Ala
			290			295					300				
55	Thr	Gly	Arg	Leu	Arg	Phe	Gly	Ile	Asp	Phe	Thr	Pro	Glu	Trp	Ser
			305			310					315				320
Asn	Leu	Tyr	Gln	Asn	Val	Phe	Leu	Gly	Asp	Ala	Ile	Pro	Val	Gly	Gly
				325					330					335	
Ser	Ile	Trp	Gly	Val	Tyr	Gly	Glu	Ser	Lys	Lys	Asn	Leu	Asn	Arg	Ser
			340					345					350		
60	Ser	Thr	Ser	Phe	Glu	Leu	Leu	Gly	Lys	His	Gly	Cys	His	Thr	Leu
			355					360					365		
Phe	Ser	Pro	Tyr	Phe	Asn	Ile	Glu	Lys	Ser	Glu	Asn	Tyr	Asn	Asn	Ala
			370			375					380				
65	Asp	Pro	Thr	Gly	Phe	Ile	Asn	Tyr	Lys	Ser	Asp	Tyr	Tyr	Thr	Tyr
			385			390					395				400
Ala	Leu	Leu	Gln	Asp	Lys	Ile	Ser	Phe	Gly	Gly	Gln	Asn	Ile	Val	Leu
				405					410					415	
Gly	Val	Asp	Ser	Arg	Asn	Met	Thr	Met	Glu	Ser	Glu	Arg	Phe	Glu	Gln
			420					425					430		
70	Ala	Gly	Val	Asn	Thr	Lys	Pro	Tyr	Asn	Pro	Gly	Tyr	Ala	Thr	Asn
			435					440					445		
Ile	Gly	Leu	Phe	Gly	Gln	Ala	Asn	Phe	Tyr	Leu	Leu	Asn	Asp	Ala	Leu
			450			455					460				
75	Ser	Ile	Ser	Ala	Gly	Ala	Arg	Ala	Asp	Phe	Met	Phe	Phe	Asp	Leu
					470					475					480

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Ala Asn Glu Tyr Leu Asn Asn Glu Ala Lys Gln Glu Thr His Asn Val  
 485 490 495  
 Ile Asn Pro Asn Val Gly Ile Lys Tyr Glu Phe Val Lys Gly Leu Thr  
 500 505 510  
 5 Ala His Gly Thr Phe Gly Ser Ala Phe Ser Ala Pro Asp Ala Phe Gln  
 515 520 525  
 Lys Ala Gly Gln Tyr Val Gly Pro Phe Gly Thr Thr Ile Gly Asn Pro  
 530 535 540  
 10 Asp Leu Lys Pro Glu Lys Ser Met Thr Trp Asp Phe Gly Ile Gly Tyr  
 545 550 555 560  
 Ser Asn Ala Arg Cys Gly Ile Gln Ala Asp Val Thr Leu Thr Tyr Phe  
 565 570 575  
 His Thr Asp His Lys Asp Leu Ile Leu Ser Ser Pro Asp Tyr Ala Asn  
 580 585 590  
 15 Asn Ile Thr Thr Tyr Ile Asn Ala Asp Lys Ala Arg Met Ser Gly Ile  
 595 600 605  
 Glu Ala Leu Leu Ser Tyr Asp Phe Gly Ser Leu Phe Ala Asn Lys Phe  
 610 615 620  
 20 Ser Leu Arg Ala Phe Ala Asn Ala Thr Ile Met Leu Asn Ser Glu Met  
 625 630 635 640  
 Lys Lys Ser Gln Thr Asp Ala Pro Trp Ser Glu Met Tyr Tyr Val Arg  
 645 650 655  
 Lys Gln Asn Ile Thr Phe Gly Ile Glu Tyr Arg Gly Lys Glu Gly Leu  
 660 665 670  
 25 Glu Val Met Leu Asn Gly Arg Phe Met Gly Arg Arg Ile Glu Gln Asn  
 675 680 685  
 Trp Tyr Ala Tyr Tyr Pro Glu Val Arg Pro Glu Leu Gln Gln Leu Leu  
 690 695 700  
 30 Ala Ala Glu Glu Pro Glu Leu Ala Ala Gln Gly Leu Leu Arg His Pro  
 705 710 715 720  
 Gln Ala Met Val Phe Asn Ala Ser Ala Tyr Tyr His Met Asn Lys Tyr  
 725 730 735  
 Leu Thr Phe Gly Val Asn Leu Asn Asn Ile Leu Asp Glu Leu Tyr Thr  
 740 745 750  
 35 Glu Lys Asp Gly Tyr His Met Pro Gly Arg Asn Ile Met Gly Lys Val  
 755 760 765  
 Met Val Asn Phe  
 770

40 (2) INFORMATION FOR SEQ ID NO:322

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 484 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
 45  
 (ii) MOLECULE TYPE: protein  
 (iii) HYPOTHETICAL: YES  
 50  
 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Porphyromonas gingivalis  
 55  
 (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...484  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:322

60 Gly Arg Ala Ser Ser Pro Tyr Arg Gln Met Asp Gly Ile Leu Asn Asp  
 1 5 10 15  
 Glu Tyr Arg Gln Ala Ser Met Asn Arg Phe Ser Asn His Trp Pro Cys  
 20 25 30  
 65 Ile Leu Val Gly Phe Val Leu Trp Phe Val Ser Ala Ser Arg Thr Val  
 35 40 45  
 Ala Gln Asn Ala Ser Glu Thr Thr Val Ser Tyr Asp Thr Asp Thr Ala  
 50 55 60  
 Val Leu Ser Glu Ala Asp Val Leu Arg Ile Ala Ser Glu Asn Ala  
 65 70 75 80  
 70 Thr Val Lys Val Ala Asp Met Asp Val Arg Lys Gln Glu Tyr Ala Arg  
 85 90 95  
 Arg Ala Ala Arg Ala Asp Leu Phe Pro Lys Val Asp Leu Asn Gly Val  
 100 105 110  
 75 Tyr Ser His Thr Leu Lys Lys Gln Val Leu Tyr Ile Asp Met Pro Gly  
 115 120 125



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Phe Ser Ser Ser Glu Gly Ile Glu Met Gly Arg Thr His Asn Thr Gln  
 130 135 140  
 Gly Gly Val Asn Val Ser Met Pro Leu Val Ser Ala Gln Leu Trp Lys  
 145 150 155 160  
 5 Ser Ile Ala Met Thr Gly Glu Gln Leu Asp Leu Ala Leu Glu Lys Ala  
 165 170 175  
 Arg Ser Ser Arg Ile Asp Leu Val Ala Glu Val Lys Lys Ala Tyr Leu  
 180 185 190  
 10 Ser Val Leu Leu Ala Glu Asp Ser Tyr Gly Val Phe Lys Arg Ser Tyr  
 195 200 205  
 Asp Asn Ala Leu Ala Asn Tyr Lys Asn Ile Ser Asp Lys Phe Asp Arg  
 210 215 220  
 Gly Leu Val Ala Glu Tyr Asp Lys Ile Arg Ala Asn Val Gln Val Arg  
 225 230 235 240  
 15 Asn Ile Glu Pro Asn Leu Leu Gln Ala Gln Asn Ser Val Ala Leu Ala  
 245 250 255  
 Leu Trp Gln Leu Lys Val Leu Met Ser Met Glu Val Glu Thr Pro Ile  
 260 265 270  
 20 Arg Leu Ser Gly Ser Leu Ser Asp Tyr Lys Glu Gln Val Tyr Thr Gly  
 275 280 285  
 Tyr Phe Ala Ala Asp Thr Leu Ile Ser Asn Asn Ser Ser Leu Arg Gln  
 290 295 300  
 Leu Asp Ile Gln Arg Arg Leu Ala Val Ser Ala Asp Lys Leu Asn Lys  
 305 310 315 320  
 25 Tyr Ser Phe Leu Pro Thr Leu Asn Leu Gly Gly Gln Tyr Thr Tyr Ser  
 325 330 335  
 Leu Asn Ser Asn Asp Ile Lys Phe Trp Gly Glu Gly Gln Arg Trp Thr  
 340 345 350  
 30 Pro Phe Ser Thr Ile Ser Leu Ser Leu Tyr Ile Pro Ile Phe Asn Gly  
 355 360 365  
 Gly Lys Arg Leu Tyr Asn Val Lys Gln Ser Ala Leu Ser Ile Arg Gln  
 370 375 380  
 Ile Asp Leu Gln Arg Arg His Ile Glu Gln Ser Ile Arg Met Gly Ile  
 385 390 395 400  
 35 Lys Asn Gln Asn Asp Arg Leu Arg Thr Cys Met Gln Arg Phe Val Ala  
 405 410 415  
 Ser Glu Glu Ala Val Arg Ser Ala Glu Lys Gly Tyr Gln Ile Ala Glu  
 420 425 430  
 40 Lys Arg Tyr Gln Thr Gly Glu Gly Thr Leu Val Glu Leu Asn Asp Ala  
 435 440 445  
 Asp Val Ala Leu Leu Gln Ala Arg Leu Asn Tyr Asn Gln Ala Ile Phe  
 450 455 460  
 Asp Phe Met Thr Ala Lys Ala Glu Leu Asp Lys Met Asn Gly Met Gly  
 465 470 475 480  
 45 Ile Pro Glu Gln

## (C) INFORMATION FOR SEQ ID NO:323

- 50 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 540 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
 55 (ii) MOLECULE TYPE: protein  
 (iii) HYPOTHETICAL: YES  
 (vi) ORIGINAL SOURCE:  
 60 (A) ORGANISM: Porphyromonas gingivalis  
 (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...540  
 65 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:323

Phe His Asn Phe Asp Phe Leu Asn Gly Ile Lys Leu Phe Ser Met Ala  
 1 5 10 15  
 70 Asn Asn Thr Leu Leu Ala Lys Thr Arg Arg Tyr Val Cys Leu Val Gly  
 20 25 30  
 Phe Cys Trp Leu Met Ala Met Met His Leu Ser Gly Gln Glu Val Thr  
 35 40 45  
 75 Met Trp Gly Asp Ser His Gly Val Ala Pro Asn Gln Val Arg Arg Thr  
 50 55 60

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5 Leu Val Lys Val Ala Leu Ser Glu Ser Leu Pro Pro Gly Ala Lys Gln  
 65 70 75 80  
 Ile Arg Ile Gly Phe Ser Leu Pro Lys Glu Thr Glu Glu Lys Val Thr  
 85 90 95  
 10 Ala Leu Tyr Leu Leu Val Ser Asp Ser Leu Ala Val Arg Asp Leu Pro  
 100 105 110  
 Asp Tyr Lys Gly Arg Val Ser Tyr Asp Ser Phe Pro Ile Ser Lys Glu  
 115 120 125  
 15 Asp Arg Thr Thr Ala Leu Ser Ala Asp Ser Val Ala Gly Arg Arg Phe  
 130 135 140  
 Phe Tyr Leu Ala Ala Asp Ile Gly Pro Val Ala Ser Phe Ser Arg Ser  
 145 150 155 160  
 Asp Thr Leu Thr Ala Arg Val Glu Glu Val Ala Val Asp Gly Arg Pro  
 165 170 175  
 20 Leu Pro Leu Lys Glu Leu Ser Pro Ala Ser Arg Arg Leu Tyr Arg Gly  
 180 185 190  
 Tyr Glu Ala Leu Phe Val Pro Gly Asp Gly Gly Ser Arg Asn Tyr Arg  
 195 200 205  
 25 Ile Pro Ala Ile Leu Lys Thr Ala Asn Gly Thr Leu Ile Ala Met Ala  
 210 215 220  
 Asp Arg Arg Lys Tyr Asn Gln Thr Asp Leu Pro Glu Asp Ile Asp Ile  
 225 230 235 240  
 Val Met Arg Arg Ser Thr Asp Gly Gly Lys Ser Trp Ser Asp Pro Arg  
 245 250 255  
 30 Ile Ile Val Gln Gly Glu Gly Arg Asn His Gly Phe Gly Asp Val Ala  
 260 265 270  
 Leu Val Gln Thr Gln Ala Gly Lys Leu Leu Met Ile Phe Val Gly Gly  
 275 280 285  
 Val Gly Leu Trp Gln Ser Thr Pro Asp Arg Pro Gln Arg Thr Tyr Ile  
 290 295 300  
 35 Ser Glu Ser Arg Asp Glu Gly Leu Thr Trp Ser Pro Pro Arg Asp Ile  
 305 310 315 320  
 Thr His Phe Ile Phe Gly Lys Asp Cys Ala Asp Pro Gly Arg Ser Arg  
 325 330 335  
 40 Trp Leu Ala Ser Phe Cys Ala Ser Gly Gln Gly Leu Val Leu Pro Ser  
 340 345 350  
 Gly Arg Ile Thr Phe Val Ala Ala Ile Arg Glu Ser Gly Gln Glu Tyr  
 355 360 365  
 45 Val Leu Asn Asn Tyr Val Leu Tyr Ser Asp Asp Glu Gly Asp Thr Trp  
 370 375 380  
 Gln Leu Ser Asp Cys Ala Tyr Arg Arg Gly Asp Glu Ala Lys Leu Ser  
 385 390 395 400  
 Leu Met Pro Asp Gly Arg Val Leu Met Ser Ile Arg Asn Gln Gly Arg  
 405 410 415  
 50 Gln Glu Ser Arg Gln Arg Phe Phe Ala Leu Ser Ser Asp Asp Gly Leu  
 420 425 430  
 Thr Trp Glu Arg Ala Lys Gln Phe Glu Gly Ile His Asp Pro Gly Cys  
 435 440 445  
 55 Asn Gly Ala Met Leu Gln Val Lys Arg Asn Gly Arg Asp Gln Val Leu  
 450 455 460  
 His Ser Leu Pro Leu Gly Pro Asp Gly Arg Arg Asp Gly Ala Val Tyr  
 465 470 475 480  
 Leu Phe Asp His Val Ser Gly Arg Trp Ser Ala Pro Val Val Val Asn  
 485 490 495  
 60 Ser Gly Ser Ser Ala Tyr Ser Asp Met Thr Leu Leu Ala Asp Gly Thr  
 500 505 510  
 Ile Gly Tyr Phe Val Glu Glu Gly Asp Glu Ile Ser Leu Val Phe Ile  
 515 520 525  
 Arg Phe Val Leu Asp Asp Leu Phe Asp Val Arg Gln  
 530 535 540

(2) INFORMATION FOR SEQ ID NO:324

- 65 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 293 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
  
 70 (ii) MOLECULE TYPE: protein  
 (iii) HYPOTHETICAL: YES  
 (vi) ORIGINAL SOURCE:  
 75 (A) ORGANISM: Porphyromonas gingivalis

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## (ix) FEATURE:

(A) NAME/KEY: misc\_feature  
(B) LOCATION 1...293

5

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:324

Lys Ser Pro Ser Asp Ser Ala Leu Pro Ser Val Trp Ser Ala Asn Thr  
 1 5 10 15  
 Ile Ser Gly Leu Val Gly Gly Lys Arg Ile Thr Leu Leu Ile Leu Tyr  
 10 20 25 30  
 Ser Met Ala Ile Arg Ser Ser Asn Ile Glu Ser Ile Gln Cys Phe Val  
 35 40 45  
 Met Lys Lys Glu Lys Leu Trp Ile Ala Ile Val Ala Gly Leu Ala Phe  
 50 55 60  
 Val Leu Gly Leu Tyr Ala Leu Gly Arg Ser Val Ala Gln Leu Arg Arg  
 15 65 70 75 80  
 Ser Gln Pro Ser Val Thr Val Thr Gly Met Ala Glu Arg Asn Phe Lys  
 85 90 95  
 Ser Asp Leu Ile Val Trp Thr Ala Ser Tyr Gln Leu Gln Met Met Asp  
 100 105 110  
 Leu Glu Ser Ala Tyr Lys Ala Leu Lys Glu Lys Gln Ile Leu Val Ala  
 115 120 125  
 Asp Tyr Leu Lys Asn Lys Gln Leu Pro Asp Ser Ser Tyr Ile Phe Ser  
 130 135 140  
 Ser Val Ala Ile Ser Lys Glu Tyr Asn Tyr Tyr Tyr Asp Pro Arg Gln  
 145 150 155 160  
 Glu Gln Asn Val Arg Thr Phe Ala Gly Tyr Leu Leu Ser Gln Thr Val  
 165 170 175  
 Thr Val Thr Ser Gln Asp Ile Glu His Val Glu Lys Ile Ser Arg Asp  
 180 185 190  
 Ile Thr Glu Leu Ile Asn Gln Gly Val Glu Ile Thr Ser Asp Arg Pro  
 195 200 205  
 Ala Tyr Tyr Tyr Thr Lys Leu Asn Asp Leu Lys Val Glu Met Leu Arg  
 210 215 220  
 Asn Ala Ser Glu Asp Ala Phe Asn Arg Ala Ser Val Ile Ala Glu Gly  
 225 230 235 240  
 Ser Gly Ser Ser Val Gly Lys Met Leu Ser Ser Ser Met Gly Val Phe  
 245 250 255  
 Gln Ile Val Gly Leu Asn Ser Asn Glu Asp Tyr Ser Trp Gly Gly Ser  
 260 265 270  
 Phe Asn Thr Ser Ser Lys Met Lys Thr Ala Ser Ile Thr Val Lys Ala  
 275 280 285  
 Ser Phe Ala Leu Lys  
 290

45

## (2) INFORMATION FOR SEQ ID NO:325

## (i) SEQUENCE CHARACTERISTICS:

50

(A) LENGTH: 280 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

55

## (iii) HYPOTHETICAL: YES

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: Porphyromonas gingivalis

60

## (ix) FEATURE:

(A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...280

65

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:325

Gly Lys Leu Gln Met Lys Lys Thr Ile Ala Ile Ile Ala Ser Ala Leu  
 1 5 10 15  
 Leu Ala Leu Gly Ala Val Gly Cys Lys Lys Asn Ala Asp Thr Thr Ala  
 20 25 30  
 Val Ser Glu Lys Asp Ser Ile Ala Leu Ser Met Gly Ile Leu Tyr Gly  
 35 40 45  
 Gln Asp Phe Ala Asn Gln Phe Glu Met Ser Arg Leu Gln Gly Gln Pro  
 50 55 60  
 Ile Asp Ser Val Ala Phe Leu Asp Gly Phe Lys Tyr Gly Ile Asp Thr  
 65 70 75 80

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Thr Arg Phe Ser Tyr Asn Leu Gly Ala Ile Tyr Ala Ser Asn Ile Ala  
 85 90 95  
 Arg Gln Leu Ala His Asp Ser Ile Asp Ile Asp Lys Phe Tyr Ala Ala  
 100 105 110  
 5 Met Arg Ala Ala Leu Leu Lys Asp Thr Val Ser Ile Ala Met Lys Pro  
 115 120 125  
 Ala Asp Ala Gln Ala Phe Met Gln Arg Ile Gln Ala Lys Lys Gln Arg  
 130 135 140  
 10 Glu Asn Asn Met Lys Gln Phe Gly Gln Asn Ile Glu Lys Gly Asn Glu  
 145 150 155 160  
 Tyr Ile Asp Thr Phe Lys Lys Glu Asp Gly Val Thr Val Thr Thr  
 165 170 175  
 Gly Leu Ala Tyr Lys Thr Leu Gln Glu Gly Thr Gly Ala Thr Pro Ser  
 180 185 190  
 15 Leu Ala Asp Thr Val Arg Val Lys Tyr Val Gly Thr Leu Val Asp Gly  
 195 200 205  
 Lys Glu Phe Asp Lys Asn Glu Glu Gly Ile Glu Phe Ala Val Thr Gly  
 210 215 220  
 20 Val Ile Lys Gly Trp Thr Glu Met Leu Gln Leu Met Lys Val Gly Gln  
 225 230 235 240  
 Lys Val Arg Val Val Ile Pro Gln Glu Leu Ala Tyr Gly Glu Thr Gly  
 245 250 255  
 Asn Tyr Thr Ile Glu Pro Phe Ser Thr Leu Thr Phe Glu Met Glu Leu  
 260 265 270  
 25 Ile Gly Ile Lys Pro Gly Lys Lys  
 275 280

(2) INFORMATION FOR SEQ ID NO:326

- 30 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 803 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
 35 (ii) MOLECULE TYPE: protein  
 (iii) HYPOTHETICAL: YES  
 (vi) ORIGINAL SOURCE:  
 40 (A) ORGANISM: Porphyromonas gingivalis  
 (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...803  
 45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:326

Cys Arg Lys Gln Lys Leu Ser Asn Pro Lys Arg Ser Arg Tyr Pro Cys  
 1 5 10 15  
 50 Arg Arg Ile Ser Phe Arg Gln Ser Asp Lys Asn Pro Met Lys Val Leu  
 20 25 30  
 Arg Gln Val Phe Leu Pro Ile Leu Phe Val Leu Leu Thr Gly Ala Cys  
 35 40 45  
 55 Ser Thr Thr Lys Asn Leu Pro Glu Gly Glu Gln Leu Tyr Ile Gly Met  
 50 55 60  
 Gly Lys Thr Gln Ile Leu Arg Gln Asp Lys Ser His Ala Gly Gln Gln  
 65 70 75 80  
 Ala Leu Thr Glu Val Glu Ser Thr Leu Lys Val Thr Pro Asn Gly Ala  
 85 90 95  
 60 Ile Phe Gly Ser Ala Ser Ala Ser Leu Pro Lys Ile Pro Phe Gly Leu  
 100 105 110  
 Trp Leu Tyr Asn Ser Phe Val Gly Asp Ser Thr Val Ile Ser Lys Trp  
 115 120 125  
 65 Ile Phe Asp Lys Phe Ala Ala Lys Pro Val Phe Ile Ser Gln Val Lys  
 130 135 140  
 Ser Asp Ser Arg Ala Lys Val Ala Thr Asn Ile Leu Arg Glu His Gly  
 145 150 155 160  
 Tyr Phe Asp Ala Lys Val Lys Ser Ser Val Thr Thr Leu Lys Lys Asp  
 165 170 175  
 70 Ser Leu Lys Ala Lys Ile Ser Tyr Thr Val Asp Met Ala Ser Pro Tyr  
 180 185 190  
 His Tyr Asp Ser Ile Ile Pro Leu Pro Ile Ser Thr Phe Pro Asp Ser  
 195 200 205  
 75 Ile Leu Ala Tyr Arg Gln Thr Pro Ser Leu Ile Arg Lys Gly Asp Gln  
 210 215 220

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	Phe	Asn	Leu	Ala	Lys	Leu	His	Glu	Glu	Arg	Gln	Thr	Ile	Ser	Ala	Leu
	225					230					235					240
	Leu	Arg	Asp	Asn	Gly	Tyr	Tyr	Tyr	Phe	Arg	Pro	Gln	Asp	Ile	Ile	Tyr
					245					250					255	
5	Glu	Ala	Asp	Thr	Leu	Leu	Val	Arg	Gly	Ala	Val	Cys	Leu	Arg	Ala	Lys
				260					265					270		
	Leu	Ser	Glu	Asp	Thr	Pro	Pro	Gln	Ala	Met	Arg	Pro	Trp	Arg	Ile	Gly
			275					280					285			
10	Lys	Arg	Thr	Ala	Val	Leu	Leu	Gly	Met	Asn	Gly	Glu	Ser	Pro	Thr	Asp
	290						295					300				
	Ser	Leu	Glu	Val	Glu	Asp	Met	Lys	Val	Leu	Tyr	Tyr	Arg	Lys	Met	Pro
	305					310					315				320	
	Val	Arg	Pro	Lys	Ile	Leu	Ala	Lys	Arg	Phe	Arg	Phe	Phe	Ser	Gly	Asn
					325					330					335	
15	Leu	Tyr	Arg	Gln	Lys	Asp	Asp	Glu	Thr	Thr	Arg	Lys	Ser	Leu	Ala	Arg
				340					345						350	
	Leu	Gly	Ala	Phe	Ser	Val	Ile	Asp	Leu	Asn	Phe	Leu	Gln	Arg	Asp	Ser
			355					360					365			
20	Ile	Ser	Gly	Leu	Leu	Asp	Val	Arg	Leu	Leu	Thr	Thr	Leu	Asp	Lys	Pro
	370					375						380				
	Trp	Asp	Ala	Ser	Leu	Glu	Thr	Leu	Phe	Thr	Ser	Lys	Ser	Asn	Asp	Phe
	385					390					395					400
	Ile	Gly	Pro	Gly	Leu	Asn	Phe	Ala	Leu	Ala	Arg	Arg	Asn	Val	Phe	Gly
					405					410					415	
25	Gly	Gly	Glu	Asn	Leu	Ser	Trp	Asn	Ile	Gly	Gly	Ser	Tyr	Glu	Trp	Glu
				420					425					430		
	Thr	Gly	Asn	Arg	Pro	Glu	Asn	Ser	Ser	Asn	Arg	Leu	Ile	Asp	Ile	Asn
			435					440					445			
30	Ser	Tyr	Asn	Met	Asn	Thr	Ala	Val	Asn	Leu	Ser	Phe	Pro	Ser	Ile	Val
			450				455						460			
	Phe	Pro	Gly	Leu	Leu	Asp	Lys	Tyr	Tyr	Tyr	Tyr	Pro	Thr	Thr	Thr	Thr
	465					470				475						480
	Phe	Gln	Ala	Ser	Ala	Thr	Ala	Leu	Asn	Arg	Ala	His	Tyr	Phe	Ser	Met
					485					490					495	
35	Tyr	Ser	Phe	Gly	Phe	Ser	Thr	Thr	Tyr	Glu	Phe	Gln	Pro	Ser	Lys	Glu
				500					505					510		
	His	Arg	His	Ala	Ile	Phe	Pro	Leu	Lys	Leu	Asn	Tyr	Asn	Leu	Leu	Gly
				515				520					525			
40	His	Gln	Thr	Glu	Thr	Phe	Gln	Ala	Ile	Thr	Ala	Asn	Asn	Pro	Pro	Leu
				530			535					540				
	Leu	Leu	Ser	Leu	Gln	Ser	Gln	Phe	Leu	Ala	Gln	Met	Gly	Tyr	Ile	Tyr
	545					550					555					560
	Thr	Phe	Asn	Lys	Ser	Val	Ser	Glu	Lys	Ser	Pro	His	His	Leu	Trp	Met
				565						570					575	
45	Gln	Phe	Gly	Leu	Ser	Glu	Ala	Gly	Asn	Leu	Leu	Asn	Leu	Ile	Tyr	Leu
				580					585					590		
	Ala	Ala	Gly	Lys	Lys	Tyr	Ser	Asp	Thr	Lys	Asn	Phe	Val	Gly	Val	Pro
			595					600					605			
50	Phe	Ser	Gln	Phe	Ile	Lys	Ala	Thr	Gly	Glu	Leu	Arg	Tyr	Ser	Tyr	Thr
			610				615					620				
	Ile	Asp	Arg	Asn	Gln	Ser	Leu	Ala	Thr	Arg	Phe	Gly	Thr	Gly	Val	Ile
	625					630				635					640	
	Tyr	Ser	Tyr	Gly	Asn	Met	Arg	Val	Ala	Pro	Tyr	Ser	Glu	Gln	Phe	Tyr
				645						650					655	
55	Val	Gly	Gly	Ala	Asn	Ser	Ile	Arg	Ala	Phe	Thr	Val	Arg	Ser	Ile	Gly
				660					665					670		
	Pro	Gly	Arg	Phe	Asn	Pro	Asp	Ser	Asp	Asn	Gln	Tyr	Ser	Tyr	Leu	Asp
			675					680					685			
60	Gln	Val	Gly	Glu	Phe	Lys	Leu	Glu	Ala	Asn	Val	Glu	Tyr	Arg	Gly	Lys
			690				695					700				
	Leu	Phe	Gly	Asp	Leu	His	Ala	Ala	Val	Phe	Leu	Asp	Ala	Gly	Asn	Val
	705					710				715					720	
	Trp	Leu	Leu	Arg	Glu	Asp	Ser	Ser	Arg	Pro	Gly	Gly	Ala	Leu	Ser	Glu
				725						730					735	
65	Val	Gly	Ser	Val	Ser	Asn	Phe	Leu	Asn	Ser	Ile	Ala	Leu	Gly	Thr	Gly
				740					745					750		
	Val	Gly	Leu	Arg	Tyr	Asp	Leu	Ala	Phe	Leu	Val	Val	Arg	Val	Asp	Val
			755					760					765			
70	Gly	Phe	Gly	Leu	His	Leu	Pro	Tyr	Asn	Thr	Gly	Lys	Lys	Gly	Tyr	Tyr
			770				775					780				
	Asn	Ile	Pro	Arg	Phe	Lys	Asp	Ala	Ile	Gly	Phe	His	Leu	Ala	Val	Gly
	785					790					795					800
	Tyr	Pro	Phe													
75																

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## (2) INFORMATION FOR SEQ ID NO:327

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 783 amino acids  
 (E) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...783

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:327

1 Ser Leu Ser Pro Tyr Ile Arg Phe Pro Met Ser Ser His Ser Val Arg  
 5 5 10 15  
 Tyr Leu Ile Gly Ile Ala Gly Cys Leu Leu Leu Met Leu Ala Ser Ser  
 20 25 30  
 25 Cys Ser Val Thr Arg Tyr Val Pro Asp Gly Ser Arg Leu Leu Asp Arg  
 35 40 45  
 Val Thr Ile Ala Ser Glu Thr Gly Ser Ile Ala Leu Pro Glu Asp Ile  
 50 55 60  
 30 Arg Asp Tyr Thr Leu Gln Gln Pro Asn Tyr Arg Leu Phe Gly Met Thr  
 65 70 75 80  
 Arg Trp Leu Leu Arg Val Tyr Ser Ser Ser Asn Pro Asn Ser Asn Ser  
 85 90 95  
 Trp Trp Asn Arg Ser Leu Arg Lys Met Gly Glu Pro Pro Val Leu Ile  
 100 105 110  
 35 Asp Ser Val Leu Thr Asp Arg Thr Ala Asn Arg Leu Ala Lys Ala Met  
 115 120 125  
 Ala Gly Asp Gly Phe Leu Asp Ala Thr Ala Arg Ala Val Val Asp Thr  
 130 135 140  
 40 Gly Leu Tyr Lys Lys Ala Arg Ile Thr Tyr Leu Ile Gln Pro Gly Ser  
 145 150 155 160  
 Arg Tyr Tyr Ile Arg Asn Met Ala Leu Asp Val Lys Asn Pro Leu Leu  
 165 170 175  
 Pro Pro Val Ala Leu Gly Asn Ser Leu Pro Ser Ala Tyr Lys Val Gly  
 180 185 190  
 45 Ile Ser Glu Gly Ser Pro Leu Ser Pro Ile Val Leu Asp Glu Glu Arg  
 195 200 205  
 Lys Ala Ile Ala Arg His Met Arg Asn Asn Gly Phe Trp Lys Phe Ser  
 210 215 220  
 50 Ala Glu Asp Val Tyr Tyr Glu Ala Asp Thr Thr Val Ser Gly Gly Ser  
 225 230 235 240  
 Gly Thr Lys Ser Ala Asp Leu Lys Leu Val Val Asn Gly Ile Gly Arg  
 245 250 255  
 Tyr Pro Tyr Arg Ile Gly Arg Val Phe Phe His Ala Asp Tyr Asp Pro  
 260 265 270  
 55 Leu Glu Ser Asp Phe Arg Val Gln Glu Leu Pro Arg Ile Asp Ser Ile  
 275 280 285  
 Ser Arg Gly Asp Tyr Thr Val Tyr Tyr Gly Ser Arg Gly Arg Tyr Ile  
 290 295 300  
 60 Arg Ala Ser Ala Leu Thr Arg Ser Val Ser Val Thr Pro Gly Ala Phe  
 305 310 315 320  
 Phe Cys Glu Asp Asp Val Glu Arg Ser Tyr Ile Lys Leu Asn Ala Leu  
 325 330 335  
 Pro Ile Val Arg Asn Val Asn Ile Arg Phe Val Glu His Asn Gly Lys  
 340 345 350  
 65 Asp Glu Ile Ala Leu Ala Asp Ser Ser Arg Leu Val Asp Cys Tyr Ile  
 355 360 365  
 Leu Thr Val Pro Ala Lys Ser Lys Ser Phe Glu Ala Glu Val Leu Gly  
 370 375 380  
 70 Thr Asn Ser Ala Gly Asp Phe Gly Ala Ala Leu Ser Leu Gly Phe Thr  
 385 390 395 400  
 Asp Arg Asn Leu Phe Arg Gly Ala Glu Met Phe Asn Ile Lys Leu Lys  
 405 410 415  
 Gly Ala Tyr Glu Ala Ile Arg Lys Gly Ser His Ser Phe Met Glu Tyr  
 420 425 430  
 75 Gly Val Glu Ser Ser Leu Arg Phe Pro Arg Leu Leu Phe Pro Phe Ile

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435 440 445  
 Ser Asp Glu Thr Arg Arg Arg Leu Arg Ala Ser Thr Glu Trp Lys Ile  
 450 455 460  
 Gly Tyr Asn Tyr Gln Thr Arg Pro Glu Phe Asp Arg Val Ile Leu Ser  
 465 470 475 480  
 Ala Gln Leu Asn Tyr Ser Trp Gln Thr Tyr Leu His Asn Arg Leu Arg  
 485 490 495  
 His Thr Ile Arg Leu Leu Asp Val Asp Tyr Leu His Leu Pro Tyr Ile  
 500 505 510  
 10 Asp Pro Asp Phe Ala Gln Ser Leu Pro Pro Thr Thr Ala Leu Tyr Asn  
 515 520 525  
 Tyr Thr Glu Gln Phe Ile Leu Gly Ser Ala Tyr Ile Leu Asn Tyr Thr  
 530 535 540  
 15 Thr Ala Ser Ser Met Glu Arg Thr Val Ser Asn Pro Phe Thr Ala Arg  
 545 550 555 560  
 Phe Ser Ile Gln Thr Ala Gly Asn Leu Leu Gln Ala Ile Ser Tyr Leu  
 565 570 575  
 Thr Asp Ser Pro Lys Asp Glu His Gly Leu Tyr Lys Met Phe Gly Leu  
 580 585 590  
 20 His Tyr Ala Gln Phe Val Lys Leu Asp Leu Asp Leu Ala Lys Thr Val  
 595 600 605  
 Leu Leu Glu Lys Asp Asn Thr Leu Ala Leu His Leu Gly Phe Gly Leu  
 610 615 620  
 25 Ala Phe Pro Tyr Gly Asn Ala Arg His Ile Pro Phe Glu Leu Arg Tyr  
 625 630 635 640  
 Phe Ala Gly Gly Ser Asn Ser Val Arg Gly Trp Ser Val Arg Thr Leu  
 645 650 655  
 Gly Pro Gly Ser Met Lys Met Thr Pro Asp Lys Thr Phe Phe Asp Gln  
 660 665 670  
 30 Met Gly Asp Ile Arg Leu Asp Leu Asn Val Glu Tyr Arg Thr Lys Leu  
 675 680 685  
 Phe Trp Lys Phe Arg Ala Ala Ala Phe Val Asp Ala Gly Asn Val Trp  
 690 695 700  
 35 Thr Ile Lys Glu Tyr Glu Asn Gln Glu Asp Gly Leu Phe Arg Phe Asp  
 705 710 715 720  
 Arg Phe Tyr Lys Glu Ile Ala Leu Ala Tyr Gly Leu Gly Leu Arg Leu  
 725 730 735  
 Asp Phe Asp Tyr Phe Leu Val Arg Leu Asp Ala Gly Leu Lys Ala Tyr  
 740 745 750  
 40 Asp Pro Gln Gln Thr Gly Arg Tyr Lys Trp Ala Ile Thr Arg Pro Asn  
 755 760 765  
 Leu Ser Ser Asn Phe Ala Trp His Ile Ala Val Gly Tyr Pro Phe  
 770 775 780  
 45 (2) INFORMATION FOR SEQ ID NO:328  
 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 875 amino acids  
 (B) TYPE: amino acid  
 50 (D) TOPOLOGY: linear  
 (ii) MOLECULE TYPE: protein  
 (iii) HYPOTHETICAL: YES  
 55 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Porphyromonas gingivalis  
 (ix) FEATURE:  
 (A) NAME/KEY: misc feature  
 60 (B) LOCATION 1...875  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:328  
 65 Val Glu Ser Lys Leu Leu Cys Leu Met Arg Lys Arg Ile Leu Gln Leu  
 1 5 10 15  
 Phe Leu Thr Ala Leu Leu Leu Ala Leu Gly Ser Ser Leu Ala Ile Ala  
 20 25 30  
 70 Gln Thr Val Val Thr Gly Lys Val Ile Asp Ser Glu Thr Ser Glu Pro  
 35 40 45  
 Leu Ile Gly Val Ser Val Ser Thr Gly Gln Gly Ala Ser Leu Arg Gly  
 50 55 60  
 Val Thr Thr Asp Met Asp Gly Gly Phe Arg Phe Glu Val Pro Ala Lys  
 65 70 75 80  
 75 Ser Val Leu Thr Phe Arg Cys Val Gly Tyr Ala Thr Val Thr Arg Ser

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				85					90				95				
	Ile	Gly	Arg	Gly	Ser	Gln	Glu	Asp	Leu	Gly	Thr	Ile	Leu	Leu	Asp	Pro	
				100					105				110				
5	Gln	Ala	Ile	Gly	Leu	Asp	Glu	Ile	Gln	Val	Ile	Ala	Ser	Val	Val	Pro	
			115					120					125				
	Lys	Asp	Arg	Met	Thr	Pro	Val	Pro	Val	Ser	Asn	Ile	Arg	Val	Ala	Asp	
			130				135						140				
	Ile	Gln	Ala	Ala	Ser	Leu	Asn	Val	Glu	Phe	Pro	Glu	Leu	Val	Lys	Ser	
			145			150					155					160	
10	Thr	Pro	Ser	Thr	Tyr	Thr	Thr	Lys	Gly	Ser	Gly	Gly	Phe	Gly	Asp	Gly	
				165						170					175		
	Arg	Thr	Asn	Val	Arg	Gly	Phe	Asp	Thr	Tyr	Asn	Phe	Gly	Val	Leu	Ile	
				180				185						190			
15	Asn	Gly	Val	Pro	Val	Asn	Gly	Met	Glu	Asp	Gly	Lys	Val	Tyr	Trp	Ser	
			195					200					205				
	Asn	Trp	Ser	Gly	Leu	Met	Asn	Gln	Ala	Ser	Thr	Ile	Gln	Ile	Gln	Arg	
			210			215						220					
	Gly	Leu	Gly	Ala	Ser	Lys	Leu	Gly	Ile	Ser	Ser	Val	Gly	Gly	Thr	Met	
			225			230				235					240		
20	Asn	Ile	Ile	Thr	Lys	Thr	Thr	Asp	Ala	Asn	Thr	Gly	Gly	Ser	Ala	Tyr	
				245						250					255		
	Val	Gly	Met	Gly	Asn	Asp	Gly	Leu	His	Lys	Glu	Ser	Phe	Ser	Ile	Ser	
				260				265						270			
25	Thr	Gly	Met	Asn	Asp	Gly	Trp	Ala	Ile	Thr	Ile	Ala	Gly	Ser	His	Met	
			275					280					285				
	Thr	Gly	Leu	Gly	Tyr	Val	Lys	Gly	Leu	Lys	Gly	Arg	Ala	Phe	Ser	Tyr	
			290				295					300					
	Phe	Phe	Asn	Val	Ser	Lys	Phe	Asn	Glu	Arg	His	Thr	Leu	Ser	Leu		
			305			310				315					320		
30	Thr	Gly	Phe	Gly	Ala	Pro	Gln	Trp	His	Asn	Gln	Arg	Ser	Ser	Lys	Tyr	
				325						330					335		
	Ser	Val	Ala	Asp	Tyr	Asp	Lys	Tyr	Gly	Ile	Arg	His	Asn	Gln	Ser	Phe	
				340					345					350			
35	Gly	Tyr	Leu	Arg	Gly	Glu	Leu	Thr	Pro	Thr	Ala	Tyr	Ala	Tyr	Asn	Thr	
			355					360					365				
	Tyr	His	Lys	Pro	Gln	Phe	Ser	Leu	Asn	His	Phe	Trp	Lys	Met	Asp	Glu	
			370				375					380					
	Asn	Thr	Ser	Leu	Tyr	Thr	Ala	Unk	Tyr	Ala	Ser	Leu	Ala	Thr	Gly	Gly	
			385			390				395					400		
40	Gly	Arg	Arg	Ala	Tyr	Gly	Lys	Asn	Ser	Lys	Trp	Val	Leu	Ile	Asn	Tyr	
				405						410					415		
	Asn	Thr	Gly	Gln	Pro	Tyr	Glu	Gln	Thr	Lys	Val	Thr	Pro	Asp	Gly	Leu	
				420					425					430			
45	Ile	Asp	Tyr	Asp	Ala	Val	Leu	Ala	Ala	Asn	Ala	Ala	Ala	Ser	Asn	Gly	
			435					440					445				
	Ser	Glu	Ala	Ile	Phe	Ala	Leu	Gly	Ser	Asn	Ser	His	Lys	Trp	Phe	Gly	
			450				455					460					
	Leu	Leu	Ser	Ser	Phe	Lys	Lys	Lys	Leu	Asn	Ser	Ser	Leu	Thr	Leu	Thr	
			465			470					475				480		
50	Ala	Gly	Tyr	Asp	Gly	Arg	Tyr	Tyr	Arg	Gly	Asp	His	Tyr	Asp	Lys	Ile	
				485					490					495			
	Thr	Asp	Leu	Leu	Gly	Gly	Ser	Tyr	Tyr	Ile	Glu	Asp	Pro	Lys	Thr	Lys	
				500					505					510			
55	Leu	Ala	Tyr	His	Ala	Glu	Gly	Gln	Gln	Leu	Lys	Val	Gly	Asp	Ile	Val	
			515					520					525				
	Asn	Arg	Asp	Tyr	Thr	Gly	Glu	Ile	Met	Trp	His	Gly	Leu	Phe	Ala	Gln	
			530				535					540					
	Met	Glu	His	Ser	Ser	Glu	Trp	Ile	Asp	Ala	Phe	Val	Ser	Gly	Ser	Ile	
			545			550				555					560		
60	Asn	Tyr	Glu	Leu	Tyr	Arg	Asn	His	Asn	Tyr	Gly	Gly	Ser	Lys	Ser	Thr	
				565						570					575		
	Gly	Tyr	Leu	Pro	Gly	Val	Ser	Pro	Trp	Lys	Ser	Phe	Leu	Pro	Trp	Ser	
				580					585					590			
65	Gly	Lys	Ala	Gly	Leu	Ser	Tyr	Lys	Phe	Ala	Gln	Gly	His	Asn	Val	Phe	
			595					600					605				
	Ala	Asn	Gly	Gly	Phe	Phe	Thr	Arg	Ala	Pro	Leu	Phe	Gly	Asn	Ile	Tyr	
			610				615					620					
	Ala	Ala	Gly	Ala	Ile	Ile	Pro	Asn	Asp	Lys	Ala	Asn	Met	Glu	Lys	Val	
			625			630				635					640		
70	Leu	Thr	Gly	Glu	Val	Gly	Tyr	Gly	Phe	Thr	Asn	His	Lys	Asn	Phe	Glu	
				645						650					655		
	Phe	Asn	Ile	Asn	Gly	Tyr	Tyr	Thr	Lys	Trp	Met	Asp	Arg	Val	Thr	Ser	
				660					665					670			
75	Lys	Arg	Ile	Gly	Asn	Glu	Tyr	Val	Tyr	Leu	Asn	Gly	Val	Asp	Ala	Val	
			675					680					685				

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His Cys Gly Val Glu Ala Glu Val Ser Tyr Arg Pro Ile Arg Gln Ile  
 690 695 700  
 Asp Leu Arg Gly Met Phe Ser Leu Gly Asp Trp Thr Trp Gln Asn Asn  
 705 710 715 720  
 5 Val Ser Tyr Thr Ser Tyr Asp Glu Ala Gly Asn Glu Thr Gly Gln Asp  
 725 730 735  
 Ile Thr Tyr Ile Lys Gly Leu His Val Gly Asp Ala Ala Gln Met Thr  
 740 745 750  
 10 Ala Ala Val Ser Ala Asp Ile Glu Leu Phe Lys Gly Phe His Val Ile  
 755 760 765  
 Gly Lys Tyr Asn Phe Leu Gly Lys Asn Tyr Ala Gly Phe Asn Pro Ala  
 770 775 780  
 Thr Arg Asn Ala Gln Gln Tyr Glu Ala Asp Gly Lys Glu Ile Val Glu  
 785 790 795 800  
 15 Ser Trp Lys Leu Pro Asp Val Gly Leu Phe Asp Leu Ser Ala Ser Tyr  
 805 810 815  
 Asn Phe Lys Leu Gly Ser Leu Ser Thr Thr Phe Tyr Phe Asn Met Asp  
 820 825 830  
 20 Asn Val Ala Asp Lys Arg Tyr Val Ser Asp Ala Asp Asp Asn Ile Ile  
 835 840 845  
 Gly Lys Lys His Asp Glu Ala Ser Ala Leu Val Trp Tyr Gly Phe Gly  
 850 855 860  
 Arg Thr Trp Ser Thr Gly Ile Arg Val Asn Phe  
 865 870 875  
 25

(2) INFORMATION FOR SEQ ID NO:329

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 460 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
 (ii) MOLECULE TYPE: protein  
 (iii) HYPOTHETICAL: YES  
 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: *Porphyromonas gingivalis*  
 (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...460  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:329

45 Asn Arg Cys Asn Pro Ser Arg Gln Tyr Phe His Leu Ser Gln Asn Asp  
 1 5 10 15  
 Val Gly Arg Ser Leu Arg Ala Phe Leu Ile His Leu Ser Met Lys Phe  
 20 25 30  
 50 Ser Ile Arg Leu Phe Leu Cys Ile Ile Phe Leu Leu Ser Ala Phe Ile  
 35 40 45  
 Leu Pro Ala Leu Gly Gln Lys Ser Lys Gln Val Gln Arg Leu Glu Lys  
 50 55 60  
 55 Gln Arg Lys Glu Ala Leu Lys Ala Ile Glu Lys Thr Asp Arg Glu Leu  
 65 70 75 80  
 Arg Asn Thr Lys Lys Asp Lys Gln Asp Lys Gln Lys His Leu Asn Leu  
 85 90 95  
 Leu Asn Lys Gln Val Ala Gln Arg Lys Gln Met Val Gln Leu Leu Asp  
 100 105 110  
 60 Asn Glu Val Lys Glu Leu Gln Ser Asp Ile Asp Ser Met Thr Gly Val  
 115 120 125  
 Cys His Gln Leu Ser Val Glu Glu Lys Ala Arg Ser Asp Glu Tyr Ala  
 130 135 140  
 65 Gln Ala Leu Gln Ser Met Gln Lys Arg Lys Arg Ser Leu Asp Arg Ile  
 145 150 155 160  
 Leu Phe Ile Ser Ser Ala Lys Ser Phe Asp Glu Gly Met Arg Arg Met  
 165 170 175  
 Arg Phe Leu Glu Gln Tyr Ala Ser Ala Tyr Lys Leu Ala Ser Val Arg  
 180 185 190  
 70 Leu Arg Asp Thr Arg Ser Lys Leu Glu Thr Glu Arg Ala Thr Val Glu  
 195 200 205  
 Asp Ala Lys Lys Glu Lys Gly His Leu Leu Val Ile Arg Glu Glu Glu  
 210 215 220  
 75 Lys Lys Lys Leu Glu Gly Gln Gln Ala Glu Gln Arg Arg Gln Val Gln  
 225 230 235 240

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Ala Leu Gly Ala Lys Gln Lys Asp Leu Glu Ala Gln Leu Arg Lys Gln  
 245 250 255  
 Lys Lys Gln Ala Glu Ala Leu Asn Arg Lys Ile Glu Lys Gln Ile Ala  
 260 265 270  
 5 Lys Glu Ile Glu Ala Ala Glu Arg Arg Ala Arg Glu Glu Arg Glu Arg  
 275 280 285  
 Leu Ala Arg Glu Ala Lys Ala Lys Gly Lys Pro Val Pro Ala Glu Pro  
 290 295 300  
 10 Glu Arg Lys Ala Glu Thr Lys Gly Gly Tyr Ala Met Asp Ala Ser Glu  
 305 310 315 320  
 Arg Ala Leu Ser Gly Ser Phe Ala Gln Asn Lys Gly Arg Leu Pro Gly  
 325 330 335  
 Pro Val Arg Gly Arg Tyr Arg Ile Val Ser Asp Phe Gly Val His Gln  
 340 345 350  
 15 His Ser Glu Leu Lys Lys Val Gln Val Asn Asn Gly Gly Ile Asp Ile  
 355 360 365  
 Ala Val Ala Thr Gly Ser Asp Ala Thr Ser Val Phe Asp Gly Val Val  
 370 375 380  
 20 Ser Ser Val Phe Val Ile Pro Gly Tyr Asn Ser Ala Val Met Val Arg  
 385 390 395 400  
 His Gly Asn Tyr Ile Thr Val Tyr Ala Asn Leu Ser Lys Val Tyr Val  
 405 410 415  
 Asn Ser Gly Thr Arg Val Lys Thr Gly Gln Ala Leu Gly Arg Ala Tyr  
 420 425 430  
 25 Thr Asp Pro Ser Asn Asn Gln Thr Thr Ile Ile His Phe Glu Ile Trp Lys  
 435 440 445  
 Glu Arg Ser Lys Gln Asn Pro Arg Leu Trp Leu Arg  
 450 455 460

30 (2) INFORMATION FOR SEQ ID NO:330

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 342 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

35 (ii) MOLECULE TYPE: protein

40 (iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Porphyromonas gingivalis

45 (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...342

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:330

50 Ser Phe Tyr Gln Glu Ile Asp Arg Leu Met Lys Lys Tyr Leu Leu Tyr  
 1 5 10 15  
 Ala Ser Leu Leu Thr Ser Val Leu Leu Phe Ser Cys Ser Lys Asn Asn  
 20 25 30  
 55 Pro Asn Glu Pro Val Glu Asp Arg Ser Ile Glu Ile Ser Ile Arg Val  
 35 40 45  
 Asp Asp Phe Thr Lys Thr Gly Glu Ala Val Arg Tyr Glu Arg Asn Gln  
 50 55 60  
 Gly Ser Ala Ala Glu Arg Leu Ile Thr Asn Leu Tyr Leu Leu Leu Phe  
 65 70 75 80  
 60 Asp Gln Ser Gly Ala Asn Pro Ala Lys Tyr Tyr Ile Thr Gly Asn Thr  
 85 90 95  
 Phe Thr Gly Gly Thr Trp Leu Pro Asp Asp Met Lys Val Lys Leu Asp  
 100 105 110  
 65 Met Thr Gln Ser Glu Ala Gly Glu Arg Lys Val Tyr Val Val Ala Asn  
 115 120 125  
 Val Asp Asn Ala Val Lys Thr Ala Leu Asp Ala Val Ala Asn Glu Ser  
 130 135 140  
 Asp Leu Gln Thr Val Lys Arg Thr Thr Ala Met Pro Trp Ser Thr Asp  
 145 150 155 160  
 70 Ile Ala Ser Pro Phe Leu Met Ser Gly Asn Lys Thr His Asp Phe Leu  
 165 170 175  
 Ala Asn Arg Leu Leu Asp Asn Val Pro Leu Val Arg Ala Ile Ala Lys  
 180 185 190  
 75 Val Glu Leu Asn Ile Ser Leu Ser Glu Lys Phe Gln Ile Val Pro Ile  
 195 200 205

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5 Ile Val Asn Gly Ser Leu Ser Glu Phe Lys Phe Arg Tyr Val Asn Phe  
 210 215 220  
 Asp Lys Glu Thr Tyr Val Val Lys Pro Thr Thr Lys Pro Asp Asn Leu  
 225 230 235 240  
 10 Ile Ser Ser Ala Asn Gly Val Trp Pro Gln Ile Thr Asp Trp Thr Val  
 245 250 255  
 Trp Gly Ala Ser Leu Asn Thr Ser Pro Ala Pro Asp Ala Gly Thr Gly  
 260 265 270  
 Tyr Thr Leu Asp Ala Asn Gly Lys Val Thr Ala Leu Arg Ile Val Thr  
 275 280 285  
 Tyr Leu Asn Glu Arg Asp Ser Lys Gly Ala Thr Val Glu Val Ala Leu  
 290 295 300  
 15 Pro Arg Val Asp Asp Gly Thr Leu Pro Pro Pro Glu Phe Gly Pro Glu  
 305 310 315 320  
 Leu Tyr Arg Leu Pro Leu Pro Asp Lys Ile Leu Arg Asn His Trp Tyr  
 325 330 335  
 Lys Tyr Glu Val Glu Ile  
 340

20 (2) INFORMATION FOR SEQ ID NO:331  
 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 329 amino acids  
 (B) TYPE: amino acid  
 25 (D) TOPOLOGY: linear  
 (ii) MOLECULE TYPE: protein  
 (iii) HYPOTHETICAL: YES  
 30 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Porphyromonas gingivalis  
 (ix) FEATURE:  
 35 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...329  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:331

40 Asn Leu Arg Thr Gln Pro Phe Phe Leu Val Asp Leu Gln Ser Met Ile  
 1 5 10 15  
 Arg Thr Ile Leu Ser Arg Tyr Val Ser Ser Asn Phe Trp Ser Arg Gly  
 20 25 30  
 45 Ala Thr Phe Phe Phe Thr Ile Phe Pro Ala Phe Ile Leu Ala Ala Thr  
 35 40 45  
 Ala Leu Pro Ala Cys Gly Gly Gly Thr Ala Ser Gly Ser Asp Arg Thr  
 50 55 60  
 Leu Ala Val Thr Ile Glu Pro Gln Lys Tyr Phe Ile Glu Ser Ile Ala  
 65 70 75 80  
 50 Asp Lys Ser Val Gln Val Val Ala Leu Val Pro Ala Gly Ser Asn Pro  
 85 90 95  
 Glu Glu Tyr Asp Pro Ser Pro Thr Val Met Lys Arg Leu Ser Glu Ala  
 100 105 110  
 55 Asp Ala Tyr Phe Tyr Ile Gly Gly Leu Gly Phe Glu Gln Arg Asn Leu  
 115 120 125  
 Ala Ala Ile Arg Asp Asn Asn Pro Lys Leu Pro Leu Phe Glu Met Gly  
 130 135 140  
 Lys Ala Leu Ala Asp Ala Gly Ser Ala Asp Leu His Gly Ser Cys Thr  
 145 150 155 160  
 60 Asp His Ser His Thr Asp Leu His Ala His Asp Pro His Tyr Trp Ser  
 165 170 175  
 Ser Val Val Gly Ala Lys Ala Leu Ser Arg Ala Ala Tyr Asp Ala Leu  
 180 185 190  
 65 Val Glu Leu Tyr Pro Asn Glu Lys Asp Lys Trp Asp Lys Gly His Asp  
 195 200 205  
 Arg Leu Asn Gly Arg Ile Asp Ser Val Lys Arg Leu Val Asp Thr Met  
 210 215 220  
 Phe Ala Asn Gly Lys Ala Asp Lys Ala Phe Val Ile Tyr His Pro Ser  
 225 230 235 240  
 70 Leu Ser Phe Phe Ala Gln Glu Phe Gly Leu Arg Gln Ile Val Ile Glu  
 245 250 255  
 Glu Asp Gly Lys Glu Pro Thr Ala Ala His Leu Arg Arg Val Ile Asp  
 260 265 270  
 75 Gln Ala Arg Ala Asp Gly Val Arg Ile Val Phe Ile Gln Pro Glu Phe  
 275 280 285

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Glu Thr Arg Gln Ala Glu Asp Ile Ala Arg Glu Ile Gly Ala Arg Pro  
 290 295 300  
 Val Arg Ile Asn Pro Leu Arg Ser Ser Trp Glu Glu Glu Ile Leu His  
 305 310 315 320  
 5 Ile Ala Arg Ala Leu Ala His Glu Arg  
 325

(2) INFORMATION FOR SEQ ID NO:332

- 10 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 878 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear
- 15 (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- 20 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Porphyromonas gingivalis
- (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...878
- 25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:332

Ala Asp Ser Ile Arg Tyr Pro Leu Tyr Phe Phe Gly Arg Asn Arg Lys  
 1 5 10 15  
 30 Lys Cys Phe Arg Glu Pro Ile Pro Thr Leu Tyr Asn Lys Asn Met Ile  
 20 25 30  
 Gly Lys Lys Ile Phe Phe Ile Leu Leu Ala Leu Ile Ala Phe Ser Gly  
 35 35 40 45  
 Leu Asn Ala Ala Thr Asp Thr Glu Phe Lys Tyr Pro Thr Asp Ala Asn  
 50 55 60  
 35 Ile Ile Gly His Val Lys Asp Ser Lys Thr Gly Glu His Leu Val Gly  
 65 70 75 80  
 Ile Thr Ile Ala Ile Lys Gly Thr Thr Phe Gly Thr Ser Thr Asp Ala  
 85 90 95  
 40 Thr Gly His Tyr Tyr Leu Arg Asn Leu Arg Pro Gly Glu Ile Thr Leu  
 100 105 110  
 Ile Met Arg Gly Met Gly Tyr Lys Ser Gln Glu Arg Val Val Arg Val  
 115 120 125  
 45 Glu Lys Asp Lys Thr Ile Glu Val Asn Phe Glu Ala Glu Glu Asp Ala  
 130 135 140  
 Ile Asn Leu Asp Glu Val Val Ile Ser Ala Asn Arg Glu Leu Thr Leu  
 145 150 155 160  
 Arg Arg Leu Ala Pro Thr Leu Val Asn Val Leu Asn Glu Lys Val Phe  
 165 170 175  
 50 Ser Gln Val Asn Ala Ser Asn Leu Ala Gln Gly Leu Ser Phe Gln Pro  
 180 185 190  
 Gly Val Arg Val Glu Asn Asn Cys Gln Asn Cys Gly Phe Asn Gln Val  
 195 200 205  
 55 Arg Ile Asn Gly Leu Asp Gly Arg Tyr Ala Gln Ile Leu Ile Asp Ser  
 210 215 220  
 Arg Pro Ile Met Ser Ala Leu Ala Gly Val Tyr Gly Leu Glu Gln Ile  
 225 230 235 240  
 Pro Ala Asn Met Ile Glu Arg Val Glu Val Val Arg Gly Gly Gly Ser  
 245 250 255  
 60 Ala Leu Tyr Gly Ser Ser Ala Ile Ala Gly Val Val Asn Ile Ile Thr  
 260 265 270  
 Lys Glu Pro Ser His Asn Ser Phe Thr Phe Asn Glu Ser Leu Ser Phe  
 275 280 285  
 65 Thr Gly Phe Ser Lys Leu Asp Asn Asn Thr Asn Phe Asn Ala Ser Ile  
 290 295 300  
 Val Ser Asp Asp Asn Arg Ala Gly Ala Met Val Phe Gly Gln Ala Arg  
 305 310 315 320  
 Tyr Arg Asn His Trp Asp Ala Asn Asn Asp Gly Tyr Ser Glu Leu Gly  
 325 330 335  
 70 Lys Ile Asp Ala Arg Ser Leu Gly Ala His Ser Tyr Leu Arg Leu Ser  
 340 345 350  
 Asp Tyr Ser Lys Leu Thr Gly Glu Phe His Thr Ile Ser Glu Phe Arg  
 355 360 365  
 75 Arg Gly Gly Asp Arg Ile Asp Leu Pro Pro His Val Val Gly Val Ala  
 370 375 380

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Glu Gln Thr Asp His Ser Val Phe Ser Gly Asn Leu Lys Tyr Asp Leu  
 385 390 395 400  
 Phe Ser Ser Asn Tyr Lys His His Phe Gln Ala Tyr Thr Ser Gly Gln  
 405 410 415  
 5 Ile Val Asn Arg Lys Ser Tyr Tyr Gly Gly Ile Gly Glu Ile Asp Val  
 420 425 430  
 Asn Gly His Pro Gly Gly Thr Glu Gly Tyr Pro Ile Pro Gln Asp Gln  
 435 440 445  
 10 Tyr Gly Asn Asn Tyr Gly Val Thr Lys Gly Lys Thr Tyr Met Gly Gly  
 450 455 460  
 Ile Gln Tyr Ser Tyr Asp Leu Asp Lys Phe Leu Leu Met Pro Ser Gln  
 465 470 475 480  
 Leu Leu Phe Gly Ala Glu Tyr Thr Arg Asp Glu Leu Asn Asp Val Met  
 485 490 495  
 15 Pro Ile Leu Ser Trp Gln Thr Gly Glu Asp Ala Asn Gly Asn Thr Ile  
 500 505 510  
 Pro Leu Tyr Pro Glu Leu Asp Gln Asn Ile Asn Asn Tyr Ser Leu Phe  
 515 520 525  
 20 Gly Gln Asn Glu Trp Lys Asn Asp Arg Trp Ser Ile Leu Val Gly Ala  
 530 535 540  
 Arg Leu Asp Lys His Ser Glu Val Lys Asp Met Ile Leu Ser Pro Arg  
 545 550 555 560  
 Thr Thr Leu Arg Phe Asn Val Asn Pro Asp Ile Asn Leu Arg Ala Thr  
 565 570 575  
 25 Tyr Ala Lys Gly Phe Arg Ala Pro Gln Val Phe Asp Glu Asp Leu His  
 580 585 590  
 Val Gly Val Val Gly Gly Glu Ala Gln Lys Val Phe Asn Asp Pro Asn  
 595 600 605  
 30 Leu Lys Pro Glu Ile Ser His Ala Phe Ser Leu Ser Ala Asp Met Tyr  
 610 615 620  
 His Arg Phe Gly Asn Val Gln Thr Asn Phe Leu Val Glu Gly Phe Tyr  
 625 630 635 640  
 Thr Arg Leu Leu Asp Val Phe Thr Asn Glu Glu Gln Pro Asp Gln His  
 645 650 655  
 35 Asp Gly Ile Lys Arg Tyr Thr Arg Ile Asn Gly Ser Gly Ala Lys Val  
 660 665 670  
 Phe Gly Leu Asn Leu Glu Gly Lys Val Ala Tyr Lys Ser Phe Gln Leu  
 675 680 685  
 40 Gln Ala Gly Leu Thr Leu Ala Ser Asn Lys Tyr Asp Glu Ala Gln Glu  
 690 695 700  
 Trp Gly Leu Asn Thr Val Lys Asp Thr Asn Gly Ala Phe Val Thr Glu  
 705 710 715 720  
 Ala Asn Ala Asn Gly Gln Gln Glu Tyr Lys Asn Glu Ser Met Thr Asp  
 725 730 735  
 45 Thr Gln Ile Thr Arg Thr Pro Ser Val Tyr Gly Tyr Phe Thr Leu Ala  
 740 745 750  
 Tyr Asn Pro Ala His Ser Trp Asn Ile Ala Leu Thr Gly Ala Tyr Thr  
 755 760 765  
 50 Gly Gln Met Tyr Val Pro His Ala Ile Glu Tyr Gly Val Lys Ser Ala  
 770 775 780  
 Glu Leu Asp Ile Met Gln Asn Asn Pro Glu Ile Thr Asp Glu Thr Gly  
 785 790 795 800  
 Lys Ala Pro Arg Ile Asp Glu Leu Lys Lys Thr Pro Ala Phe Phe Asp  
 805 810 815  
 55 Leu Gly Leu Lys Val Gly Tyr Asp Phe His Val Phe Gln Ala Thr Glu  
 820 825 830  
 Val Gln Leu Tyr Val Gly Met Asn Asn Ile Phe Asn Ser Phe Gln Lys  
 835 840 845  
 60 Asp Phe Asp Arg Gly Ala Ala Arg Asp Ser Gly Tyr Ile Tyr Gly Pro  
 850 855 860  
 Thr Gln Pro Arg Thr Gly Tyr Met Gly Leu Val Val Lys Phe  
 865 870 875

(2) INFORMATION FOR SEQ ID NO:333

65

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 206 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

70

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

75

(vi) ORIGINAL SOURCE:

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(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

(A) NAME/KEY: misc\_feature  
(B) LOCATION 1...206

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:333

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Lys Gln Ile Val Met Thr Val Lys Arg Ala Val Arg Ile Ala Leu Leu  
 1 5 10 15  
 Thr Leu Ile Gly Ile Leu Phe Ser Ser Pro Ser Leu Val Arg Ala Gln  
 20 25 30  
 Ser Leu Phe Ser Thr Glu His Val Leu Gln Leu Tyr Asn Lys Ile Leu  
 35 40 45  
 Tyr Gly Glu Ser Ala Ala Asp Thr Val Ala Glu Lys Thr Ala Gly Glu  
 50 55 60  
 Ser Ala Phe Pro Phe Ile Asp Lys Leu Ile Asn Leu Gly Arg Thr Phe  
 65 70 75 80  
 Leu Gly Lys Pro Tyr Arg Tyr Arg Gly Pro Ser Pro Trp Pro Met Asp  
 85 90 95  
 Cys Ser Gly Tyr Val Ser Tyr Leu Tyr Ser Lys Phe Asp Ile Lys Leu  
 100 105 110  
 Pro Arg Gly Ala Ala Ala Gln Ser Gln Tyr Thr Asn Pro Ile Glu Arg  
 115 120 125  
 Glu Asp Val Arg Pro Gly Asp Leu Leu Phe Phe Lys Gly Arg Asn Ala  
 130 135 140  
 Arg Ser Asn Arg Ile Gly His Val Ala Leu Val Val Ser Val Asp Glu  
 145 150 155 160  
 Asp Asp Ile Thr Met Met His Ser Arg Asn Ser Arg Gly Ile Val Ile  
 165 170 175  
 Glu Lys Leu Asn Arg Ser Ala Tyr Phe Ser Arg Arg Leu Val Ser Tyr  
 180 185 190  
 Gly Arg Val Pro Gly Ala Lys Arg Val Ile Pro Arg Lys Ser  
 195 200 205

35

(2) INFORMATION FOR SEQ ID NO:334

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 467 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

40

(ii) MOLECULE TYPE: protein

45

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Porphyromonas gingivalis

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(ix) FEATURE:

(A) NAME/KEY: misc\_feature  
(B) LOCATION 1...467

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:334

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Lys Gly Thr Trp Asn Arg Lys Asn Arg Arg Glu Glu Met Lys Arg Thr  
 1 5 10 15  
 Ile Leu Leu Thr Ala Leu Thr Val Leu Ser Ser Leu Ser Leu Leu Arg  
 20 25 30  
 Ala Gln Asn Glu Ser Glu Ala Ser Thr Asn Pro Met Ser Gly Leu Ser  
 35 40 45  
 Leu Glu Asp Cys Ile Arg Ile Ala Lys Glu Arg Asn Leu Asn Leu Arg  
 50 55 60  
 Arg Gln Glu Ile Glu Gln Glu Asn Arg Ile Ile Ser Leu Asp Ala Ala  
 65 70 75 80  
 Arg His Ser Phe Leu Pro Ser Val Asn Ala Gly Ile Gly His Asn Tyr  
 85 90 95  
 Ser Phe Gly Arg Ser Lys Asp Lys Thr Gly Val Thr Val Asp Arg Ser  
 100 105 110  
 Ser Met Asn Thr Asn Leu Ser Ile Gly Ala Ser Val Glu Val Phe Ser  
 115 120 125  
 Gly Thr Arg Arg Leu His Asp Leu Lys Gln Gln Lys Tyr Asn Val Glu  
 130 135 140  
 Asp Gly Ile Ala Arg Leu Gln Lys Ala Arg Glu Asp Leu Ser Leu Gln  
 145 150 155 160

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Ile Ala Ala Leu Tyr Ile Asn Leu Leu Phe Arg Gln Glu Met Thr Arg  
 165 170 175  
 Thr Ala Glu Thr Gln Leu Ala Leu Ile Arg Glu Gln Arg Asn Arg Thr  
 180 185 190  
 5 Ala Glu Met Val Arg Val Gly Lys Trp Ala Glu Gly Lys Leu Leu Asp  
 195 200 205  
 Ile Asn Ala Gln Met Ala Lys Asp Glu Gln Leu Leu Val Gln Tyr Arg  
 210 215 220  
 10 Ser Glu Glu Glu Leu Ala Arg Leu Asp Leu Gly Gln Ala Leu Glu Leu  
 225 230 235 240  
 Glu His Pro Glu Ser Ile Ala Val Lys Ala Pro Asp Thr Asp Val Leu  
 245 250 255  
 Val Ala Glu Arg Leu Gly Ser Leu Leu Ala Pro Glu Glu Ile Tyr Arg  
 260 265 270  
 15 Thr Ala Leu Gly Leu Lys Pro Ala Leu His Ser Ser Glu Leu Gln Ile  
 275 280 285  
 Ala Ser Ala Arg Glu Gly Leu Ala Ser Ala Arg Ala Ala Tyr Phe Pro  
 290 295 300  
 20 Thr Leu Ser Leu Ser Ala Gly Tyr Ser Asn Gly Tyr Phe Arg Asp Leu  
 305 310 315 320  
 Gly Lys Glu Tyr Ala Ala Ile Asn Pro Ser Phe Ser Glu Gln Trp Lys  
 325 330 335  
 Asn Asn Gly Ser Tyr Ser Ile Gly Leu Ser Leu Asn Ile Pro Ile Phe  
 340 345 350  
 25 Ser Ala Met Gln Thr Gln Asp Arg Val Arg Ser Ser Arg Leu Gln Ile  
 355 360 365  
 Arg Ser Ser Glu Leu Arg Leu Val Glu Glu Lys Lys Ala Leu Tyr Lys  
 370 375 380  
 30 Glu Ile Arg Gln Ala Tyr Ser Asn Ala Val Ala Ala Asp Lys Ala Ile  
 385 390 395 400  
 Ala Ala Ala Glu Asn Ser Lys Ala Ala Thr Leu Lys Ala Tyr Glu Tyr  
 405 410 415  
 Ala Arg Asp Ser Phe Glu Ala Gly Arg Leu Ser Ala Tyr Glu Tyr Ala  
 420 425 430  
 35 Glu Ala Lys Thr Lys Tyr Ala Leu Ser Gln Val Glu Glu Leu Arg Ala  
 435 440 445  
 Lys Tyr Asp Phe Ile Tyr Lys Ala Lys Val Leu Asp Phe Tyr Gln Gly  
 450 455 460  
 40 Lys Asp Phe  
 465

## (2) INFORMATION FOR SEQ ID NO:335

- 45 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 451 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
 50 (ii) MOLECULE TYPE: protein  
 (iii) HYPOTHETICAL: YES  
 (vi) ORIGINAL SOURCE:  
 55 (A) ORGANISM: Porphyromonas gingivalis  
 (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...451  
 60 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:335

Lys Thr Ser Tyr Arg Asn Asn Met Arg Phe Gln His Tyr Leu Ile Cys  
 1 5 10 15  
 65 Thr Ala Ala Val Ala Ala Leu Ala Ala Asn Pro Leu Thr Gly Gln Ser  
 20 25 30  
 Asn Met Thr Leu Glu Glu Cys Ile Asp Tyr Ala Arg Arg His Ser Ser  
 35 40 45  
 Ala Val Ala Leu Ser Ala Ala Glu Leu Glu Gln Ser Lys Ala Asp Tyr  
 50 55 60  
 70 Leu Gln Ala Val Gly Asn Phe Leu Pro Arg Val Ser Ala Gly Thr Gly  
 65 70 75 80  
 Ala Ser Trp Asn Phe Gly Arg Gly Leu Asp Ala Glu Thr Asn Thr Tyr  
 85 90 95  
 75 Thr Asp Ile Asn Ser Phe Asn Asn Ser Tyr Ser Ile His Ala Thr Met  
 100 105 110

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Thr Leu Phe Asp Gly Leu Gln Ser Val Tyr Arg Leu Arg Met Ala His  
 115 120 125  
 Ala Arg Arg Glu Ala Ser Arg Leu Ser Val Arg Glu Gln Gln Glu Leu  
 130 135 140  
 5 Ala Ala Leu Gly Thr Thr Glu Ala Tyr Tyr Asp Leu Val Tyr Ala Arg  
 145 150 155 160  
 Gln Met Gln Glu Leu Ala Met Gln Lys Tyr Glu Glu Ser Ser Arg Leu  
 165 170 175  
 10 His Arg Gln Thr Ala Arg Met Glu Glu Leu Gly Met Lys Ser Arg Pro  
 180 185 190  
 Asp Val Leu Glu Met Gln Ser Arg Met Ala Gly Asp Arg Leu Ala Leu  
 195 200 205  
 Thr Gln Ala Asp Asn Gln Cys Ile Ala Leu Ile Arg Leu Lys Glu  
 210 215 220  
 15 Lys Met Asn Phe Pro Ile Asp Asp Glu Leu Val Val Asp Asp Met Pro  
 225 230 235 240  
 Ala Asp Ser Leu Ser Ala Asp Met Ala Glu Ser Asp Ser Ser Ala Gly  
 245 250 255  
 20 Val Phe Ala Arg Ala Ala His His His Pro Val Leu Leu Arg Ala Lys  
 260 265 270  
 Leu Asp Glu Gln Ala Ala Thr Asp Arg Leu Arg Ala Ala Arg Gly Ala  
 275 280 285  
 Phe Leu Pro Ser Val Ser Val Ser Gly Gly Trp Asn Thr Gly Phe Ser  
 290 295 300  
 25 Arg Phe Leu Asn Gly Ser Asp Tyr Thr Pro Phe Ser Glu Gln Phe Arg  
 305 310 315 320  
 Asn Arg Arg Gly Glu Tyr Val Ser Leu Asn Leu Ser Ile Pro Ile Phe  
 325 330 335  
 30 Ser Gly Phe Ser Leu Val Ser His Leu Arg Gln Ala Arg Ala Glu Arg  
 340 345 350  
 Arg Ala Ala Ile Val Arg Arg Gly Glu Ala Glu Arg Arg Leu Tyr Ser  
 355 360 365  
 Glu Ile Ala Gln Ala Met Ala Asp Arg Asp Ala Ala Leu Ala Ser Tyr  
 370 375 380  
 35 Arg Gln Ala Lys Glu His Thr Asp Ala Met Gln Thr Ala Tyr Glu Ala  
 385 390 395 400  
 Val Leu Gln Arg Tyr Glu Glu Gly Leu Asn Thr Ala Ile Asp Leu Thr  
 405 410 415  
 40 Thr Gln Ala Asn Arg Leu Leu Asp Ala Arg Val Gln Arg Leu Arg Ala  
 420 425 430  
 Ala Met Thr Tyr Arg Leu Lys Cys Lys Leu Ile Ala Tyr Tyr Gly Cys  
 435 440 445  
 Leu Ser Asp  
 450

(2) INFORMATION FOR SEQ ID NO:336

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 962 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Porphyromonas gingivalis*

(ix) FEATURE:

(A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...962

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:336

65 Ala Ile Phe Val Val Ser Leu Gln Ile Glu Lys Ile Thr Glu Asn Lys  
 1 5 10 15  
 Tyr Asn Ser Asp Lys Ser Met Asn Lys Phe Tyr Lys Ser Leu Leu Gln  
 20 25 30  
 70 Ser Gly Leu Ala Ala Phe Val Ser Met Ala Thr Ala Leu Thr Ala Ser  
 35 40 45  
 Ala Gln Ile Ser Phe Gly Gly Glu Pro Leu Ser Phe Ser Ser Arg Ser  
 50 55 60  
 75 Ala Gly Thr His Ser Phe Asp Ala Met Thr Ile Arg Leu Thr Pro  
 65 70 75 80



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	Asp	Phe	Asn	Pro	Glu	Asp	Leu	Ile	Ala	Gln	Ser	Arg	Trp	Gln	Ser	Gln
					85					90					95	
	Arg	Asp	Gly	Arg	Pro	Val	Arg	Ile	Gly	Gln	Val	Ile	Pro	Val	Asp	Val
					100				105					110		
5	Asp	Phe	Ala	Ser	Lys	Ala	Ser	His	Ile	Ser	Ser	Ile	Gly	Asp	Val	Asp
			115					120					125			
	Val	Tyr	Arg	Leu	Gln	Phe	Lys	Leu	Glu	Gly	Ala	Lys	Ala	Ile	Thr	Leu
			130				135						140			
10	Tyr	Tyr	Asp	Ala	Phe	Asn	Ile	Pro	Glu	Gly	Gly	Arg	Leu	Tyr	Ile	Tyr
			145			150					155				160	
	Thr	Pro	Asp	His	Glu	Ile	Val	Leu	Gly	Ala	Tyr	Thr	Asn	Ala	Thr	His
					165					170					175	
	Arg	Arg	Asn	Gly	Ala	Phe	Ala	Thr	Glu	Pro	Val	Pro	Gly	Ser	Glu	Leu
					180				185					190		
15	Ile	Met	Asp	Tyr	Glu	Val	Ser	Arg	Gly	Gly	Thr	Leu	Pro	Asp	Ile	Lys
			195				200						205			
	Ile	Ser	Gly	Ala	Gly	Tyr	Ile	Phe	Asp	Lys	Val	Gly	Gly	Arg	Pro	Val
			210				215					220				
20	Thr	Asp	Asn	His	Tyr	Gly	Ile	Gly	Glu	Asp	Asp	Ser	Asp	Ser	Asp	Cys
			225			230					235					240
	Glu	Ile	Asn	Ile	Asn	Cys	Pro	Glu	Gly	Ala	Asp	Trp	Gln	Ala	Glu	Lys
					245					250					255	
	Asn	Gly	Val	Val	Gln	Met	Ile	Met	Val	Lys	Gly	Gln	Tyr	Ile	Ser	Met
			260						265					270		
25	Cys	Ser	Gly	Asn	Leu	Leu	Asn	Asn	Thr	Lys	Gly	Asp	Phe	Thr	Pro	Leu
			275				280						285			
	Ile	Ile	Ser	Ala	Gly	His	Cys	Ala	Ser	Ile	Thr	Thr	Asn	Phe	Gly	Val
			290				295					300				
30	Thr	Gln	Ser	Glu	Leu	Asp	Lys	Trp	Ile	Phe	Thr	Phe	His	Tyr	Glu	Lys
			305			310					315					320
	Arg	Gly	Cys	Ser	Asn	Gly	Thr	Leu	Ala	Ile	Phe	Arg	Gly	Asn	Ser	Ile
					325					330					335	
	Ile	Gly	Ala	Ser	Met	Lys	Ala	Phe	Leu	Pro	Ile	Lys	Gly	Lys	Ser	Asp
					340				345					350		
35	Gly	Leu	Leu	Leu	Gln	Leu	Asn	Asp	Glu	Val	Pro	Leu	Arg	Tyr	Arg	Val
			355					360					365			
	Tyr	Tyr	Asn	Gly	Trp	Asp	Ser	Thr	Pro	Asp	Ile	Pro	Ser	Ser	Gly	Ala
			370				375					380				
40	Gly	Ile	His	His	Pro	Ala	Gly	Asp	Ala	Met	Lys	Ile	Ser	Ile	Leu	Lys
			385			390					395					400
	Lys	Thr	Pro	Ala	Leu	Asn	Thr	Trp	Ile	Ser	Ser	Ser	Gly	Ser	Gly	Gly
					405					410					415	
	Thr	Asp	Asp	His	Phe	Tyr	Phe	Lys	Tyr	Asp	Gln	Gly	Gly	Thr	Glu	Gly
				420				425						430		
45	Gly	Ser	Ser	Gly	Ser	Ser	Leu	Phe	Asn	Gln	Asn	Lys	His	Val	Val	Gly
			435					440					445			
	Thr	Leu	Thr	Gly	Gly	Ala	Gly	Asn	Cys	Gly	Gly	Thr	Glu	Phe	Tyr	Gly
			450				455					460				
50	Arg	Leu	Asn	Ser	His	Trp	Asn	Glu	Tyr	Ala	Ser	Asp	Gly	Asn	Thr	Ser
			465			470					475					480
	Arg	Met	Asp	Ile	Tyr	Leu	Asp	Pro	Gln	Asn	Asn	Gly	Gln	Thr	Thr	Ile
					485					490					495	
	Leu	Asn	Gly	Thr	Tyr	Arg	Asp	Gly	Tyr	Lys	Pro	Leu	Pro	Ser	Val	Pro
				500					505					510		
55	Arg	Leu	Leu	Leu	Gln	Ser	Thr	Gly	Asp	Gln	Val	Glu	Leu	Asn	Trp	Thr
			515					520					525			
	Ala	Val	Pro	Ala	Asp	Gln	Tyr	Pro	Ser	Ser	Tyr	Gln	Val	Glu	Tyr	His
			530				535					540				
60	Ile	Phe	Arg	Asn	Gly	Lys	Glu	Ile	Ala	Thr	Thr	Lys	Glu	Leu	Ser	Tyr
					545		550				555				560	
	Ser	Asp	Ala	Ile	Asp	Glu	Ser	Ile	Ile	Gly	Ser	Gly	Ile	Ile	Arg	Tyr
					565					570					575	
	Glu	Val	Ser	Ala	Arg	Phe	Ile	Tyr	Pro	Ser	Pro	Leu	Asp	Gly	Val	Glu
				580				585						590		
65	Ser	Tyr	Lys	Asp	Thr	Asp	Lys	Thr	Ser	Ala	Asp	Leu	Ala	Ile	Gly	Asp
			595					600					605			
	Ile	Gln	Thr	Lys	Leu	Lys	Pro	Asp	Val	Thr	Pro	Leu	Pro	Gly	Gly	Gly
			610				615					620				
70	Val	Ser	Leu	Ser	Trp	Lys	Val	Pro	Phe	Leu	Ser	Gln	Leu	Val	Ser	Arg
			625			630					635					640
	Phe	Gly	Glu	Ser	Pro	Asn	Pro	Val	Phe	Lys	Thr	Phe	Glu	Val	Pro	Tyr
					645					650					655	
	Val	Ser	Ala	Ala	Ala	Gln	Thr	Pro	Asn	Pro	Pro	Val	Gly	Val	Val	
				660				665					670			
75	Ile	Ala	Asp	Lys	Phe	Met	Ala	Gly	Thr	Tyr	Pro	Glu	Lys	Ala	Ala	Ile

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675 680 685  
 Ala Ala Val Tyr Val Met Pro Ser Ala Pro Asp Ser Thr Phe His Leu  
 690 695 700  
 5 Phe Leu Lys Ser Asn Thr Asn Arg Arg Leu Gln Lys Val Thr Thr Pro  
 705 710 715 720  
 Ser Asp Trp Gln Ala Gly Thr Trp Leu Arg Ile Asn Leu Asp Lys Pro  
 725 730 735  
 Phe Pro Val Asn Asn Asp His Met Leu Phe Ala Gly Ile Arg Met Pro  
 740 745 750  
 10 Asn Lys Tyr Lys Leu Asn Arg Ala Ile Arg Tyr Val Arg Asn Pro Asp  
 755 760 765  
 Asn Leu Phe Ser Ile Thr Gly Lys Lys Ile Ser Tyr Asn Asn Gly Val  
 770 775 780  
 15 Ser Phe Glu Gly Tyr Gly Ile Pro Ser Leu Leu Gly Tyr Met Ala Ile  
 785 790 795 800  
 Lys Tyr Leu Val Val Asn Thr Asp Ala Pro Lys Ile Asp Met Ser Leu  
 805 810 815  
 Val Gln Glu Pro Tyr Ala Lys Gly Thr Asn Val Ala Pro Phe Pro Glu  
 820 825 830  
 20 Leu Val Gly Ile Tyr Val Tyr Lys Asn Gly Thr Phe Ile Gly Thr Gln  
 835 840 845  
 Asp Pro Ser Val Thr Thr Tyr Ser Val Ser Asp Gly Thr Glu Ser Asp  
 850 855 860  
 25 Glu Tyr Glu Ile Lys Leu Val Tyr Lys Gly Ser Gly Ile Ser Asn Gly  
 865 870 875 880  
 Val Ala Gln Ile Glu Asn Asn Asn Ala Val Val Ala Tyr Pro Ser Val  
 885 890 895  
 Val Thr Asp Arg Phe Ser Ile Lys Asn Ala His Met Val His Ala Ala  
 900 905 910  
 30 Ala Leu Tyr Ser Leu Asp Gly Lys Gln Val Arg Ser Trp Asn Asn Leu  
 915 920 925  
 Arg Asn Gly Val Thr Phe Ser Val Gln Gly Leu Thr Ala Gly Thr Tyr  
 930 935 940  
 35 Met Leu Val Met Gln Thr Ala Asn Gly Pro Val Ser Gln Lys Ile Val  
 945 950 955 960  
 Lys Gln

## (2) INFORMATION FOR SEQ ID NO:337

40

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 702 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

45

- (ii) MOLECULE TYPE: protein  
 (iii) HYPOTHETICAL: YES

50

- (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: *Porphyromonas gingivalis*

55

- (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...702

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:337

60 Trp Lys Lys Ser Asn Pro Gln Tyr Arg Gly Arg Thr Ala Asn Tyr Arg  
 1 5 10 15  
 Asp His Tyr Asn Thr Glu Ser Tyr Leu Ser Leu Arg Arg Asn Gln Thr  
 20 25 30  
 Met Lys Tyr Leu Ile Arg Leu Phe Leu Ser Leu Met Leu Leu Ser Leu  
 35 40 45  
 65 Trp Thr Gly Cys Thr His Glu Glu Leu Ser Ile Cys Asp Gly Glu Asn  
 50 55 60  
 Thr Leu Val Leu Arg Val Glu Thr Gly Lys Ala Pro Asn Ala Arg Ala  
 65 70 75 80  
 Thr Glu Pro Gly Gln Gly Ile Tyr Asn Glu Asn Lys Val Gly Ser Ile  
 85 90 95  
 70 Ser Val Leu Phe Tyr Leu Glu Gly Gln Leu Arg Trp Gln Val Lys Ser  
 100 105 110  
 Thr Asp Tyr Gln Ile His Glu Gly Ala Tyr Ile Ile Pro Val Lys Glu  
 115 120 125  
 75 Gln Met Arg Pro Leu Phe Asn Gly Asn Asn Asn Phe Ser Ile Tyr Val

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	130		135		140	
	Val Ala Asn Leu Asp	Phe Asn Ala Pro Ala Thr	Glu Ala Ala Leu Ser			
	145	150	155			
5	Gln Phe Val Val Glu	Lys Ser Ile Glu Val Ser	Ser Thr Thr Ala Pro			
	165	170	175			
	Ala Asp Phe Val Met	Leu Ala His Gly Asn Lys	Gln Ile Asn Met Ala			
	180	185	190			
	Thr Thr Glu Gly Lys	Leu Leu Gly Asp Tyr Lys	Leu Lys Arg Val Ala			
	195	200	205			
10	Ala Lys Ile Arg Met	Ile Lys Pro Thr Ile Asn	Val Gln Gly Tyr Glu			
	210	215	220			
	Val Val Gly Asn Ile	Gln Ala Lys Phe Arg Asn	Ser Val Thr Lys Gly			
	225	230	235			
	Phe Leu Thr Thr Glu	Ala Gln Glu Ile Pro	Ala Ala Ser Tyr Lys			
15	245	250	255			
	Thr Ser Glu Tyr Leu	Asp Ile Ala Glu Ser	Ala Pro Ala Asn Ser Ile			
	260	265	270			
	His Phe Tyr Ser Tyr	Asn Lys Trp Thr Leu	Ser Thr Pro Glu Lys			
	275	280	285			
20	Arg Pro Glu Phe Phe	Ile Met Val Lys Phe Lys	Lys Thr Gly Gln Pro			
	290	295	300			
	Asp Asn Thr Ala Lys	Pro Tyr Tyr Tyr Arg	Val Pro Leu Glu Ser Gln			
	305	310	315			
	Asp Asn Gln Val Lys	Ser Asn Val Leu Tyr	Asn Leu Asn Val Lys Ile			
25	325	330	335			
	Glu Ile Leu Gly Ser	Leu Gln Glu Pro Glu	Ala Val Ser Val Asn Gly			
	340	345	350			
	Thr Leu Ala Ile Glu	Glu Trp Ile Leu His	Gln Asp Ala Phe Asn Leu			
	355	360	365			
30	Pro Ala Thr Asn Tyr	Leu Ile Val Glu Gln	His Glu Ile Phe Met Asn			
	370	375	380			
	Asn Val Asn Thr Tyr	Ser Val Lys Tyr Gln	Thr Ser Gln Lys Pro Ile			
	385	390	395			
	Ser Ile Ser Ile Gln	Ser Val Thr Phe Ser	Tyr Val Ser Ser Asp Gly			
35	405	410	415			
	Thr Gln His Asn Asp	Leu Val Ala Ser Ser	Ser Asp Gln Tyr Pro Thr			
	420	425	430			
	Ile Thr Ser Asp Asn	Thr Ser Ile Ile Ile	Thr Ser Lys Ile Pro Val			
	435	440	445			
40	Asn Asn Val Pro Lys	Lys Ile Val Phe Glu	Val Thr Asn Gly Val Ala			
	450	455	460			
	Gly Leu Lys Glu Thr	Val Thr Val Leu Gln	Tyr Pro Ala Gln Phe Ile			
	465	470	475			
	Val Asn Thr Leu Gly	Thr Ala Ser Ala Trp	Arg Pro Asp Gly Ser Leu			
45	485	490	495			
	Ala Pro Gly Leu Asn	Asn Lys Ala Ile Tyr	His Val Val Val Leu Val			
	500	505	510			
	Pro Pro Glu Asn Leu	Phe Glu Asp Gly Thr	Gln Thr Ile Ile Gly Tyr			
	515	520	525			
50	Pro Pro Thr Glu Thr	Ile Ser Phe His Lys	Lys Glu Asn Asn Thr Tyr			
	530	535	540			
	Pro Ile Val Trp Ser	Asp Thr Asn Thr Thr	Lys Gln Asp Leu Glu Thr			
	545	550	555			
	Ser Arg Met Ile Ser	Pro Ser Phe Glu Leu	Ala Ser Gln Leu Gly Ala			
55	565	570	575			
	Thr Leu Pro Met Pro	Tyr Leu Glu Tyr Trp	Pro Gly Thr Ser Tyr Leu			
	580	585	590			
	Leu Asp Tyr Ser Gly	Asn Tyr Asn Asn Lys	Arg Tyr Ala Leu Phe Asn			
	595	600	605			
60	Cys Ala Phe Tyr Trp	Glu Lys Arg Lys Val	Asn Asn Asn Glu Ile Lys			
	610	615	620			
	Phe Asp Asp Trp Arg	Leu Pro Thr Glu Ala	Glu Ile Lys Leu Ile Asp			
	625	630	635			
	Lys Leu Gln His Asn	Glu Gln Ser Ala Val	Gln Ala Ile Met Thr Gly			
65	645	650	655			
	Asn Tyr Tyr Trp Asp	Ser Tyr Ser Ala Asn	Gly Ser Tyr Lys Met Gln			
	660	665	670			
	Gly Gly Gly Gly Gln	Gly Asn Ser Ser Lys	Ala Tyr Val Arg Cys Val			
	675	680	685			
70	Arg Asp Val Lys Lys	Pro Ile Arg Asp Lys	Lys Ser Gly Lys			
	690	695	700			

(2) INFORMATION FOR SEQ ID NO:338

75

(1) SEQUENCE CHARACTERISTICS:

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(A) LENGTH: 1312 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

5 (ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

10 (vi) ORIGINAL SOURCE:

(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

(A) NAME/KEY: misc\_feature

(B) LOCATION 1...1312

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:338

Lys Arg Val Asp Ser Tyr Glu Cys Arg Gln Lys Ala Cys Lys Cys Ala  
 1 5 10 15  
 20 Ile Cys Val Ile Gln Lys Phe Thr Asn Val Lys Leu Asn Asp Met Arg  
 20 20 25 30  
 Lys Ile Leu Ser Phe Leu Met Met Cys Ser Leu His Leu Gly Leu Gln  
 35 40 45  
 25 Ser Gln Thr Trp His Gly Asp Pro Asp Ser Val Ala Ala Leu Pro Ser  
 50 55 60  
 Ile Gly Ile Gln Glu Ser Ser Cys Thr Arg Ile Thr Phe Glu Val Val  
 65 70 75 80  
 Phe Pro Gly Phe Tyr Ser Val Glu Lys Arg Glu Gly Asn Gln Val Phe  
 85 90 95  
 30 Gln Arg Ile Ser Met Pro Gly Cys Gly Ser Phe Gly Asn Leu Gly Glu  
 100 105 110  
 Ala Glu Leu Pro Val Leu Lys Lys Met Ile Ala Val Pro Glu Phe Ser  
 115 120 125  
 35 Thr Ala Asn Val Ala Val Lys Ile Lys Glu Thr Glu Thr Phe Asp Asn  
 130 135 140  
 Tyr Asn Ile Tyr Pro Asn Pro Thr Tyr Val Val Glu Glu Leu Pro Glu  
 145 150 155 160  
 Gly Gly Thr Tyr Leu Val Glu Ala Phe Ala Ile Asn Asn Asp Tyr Tyr  
 165 170 175  
 40 Ser Gln Asn Val Ser Leu Pro Ser Thr His Tyr Val Tyr Ser Gln Asp  
 180 185 190  
 Gly Tyr Phe Arg Ser Gln Arg Phe Ile Glu Val Thr Leu Tyr Pro Phe  
 195 200 205  
 45 Arg Tyr Asn Pro Val Arg Gln Glu Ile Leu Phe Ala Lys Lys Ile Glu  
 210 215 220  
 Val Thr Ile Thr Phe Asp Asn Pro Gln Pro Pro Leu Gln Lys Asn Thr  
 225 230 235 240  
 Gly Ile Phe Asn Lys Val Ala Ser Ser Ala Phe Ile Asn Tyr Glu Ala  
 245 250 255  
 50 Asp Gly Lys Ser Ala Ile Glu Asn Asp Met Val Phe Ser Arg Gly Thr  
 260 265 270  
 Thr Thr Tyr Ile Ser Gly Asn Val Ala Ser Asn Leu Pro Gln Asn Cys  
 275 280 285  
 55 Asp Tyr Leu Val Ile Tyr Asp Asp Met Phe Asn Val Asn Gln Gln Pro  
 290 295 300  
 His Asp Glu Ile Lys Arg Leu Cys Glu His Arg Ala Phe Tyr Asn Gly  
 305 310 315 320  
 Phe Asp Val Ala Ala Val Ser Ile Lys Asp Val Leu Asn Ser Phe Pro  
 325 330 335  
 60 Ser Asn Ala Thr Ser Tyr Ile Asn Glu Thr Lys Leu Lys Asn Phe Ile  
 340 345 350  
 Arg Ser Val Tyr Asn Gln Ser Asn Ala Lys Arg Thr Leu Asp Gly Lys  
 355 360 365  
 65 Leu Gly Tyr Val Leu Leu Ile Gly Lys Pro Leu Ser Lys Tyr Leu Ala  
 370 375 380  
 Asp Thr Asp Asn Thr Lys Val Pro Thr Ser Phe Ile His Asn Val Ser  
 385 390 395 400  
 Leu Ile Pro Ser His Pro Thr Phe Gly Ser Ile Cys Ala Ser Asp Tyr  
 405 410 415  
 70 Phe Phe Ser Cys Val Ser Pro Leu Asp Thr Val Gly Asp Leu Phe Ile  
 420 425 430  
 Gly Arg Phe Ser Val Thr Asn Ala His Glu Leu His Asn Leu Ile Glu  
 435 440 445  
 75 Lys Thr Ile Asn Lys Glu Ile Ser Tyr Asn Pro Ile Ala His Lys Asn  
 450 455 460

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	Ile	Leu	Tyr	Ala	Glu	Gly	Lys	Gly	Cys	Asp	Ala	Pro	Ile	Leu	Arg	Leu	
	465					470					475						480
	Phe	Leu	Lys	Glu	Ile	Ala	Ser	Gly	Tyr	Thr	Val	Asn	Ser	Ile	Leu	Lys	
				485						490						495	
5	Ser	Asn	Gln	Val	Ser	Ala	Ile	Asp	Ser	Ile	Phe	Asp	Cys	Leu	Asn	Asn	
				500					505					510			
	Gly	Ser	His	His	Phe	Tyr	Phe	Asn	Thr	His	Gly	Met	Pro	Thr	Val	Trp	
			515					520				525					
10	Gly	Ile	Gly	Gln	Gly	Leu	Asp	Val	Asn	Thr	Leu	Thr	Ala	Arg	Leu	Asn	
		530					535					540					
	Asn	Thr	Ser	Ser	Gln	Gly	Leu	Cys	Thr	Ser	Leu	Ser	Cys	Ser	Ser	Ala	
	545					550					555					560	
	Val	Ala	Asp	Ser	Thr	Ile	Arg	Ser	Leu	Gly	Glu	Val	Leu	Thr	Thr	Tyr	
					565					570						575	
15	Ala	Pro	Asn	Lys	Gly	Phe	Ser	Ala	Phe	Leu	Gly	Gly	Ser	Arg	Ala	Thr	
				580					585					590			
	Gln	Tyr	Ala	Val	Tyr	Leu	Glu	Gly	Pro	Cys	Pro	Pro	Ser	Glu	Phe	Tyr	
		595						600					605				
20	Glu	Tyr	Leu	Pro	Tyr	Ser	Leu	Tyr	His	Asn	Leu	Ser	Thr	Val	Val	Gly	
		610					615					620					
	Glu	Met	Leu	Leu	Ser	Ser	Ile	Ile	Asn	Thr	Asn	Ser	Val	Asp	Thr	Tyr	
	625					630					635					640	
	Ser	Lys	Phe	Asn	Phe	Asn	Leu	Leu	Gly	Asp	Pro	Ala	Leu	Asn	Ile	Met	
				645						650					655		
25	Ala	His	Gly	Met	Glu	Val	Ser	Asn	Cys	Ile	Thr	Leu	Pro	Asn	Asn	Thr	
			660						665					670			
	Ile	Ile	Ser	Ser	Pro	Ile	Thr	Ile	Lys	Asn	Gly	Gly	Cys	Leu	Lys	Ile	
		675					680						685				
30	Pro	Glu	Lys	Gly	Val	Leu	His	Phe	Thr	Asn	Asn	Gly	Ser	Ile	Gln	Val	
		690					695					700					
	Met	Ser	Gly	Gly	Thr	Leu	Glu	Ile	Gly	Asn	Gln	Ala	Lys	Ile	Ser	Gly	
	705					710					715					720	
	Glu	Thr	Gly	Ala	Asn	Pro	Thr	Phe	Ile	Thr	Val	Tyr	Gly	Asp	Gly	Leu	
					725					730					735		
35	Ala	Ile	Asn	Lys	Gln	Val	Glu	Ile	Asp	Asn	Ile	Asp	Arg	Leu	Asn	Leu	
			740						745					750			
	Phe	Ser	Thr	His	Ser	Val	Met	Pro	Lys	Phe	His	Phe	Asp	Ser	Val	Lys	
		755					760					765					
40	Phe	Asn	Ser	Ala	Pro	Leu	Tyr	Thr	Thr	Asn	Cys	Ile	Val	Glu	Ile	Ser	
		770					775					780					
	Asn	Cys	Glu	Phe	Thr	Asn	Arg	Ser	Asp	Ile	Ile	Ser	Lys	Asn	Cys	Asp	
	785					790					795					800	
	Leu	Ser	Val	Glu	Asn	Ser	Met	Phe	Ser	Ser	Ser	Gly	Ile	Thr	Val	Phe	
				805						810					815		
45	Lys	Pro	Met	Ala	Thr	Ser	Ser	Ile	Thr	Gly	Leu	Ser	Thr	Lys	Ala	Lys	
			820						825					830			
	Ile	Thr	Asp	Asn	Thr	Phe	Phe	Ala	Thr	Gly	Asn	Phe	Ala	Tyr	His	Ile	
		835						840					845				
50	Thr	Asn	Thr	Pro	Gly	Leu	Thr	Ala	Thr	Ser	Asn	Ala	Ala	Ile	Lys	Leu	
		850					855					860					
	Asp	Asn	Ile	Pro	Glu	Tyr	Tyr	Ile	Ser	Gly	Asn	Lys	Ile	Val	Asn	Cys	
	865					870					875					880	
	Asp	Glu	Ala	Leu	Val	Leu	Asn	Asn	Ser	Gly	Asn	Arg	Thr	Asn	Arg	Leu	
				885						890					895		
55	His	Asn	Ile	Thr	Arg	Asn	Val	Ile	Lys	Asn	Cys	Arg	Ile	Gly	Ser	Thr	
			900						905					910			
	Leu	Tyr	Asn	Ser	Tyr	Gly	Ile	Tyr	Asn	Arg	Asn	Lys	Ile	Ser	Asn	Asn	
		915						920					925				
60	His	Ile	Gly	Val	Arg	Leu	Leu	Asn	Asn	Ser	Cys	Phe	Tyr	Phe	Asp	Asn	
		930						935					940				
	Ala	Pro	Val	Ile	Asn	Glu	Glu	Asp	Lys	Gln	Thr	Phe	Ile	Ser	Asn	Arg	
	945					950					955					960	
	Thr	Trp	Gln	Leu	Tyr	Ser	Ser	Asn	Gly	Thr	Phe	Pro	Leu	Asn	Phe	His	
				965						970					975		
65	Tyr	Asn	Ser	Leu	Gln	Gly	Gly	Asp	Thr	Asp	Thr	Trp	Ile	Tyr	Asn	Asp	
			980						985					990			
	Thr	Tyr	Thr	Asn	Arg	Tyr	Ile	Asp	Val	Ser	Asn	Asn	His	Trp	Gly	Asn	
		995						1000					1005				
70	Asn	Asp	Leu	Phe	Asp	Pro	Asn	Gln	Val	Phe	Asn	Thr	Pro	Asp	Leu	Phe	
		1010						1015					1020				
	Ile	Trp	Ile	Pro	Phe	Trp	Asp	Gly	Leu	Pro	Asn	Gly	Arg	Ser	Gly	Asn	
	1025					1030					1035					1040	
	Ser	Ser	Ala	Glu	Ala	Val	Glu	Phe	Gln	Thr	Ala	Leu	Asp	Cys	Ile	Gly	
				1045						1050					1055		
75	Asn	Ser	Asp	Tyr	Leu	Ser	Ala	Lys	Val	Ala	Leu	Lys	Met	Met	Val	Glu	

SUBSTITUTE SHEET (Rule 26) (RO/AU)

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      1060      1065      1070
Thr Tyr Pro Glu Ser Asp Phe Ala Ile Ala Ala Leu Lys Glu Leu Phe
      1075      1080      1085
5  Arg Ile Glu Lys Met Ser Gly Asn Asp Tyr Glu Gly Leu Lys Asp Tyr
      1090      1095      1100
Phe Arg Ser Asn Pro Thr Ile Ile Ser Ser Gln Asn Leu Phe Pro Thr
1105      1110      1115      1120
Ala Asp Phe Leu Ser Ala Arg Cys Asp Ile Val Cys Glu Asn Tyr Gln
      1125      1130      1135
10 Ser Ala Ile Asp Trp Tyr Glu Asn Arg Leu Asn Ser Glu Ile Ser Tyr
      1140      1145      1150
Gln Asp Ser Val Phe Ala Val Ile Asp Leu Gly Asp Ile Tyr Trp Asn
      1155      1160      1165
15 Met Gln Leu Asp Ser Leu Arg Gly Thr Gly Ile Asp Leu Asn Ile Leu
      1170      1175      1180
Ser Cys Glu Gln Arg Lys Ser Leu Glu Ser His Gln Asn Val Lys Asn
1185      1190      1195      1200
Tyr Leu Leu Ser Thr Leu Pro Glu Ser Thr Gly Thr Leu Leu Pro Pro
      1205      1210      1215
20 Leu Glu Cys Asn Lys Ser Ser Leu Asp Lys Ser Lys Ile Ile Ser Ile
      1220      1225      1230
Ser Pro Asn Pro Ala Lys Ala Val Val Thr Ile Ile Tyr Tyr Thr Asp
      1235      1240      1245
25 Asn Pro Ser Cys Ser Val Ile Lys Ile Tyr Gly Ile Asn Gly Ala Ser
      1250      1255      1260
Ala Asp Ile Thr Gly Leu Pro Lys His Leu Ser Glu Gly Tyr Tyr Ser
1265      1270      1275      1280
Ile Gln Phe Asn Thr Ser Asn Phe Asp Pro Gly Phe Tyr Leu Val Thr
      1285      1290      1295
30 Leu Asn Val Asp Gln Lys Ile Ile Asp Thr Glu Lys Leu Arg Ile Lys
      1300      1305      1310

```

## (2) INFORMATION FOR SEQ ID NO:339

- 35 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 938 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear
- 40 (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- 45 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Porphyromonas gingivalis
- (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...938
- 50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:339

```

Ser Glu Asn Tyr Arg Tyr Gly Lys Ile Thr Asn Gln Ile Met Ala Ile
1      5      10      15
55 Met Met Lys Ser Ile Val Phe Arg Ala Phe Leu Thr Ile Leu Leu Ser
      20      25      30
Trp Ala Ala Ile Thr Asn Pro Thr Ala Gln Glu Ile Ser Gly Met Asn
      35      40      45
60 Ala Ser Cys Leu Ala Ala Pro Ala Gln Pro Asp Thr Ile Leu Tyr Glu
      50      55      60
Ser Phe Glu Asn Gly Pro Val Pro Asn Gly Trp Leu Glu Ile Asp Ala
65      70      75      80
Asp Ala Asp Gly Ala Thr Trp Gly Ser Pro Ser Gly Ser Phe Ser Val
      85      90      95
65 Pro Tyr Gly His Asn Gly Leu Cys Thr Tyr Ser His Ile Arg Ser Gly
      100      105      110
Ile Ser Thr Ala Gly Asn Tyr Leu Ile Thr Pro Asn Ile Glu Gly Ala
      115      120      125
70 Lys Arg Val Lys Tyr Trp Val Cys Asn Gln Tyr Ser Thr Asn Pro Glu
      130      135      140
His Tyr Ala Val Met Val Ser Thr Thr Gly Thr Ala Ile Glu Asp Phe
145      150      155      160
Val Leu Leu Phe Asp Asp Ser Ile Thr Gly Lys Pro Thr Pro Leu Val
      165      170      175
75 Trp Arg Arg Arg Ile Val Asp Leu Pro Glu Gly Thr Lys Tyr Ile Ala

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				180					185					190			
	Trp	Arg	His	Tyr	Lys	Val	Thr	Asp	Ser	His	Thr	Glu	Phe	Leu	Lys	Leu	
			195					200					205				
5	Asp	Asp	Val	Thr	Val	Tyr	Arg	Ser	Ile	Glu	Gly	Pro	Glu	Pro	Ala	Thr	
		210					215					220					
	Asp	Phe	Thr	Val	Ile	Asn	Ile	Gly	Gln	Asn	Val	Gly	Arg	Leu	Thr	Trp	
	225					230						235				240	
	Asn	Tyr	Pro	Glu	Asp	Tyr	Gln	Pro	Glu	Gly	Lys	Gly	Asn	Glu	Glu	Leu	
					245							250			255		
10	Gln	Leu	Ser	Gly	Tyr	Asn	Ile	Tyr	Ala	Asn	Gly	Thr	Leu	Leu	Ala	Gln	
				260					265						270		
	Ile	Lys	Asp	Val	Ser	Ile	Leu	Glu	Tyr	Val	Asp	Ser	Thr	Tyr	Ser	Leu	
			275						280					285			
15	Arg	Asp	Asn	Pro	Leu	Gln	Val	Glu	Tyr	Cys	Val	Thr	Ala	Val	Tyr	Asp	
		290						295				300					
	Glu	Ser	Ile	Glu	Ser	Ser	Thr	Val	Cys	Gly	Thr	Leu	His	Tyr	Ala	Thr	
	305					310						315				320	
	Asp	Ala	Ile	Leu	Tyr	Glu	Asn	Phe	Glu	Asn	Gly	Pro	Val	Pro	Asn	Gly	
					325						330				335		
20	Trp	Leu	Val	Ile	Asp	Ala	Asp	Gly	Asp	Gly	Phe	Ser	Trp	Gly	His	Tyr	
				340					345					350			
	Leu	Asn	Ala	Tyr	Asp	Ala	Phe	Pro	Gly	His	Asn	Gly	Gly	His	Cys	Ser	
			355					360					365				
25	Leu	Ser	Ala	Ser	Tyr	Val	Pro	Gly	Ile	Gly	Pro	Val	Thr	Pro	Asp	Asn	
		370					375					380					
	Tyr	Leu	Ile	Thr	Pro	Lys	Val	Glu	Gly	Ala	Lys	Arg	Val	Lys	Tyr	Trp	
	385					390					395					400	
	Val	Ser	Thr	Gln	Asp	Ala	Asn	Trp	Ala	Ala	Glu	His	Tyr	Ala	Val	Met	
				405						410					415		
30	Ala	Ser	Thr	Thr	Gly	Thr	Ala	Val	Gly	Asp	Phe	Val	Ile	Leu	Phe	Glu	
				420					425					430			
	Glu	Thr	Met	Thr	Ala	Lys	Pro	Thr	Gly	Ala	Trp	Tyr	Glu	Arg	Thr	Ile	
			435					440						445			
35	Asn	Leu	Pro	Glu	Gly	Thr	Lys	Tyr	Ile	Ala	Trp	Arg	His	Tyr	Asn	Cys	
		450					455					460					
	Thr	Asp	Ile	Tyr	Phe	Leu	Lys	Leu	Asp	Asp	Ile	Thr	Val	Phe	Gly	Thr	
	465					470					475					480	
	Pro	Ala	Ser	Glu	Pro	Glu	Pro	Val	Thr	Asp	Phe	Val	Val	Ser	Leu	Ile	
					485					490					495		
40	Glu	Asn	Asn	Lys	Gly	Arg	Leu	Lys	Trp	Asn	Tyr	Pro	Asn	Gly	Tyr	Glu	
				500					505					510			
	Pro	Asp	Lys	Thr	Asp	Asp	Lys	Asp	Pro	Leu	Gln	Leu	Ala	Gly	Tyr	Asn	
			515					520					525				
45	Ile	Tyr	Ala	Asn	Gly	Ser	Leu	Leu	Val	His	Ile	Gln	Asp	Pro	Thr	Val	
		530					535					540					
	Leu	Glu	Tyr	Ile	Asp	Glu	Thr	Tyr	Ser	Ser	Arg	Asp	Asp	Gln	Val	Glu	
	545					550					555					560	
	Val	Glu	Tyr	Cys	Val	Thr	Ala	Val	Tyr	Asn	Asp	Asn	Ile	Glu	Ser	Gln	
					565						570				575		
50	Ser	Val	Cys	Asp	Lys	Leu	Ile	Tyr	Asp	Ser	Gln	Ser	Asp	Ile	Ile	Leu	
				580					585					590			
	Tyr	Glu	Gly	Phe	Glu	Ala	Gly	Ser	Ile	Pro	Glu	Gly	Trp	Leu	Leu	Ile	
			595					600					605				
55	Asp	Ala	Asp	Gly	Asp	Asn	Val	Asn	Trp	Asp	Tyr	Tyr	Pro	Trp	Thr	Met	
		610					615						620				
	Tyr	Gly	His	Asp	Ser	Glu	Lys	Cys	Ile	Ala	Ser	Pro	Ser	Tyr	Leu	Pro	
	625					630					635					640	
	Met	Ile	Gly	Val	Leu	Thr	Pro	Asp	Asn	Tyr	Leu	Val	Thr	Pro	Arg	Leu	
					645					650					655		
60	Glu	Gly	Ala	Lys	Leu	Val	Lys	Tyr	Trp	Val	Ser	Ala	Gln	Asp	Ala	Val	
				660					665					670			
	Tyr	Ser	Ala	Glu	His	Tyr	Ala	Val	Met	Val	Ser	Thr	Thr	Gly	Thr	Ala	
			675					680					685				
65	Val	Glu	Asp	Phe	Val	Leu	Leu	Phe	Glu	Glu	Thr	Met	Thr	Ala	Lys	Ala	
		690					695					700					
	Asn	Gly	Ala	Trp	Tyr	Glu	Arg	Thr	Ile	Thr	Leu	Pro	Ala	Gly	Thr	Lys	
	705					710					715					720	
	Tyr	Ile	Ala	Trp	Arg	His	Tyr	Asp	Cys	Thr	Asp	Met	Phe	Phe	Leu	Leu	
					725					730					735		
70	Leu	Asp	Asp	Ile	Thr	Val	Tyr	Arg	Ser	Thr	Glu	Thr	Val	Pro	Glu	Pro	
				740					745					750			
	Val	Thr	Asp	Phe	Val	Val	Ser	Leu	Ile	Glu	Asn	Asn	Lys	Gly	Arg	Leu	
			755					760					765				
75	Lys	Trp	Asn	Tyr	Pro	Asn	Gly	Tyr	Glu	Pro	Asp	Lys	Thr	Asp	Asp	Lys	
		770					775					780					

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Lys Pro Leu Gln Leu Thr Gly Tyr Asn Ile Tyr Ala Asn Gly Ser Leu  
 785 790 795 800  
 Leu Val His Ile Gln Asp Pro Thr Val Leu Glu Tyr Ile Asp Glu Thr  
 805 810 815  
 5 Tyr Ser Ser Arg Asp Gly Gln Val Glu Met Glu Tyr Cys Val Thr Ala  
 820 825 830  
 Val Tyr Asn Asp Asn Ile Glu Ser Gln Ser Val Cys Asp Lys Leu Asn  
 835 840 845  
 10 Tyr Thr Ile Thr Ser Leu Asp Asn Ile Gln Ser Asp Thr Ser Leu Lys  
 850 855 860  
 Ile Tyr Pro Asn Pro Ala Ser Tyr Val Val Arg Ile Glu Gly Leu Ser  
 865 870 875 880  
 Arg Ser Lys Ser Thr Ile Glu Leu Tyr Asn Ala Leu Gly Ile Cys Ile  
 885 890 895  
 15 Leu Arg Glu Glu Thr His Ser Glu Lys Thr Glu Ile Asp Val Ser Arg  
 900 905 910  
 Leu Asn Asp Gly Val Tyr Leu Ile Lys Val Val Gly Gly Asn Lys Thr  
 915 920 925  
 20 Thr Thr Glu Lys Val Glu Ile Lys Arg Pro  
 930 935

(2) INFORMATION FOR SEQ ID NO:340

- 25 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 606 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
 30 (ii) MOLECULE TYPE: protein  
 (iii) HYPOTHETICAL: YES  
 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Porphyromonas gingivalis  
 35 (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...606  
 40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:340

Ile Ile Phe Cys Thr Ile His His Ser Glu Leu Glu Ile Met Asn Ser  
 1 5 10 15  
 45 Ile Met Lys Tyr Gln Leu Tyr Thr Ala Val Ile Met Ala Leu Ser Val  
 20 25 30  
 Ser Ser Val Cys Gly Gln Thr Pro Arg Asn Thr Glu Thr Lys Arg Pro  
 35 40 45  
 Asp Thr Leu Arg Arg Glu Leu Thr Ile Val Asn Asp Gln Thr Val Glu  
 50 55 60  
 Met Glu His Ala Asp Pro Leu Pro Ala Ala Tyr Lys Ala Ile Glu Pro  
 65 70 75 80  
 Arg Leu Lys Pro Phe Arg Pro Glu Tyr Asn Lys Arg Thr Phe Gly Phe  
 85 90 95  
 55 Val Pro Glu Val Ser Ser Ser Gly Arg Asn Asn Leu Pro Asn Ile Leu  
 100 105 110  
 Pro Thr Glu Gly His Met Lys His Arg Gly Tyr Leu Asn Ile Gly Ile  
 115 120 125  
 Gly His Thr Leu Asn Gln Arg Met Asp Ala Gly Tyr Arg Leu Ile Asp  
 130 135 140  
 60 Ala Glu Gln Glu Arg Leu Asn Leu Phe Leu Ser Tyr Arg Gly Met Lys  
 145 150 155 160  
 Ser Ala Phe Asn Thr Gly Asp Phe Asp Gly Asp Arg Lys Asp Arg Arg  
 165 170 175  
 65 Met Met Ala Gly Val Asp Tyr Glu Gln Arg Arg Pro Ser Phe Val Leu  
 180 185 190  
 Ala Thr Gly Leu Tyr Tyr Ser Asn His Tyr Phe Asn Asn Tyr Gly Arg  
 195 200 205  
 Gly Ala Thr Thr Asn Val Gly Ser Ile Pro Gln Leu Ser Thr Pro Val  
 210 215 220  
 70 Thr Pro Gln Met Asp Asn Gly Thr His Asn Val Arg Val Tyr Leu Gly  
 225 230 235 240  
 Ala Lys Asn Asp Val Ile Asp Ala Arg Ile Asp Tyr Arg Phe Phe Arg  
 245 250 255  
 75 Ser Ile Pro Tyr Leu Gly Thr Asp Pro Met Lys Ala Leu Thr Glu His  
 260 265 270

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      Thr Pro Glu Leu Asn Val Thr Met Ser Asn Glu Leu Ser Asp Asp Ile
      275                280                285
Lys Leu Gly Val Glu Val Arg Thr Gly Gly Leu Phe Phe Ala Lys Asn
      290                295                300
5  Ser Glu Met Ile Gln Thr Gly Val Leu Ser Glu Thr Asp Arg Asn Leu
      305                310                315                320
Tyr Tyr Val Glu Gly Ala Pro Thr Ile Gly Phe Val Gly Asp Ser Asp
      325                330                335
      Asn Met Gln Trp Asn Ile Gln Ala Gly Val Gly Ile Ser Ser His Phe
      340                345                350
10 Gly Ala Lys Gly Arg Leu Phe Phe Trp Pro Lys Leu Asp Ala Ser Leu
      355                360                365
Ser Ile Phe Pro Ser Trp Arg Val Tyr Ala Lys Ala Phe Gly Gly Val
      370                375                380
15 Ile Arg Asn Gly Leu Ala Asp Val Met Gln Glu Glu Met Pro Tyr Leu
      385                390                395                400
Met Pro Asn Thr Ile Val Leu Pro Ser Arg Asn Ala Leu Thr Ala Gln
      405                410                415
20 Leu Gly Val Lys Gly Asn Ile Ala Asp Val Val Arg Met Glu Val Tyr
      420                425                430
Gly Asp Phe Ser Lys Leu Thr Gly Val Pro Phe Tyr Thr Pro Thr Leu
      435                440                445
Pro Leu Tyr Asn Pro Ser Asp Leu Tyr Gln Tyr Asn Val Ser Phe Leu
      450                455                460
25 Pro Ile Tyr Ala Asp Gly Ser Arg Trp Arg Ala Gly Gly Lys Leu Glu
      465                470                475                480
Tyr Ser Tyr Arg Asp Met Leu Arg Phe Leu Val Asp Ala Ser Tyr Gly
      485                490                495
30 Lys Trp Asn Leu Asp Gly Gly Leu Val Ala Ser Met Gln Pro Asp Leu
      500                505                510
Ile Leu Lys Ala Glu Val Gly Val His Pro Ile Ala Pro Leu Asp Val
      515                520                525
Arg Leu Arg Tyr Thr Gln Leu Asn Gly Arg Tyr Arg Tyr Ser Phe Gly
      530                535                540
35 Ser Ala Gly Ser Glu Ala Leu Gly Ile Gly Asn Val His Leu Leu Ser
      545                550                555                560
Ala Asp Val Ser Tyr Lys Leu Lys Lys Asn Leu Ser Leu Tyr Leu Lys
      565                570                575
40 Ile Asp Asn Met Leu Ala Glu Thr Thr Glu Leu Ile Gly Tyr Tyr Pro
      580                585                590
Met Gln Pro Phe His Cys Phe Ala Gly Phe Ser Trp Thr Phe
      595                600                605

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45  (2) INFORMATION FOR SEQ ID NO:341
      (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 357 amino acids
          (B) TYPE: amino acid
          (D) TOPOLOGY: linear
50  (ii) MOLECULE TYPE: protein
      (iii) HYPOTHETICAL: YES
55  (vi) ORIGINAL SOURCE:
          (A) ORGANISM: Porphyromonas gingivalis
      (ix) FEATURE:
          (A) NAME/KEY: misc_feature
60  (B) LOCATION 1...357
      (xi) SEQUENCE DESCRIPTION: SEQ ID NO:341

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```

65  Asn Ser His Ala Thr Val Ser Val Ile Cys Ser Met Met Glu Lys Cys
      1         5         10        15
Ile Phe Ala His Tyr Pro His Asn Leu Val Phe Met Ile Arg Lys His
      20        25        30
Phe Gly Ile Ile Leu Gly Phe Leu Ser Leu Val Phe Ser Ala Gly Ala
      35        40        45
70  Gln Gln Glu Lys Gln Val Phe His Phe Leu Asn Leu Pro Ala Thr Ala
      50        55        60
Gln Ala Leu Ala Ala Gly Gly Lys Ala Ile Thr Ile Val Asp Asp Asn
      65        70        75        80
75  Pro Gly Leu Ala Phe Glu Asn Pro Ala Leu Leu Gly Tyr Glu Ser Gly
      85        90        95

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Gly Arg Ala Phe Leu Ser Tyr Leu Tyr Tyr Met Ser Gly Ser His Met  
 100 105 110  
 Gly Asn Ala Cys Tyr Ala Ser Ser Val Gly Glu Arg Gly Met Trp Gly  
 115 120 125  
 5 Val Gly Met Arg Phe Leu Asn Tyr Gly Ser Met Gln Gly Tyr Asp Gln  
 130 135 140  
 Asn Ala Ile Ala Thr Gly Ser Phe Ser Ala Ser Asp Ile Ala Val Gln  
 145 150 155 160  
 10 Gly Phe Tyr Ser His Glu Leu Ser Asn His Phe Arg Gly Gly Val Ser  
 165 170 175  
 Leu Lys Ala Leu Tyr Ser Ser Ile Glu Thr Tyr Ser Ser Phe Gly Leu  
 180 185 190  
 Gly Val Asp Val Gly Ile Ser Tyr Tyr Asp Asp Asp Lys Gly Tyr Ser  
 195 200 205  
 15 Ala Ser Ala Leu Phe Lys Asn Val Gly Ala Gln Leu Lys Gly Tyr Asn  
 210 215 220  
 Glu Glu Arg Glu Pro Leu Asp Trp Asp Phe Gln Leu Gly Phe Ser Arg  
 225 230 235 240  
 20 Ser Phe Ile Asn Ala Pro Phe Arg Leu His Ile Thr Leu Phe Asn Leu  
 245 250 255  
 Asn Pro His Tyr Phe Lys Arg Leu Val Pro Arg Asp Leu Ser Lys Met  
 260 265 270  
 Gln Lys Phe Leu Arg His Phe Ser Ile Gly Ala Glu Phe Thr Pro Ser  
 275 280 285  
 25 Glu Arg Phe Trp Val Gly Leu Gly Tyr Thr Pro Gln Ile Ala Gln Asp  
 290 295 300  
 Phe Glu Val Glu Gly Gly Asn Lys Trp Gly Gly Leu Ser Ala Gly Val  
 305 310 315 320  
 30 Gly Phe Thr Ser Gly Val Val Arg Val Gly Val Ser Ala Ala Thr Tyr  
 325 330 335  
 His Pro Ala Ala Leu Ser Phe Met Cys Ser Val Gly Ile Arg Leu Asp  
 340 345 350  
 Asp Lys Ser Ile Phe  
 355

(2) INFORMATION FOR SEQ ID NO:342

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 337 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(iv) ORIGINAL SOURCE:

(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

- (A) NAME/KEY: misc feature  
 (B) LOCATION 1...337

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:342

Pro Gln Pro Val Gly Leu Lys Glu Ile Thr Ile Lys Pro Met Cys Leu  
 1 5 10 15  
 Glu Pro Ile Ile Ala Pro Ile Ser Ser Glu Leu Leu Glu Gln Glu Leu  
 20 25 30  
 60 Thr Ala Asp Arg Phe Leu Arg Met Thr Asn Lys Ala Gly Asn Glu Ile  
 35 40 45  
 Tyr Val Phe Thr Ala Glu Glu Ala Pro His Cys Met Lys Glu Val Gly  
 50 55 60  
 65 Arg Leu Arg Glu Glu Ala Phe Arg His Tyr Gly Gly Thr Gly Lys  
 65 70 75 80  
 Ala Ile Asp Ile Asp Glu Phe Asp Thr Met Pro Gly Ser Tyr Lys Gln  
 85 90 95  
 Leu Ile Val Trp Asp Pro Gln Asn Lys Ala Ile Leu Gly Gly Tyr Arg  
 100 105 110  
 70 Phe Ile Tyr Gly Arg Asp Val Ala Phe Asp Thr Asp Gly Lys Pro Leu  
 115 120 125  
 Leu Ala Thr Ala Glu Met Phe Arg Phe Ser Asp Ala Phe Leu His Asp  
 130 135 140  
 75 Tyr Leu Pro Tyr Thr Val Glu Leu Gly Arg Ser Phe Val Ser Leu Gln  
 145 150 155 160

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Tyr Gln Ser Thr Arg Met Gly Thr Lys Ala Ile Phe Val Leu Asp Asn  
 165 170 175  
 Leu Trp Asp Gly Ile Gly Ala Leu Thr Val Val Asn Pro Glu Ala Leu  
 180 185 190  
 5 Tyr Phe Tyr Gly Lys Val Thr Met Tyr Lys Asp Tyr Asp Arg Arg Ala  
 195 200 205  
 Arg Asn Leu Ile Leu Tyr Phe Leu Arg Lys His Phe Ser Asp Pro Glu  
 210 215 220  
 10 Gly Leu Val Lys Pro Ile His Pro Leu Pro Ile Glu Ile Ser Ala Glu  
 225 230 235 240  
 Asp Glu Ala Leu Phe Ser Ser Ser Asp Phe Asp Thr Asn Tyr Lys Thr  
 245 250 255  
 Leu Asn Ile Glu Val Arg Lys Leu Gly Ile Asn Ile Pro Pro Leu Val  
 260 265 270  
 15 Ser Ala Tyr Ile Ala Leu Ser Pro Glu Met Arg Val Phe Gly Thr Ala  
 275 280 285  
 Val Asn Glu Ser Phe Gly Glu Val Glu Glu Thr Gly Ile Phe Ile Ala  
 290 295 300  
 20 Val Gly Lys Ile Leu Glu Glu Lys Lys Gln Arg His Ile Glu Ser Phe  
 305 310 315 320  
 Ile Leu Ser Arg Asn Glu Lys Lys Gly Leu Asp Ser Ser Asn Gly Arg  
 325 330 335  
 Ser

25

(2, INFORMATION FOR SEQ ID NO:343

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 566 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

30

(ii) MOLECULE TYPE: protein

35

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Porphyromonas gingivalis

40

(ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...566

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:343

Tyr Asp Gly Ala Arg Leu Val Tyr Thr Leu Phe Arg Asn Arg Asn Asp  
 1 5 10 15  
 Ile His Pro Met Lys Thr Ile Val Arg Tyr Ser Arg Leu Pro Val Ala  
 20 25 30  
 50 Leu Phe Phe Cys Leu Leu Gly Ala Val His Leu Ser Val Glu Ala Gln  
 35 40 45  
 Met Leu Asn Thr Pro Phe Glu Leu Ser Asp Gln Ile Val Leu Ser Pro  
 50 55 60  
 55 Thr Glu Arg Gln Tyr Arg Glu Ile Cys Val Gln Thr Lys Glu Lys Arg  
 65 70 75 80  
 Gly Ala Asp Leu Phe Pro Leu Ser Asp Lys Leu Arg Asp Ser Ala Tyr  
 85 90 95  
 Val Arg Phe Gly Ser Ala Tyr Gly Asp Ile Ala Gly Asp Tyr Leu Pro  
 100 105 110  
 60 Tyr Asn Gly Asn Asn Tyr Ser Ser Leu Ser Leu Glu Ser Gly Gly Arg  
 115 120 125  
 Ile Ser Val Arg Asn Tyr Gly Thr Leu Gln Gly Ser Ala Ser Tyr Ser  
 130 135 140  
 65 Arg Gly Met His Lys Arg Ile Gly Trp Asn Ala Leu Arg Asn Ala Glu  
 145 150 155 160  
 Ala Tyr Tyr Pro Tyr Leu Val Ser Asp Ser Thr Gly Gly Asp Tyr His  
 165 170 175  
 Phe Glu Asp Tyr Arg Leu Ala Gly Tyr Tyr Ser Phe Arg Ala Gly Arg  
 180 185 190  
 70 Leu Pro Leu Gly Ile Gly Phe Ser Tyr Arg Gly Glu Val Ala Tyr Arg  
 195 200 205  
 Leu Thr Asp Pro Arg Thr Thr Asn Thr Thr Gly Ala Leu Glu Leu Ser  
 210 215 220  
 75 Cys Ala Thr Ser Leu Thr Pro Arg Glu Asn Arg Leu Ser Leu Ser  
 225 230 235 240

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(2) INFORMATION FOR SEQ ID NO:344

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 819 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:  
(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:  
(A) NAME/KEY: misc\_feature  
(B) LOCATION 1...819

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:344

Arg	Thr	Asn	Val	Phe	Leu	Ser	Leu	Ser	His	Lys	Ile	Gly	Arg	Arg	Gly
1				5					10					15	
Ala	Ser	Cys	Ser	Asn	Arg	Asn	Ala	Trp	Met	Ala	Glu	Asn	Lys	Pro	Ser
			20					25					30		
Ser	Pro	Glu	Pro	Asp	Asn	Thr	Gly	Val	Gly	Asn	Ser	Pro	Ser	Asp	Tyr
		35					40					45			
Leu	His	Gly	Glu	Ala	Ile	Ile	Pro	Pro	Leu	Ser	Ser	Leu	Ser	Asn	Phe
	50					55					60				
Asn	Asp	Lys	Arg	Phe	Met	Lys	Lys	Leu	His	Met	Ile	Ala	Ala	Leu	Ala
65					70					75					80
Val	Leu	Pro	Phe	Cys	Leu	Thr	Ala	Gln	Ala	Pro	Val	Ser	Asn	Ser	Glu
				85					90					95	

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	Ile	Asp	Ser	Leu	Ser	Asn	Val	Gln	Leu	Gln	Thr	Val	Gln	Val	Val	Ala
				100					105					110		
	Thr	Arg	Ala	Thr	Ala	Lys	Thr	Pro	Val	Ala	Tyr	Thr	Asn	Val	Arg	Lys
			115					120					125			
5	Ala	Glu	Leu	Ser	Lys	Ser	Asn	Tyr	Gly	Arg	Asp	Ile	Pro	Tyr	Leu	Leu
		130					135					140				
	Met	Leu	Thr	Pro	Ser	Val	Val	Ala	Thr	Ser	Asp	Ala	Gly	Thr	Gly	Ile
		145				150					155					160
10	Gly	Tyr	Ser	Gly	Phe	Arg	Val	Arg	Gly	Thr	Asp	Ala	Asn	Arg	Ile	Asn
				165						170					175	
	Ile	Thr	Thr	Asn	Gly	Val	Pro	Leu	Asn	Asp	Ser	Glu	Ser	Gln	Ser	Val
				180					185					190		
	Phe	Trp	Val	Asn	Met	Pro	Asp	Phe	Ala	Ser	Ser	Ile	Glu	Asp	Leu	Gln
			195					200					205			
15	Val	Gln	Arg	Gly	Val	Gly	Thr	Ser	Thr	Asn	Gly	Ala	Gly	Ala	Phe	Gly
		210					215					220				
	Ala	Ser	Val	Asn	Met	Arg	Thr	Asp	Asn	Leu	Gly	Leu	Ala	Pro	Tyr	Gly
		225				230					235					240
20	Arg	Val	Asp	Leu	Ser	Gly	Gly	Ser	Phe	Gly	Thr	Phe	Arg	Arg	Ser	Val
				245						250					255	
	Lys	Leu	Gly	Ser	Gly	Arg	Ile	Gly	Arg	His	Trp	Ala	Val	Asp	Ala	Arg
				260					265					270		
	Leu	Ser	Lys	Ile	Gly	Ser	Asp	Gly	Tyr	Val	Asp	Arg	Gly	Ser	Val	Asp
			275					280					285			
25	Leu	Lys	Ser	Tyr	Phe	Ala	Gln	Val	Gly	Tyr	Phe	Gly	Ser	Asn	Thr	Ala
		290				295						300				
	Leu	Arg	Phe	Ile	Thr	Phe	Gly	Gly	Lys	Glu	Val	Thr	Gly	Ile	Ala	Trp
		305				310					315					320
30	Asn	Gly	Leu	Ser	Lys	Glu	Asp	Glu	Ala	Lys	Tyr	Gly	Arg	Arg	Tyr	Asn
				325						330					335	
	Ser	Ala	Gly	Leu	Met	Tyr	Val	Asp	Ala	Gln	Gly	Val	Pro	His	Tyr	Tyr
				340					345					350		
	His	Asn	Thr	Asp	Asn	Tyr	Glu	Gln	Arg	His	Tyr	His	Ala	Ile	Met	Thr
			355					360					365			
35	His	Ser	Phe	Ser	Pro	Ser	Val	Ile	Leu	Asn	Leu	Thr	Ala	His	Tyr	Thr
			370				375					380				
	Ala	Gly	Tyr	Gly	Tyr	Thr	Asp	Glu	Tyr	Arg	Thr	Gly	Arg	Lys	Leu	Lys
		385				390					395					400
40	Glu	Tyr	Ala	Leu	Gln	Pro	Tyr	Val	Glu	Asn	Ser	Val	Thr	Val	Lys	Lys
				405						410					415	
	Thr	Asp	Leu	Ile	Arg	Gln	Lys	Tyr	Leu	Asp	Asn	Asp	Phe	Gly	Gly	Leu
				420					425					430		
	Ile	Gly	Ser	Leu	Asn	Trp	His	Thr	Gly	Ala	Trp	Asp	Leu	Gln	Phe	Gly
			435					440					445			
45	Ala	Ser	Gly	Asn	Ile	Tyr	Lys	Gly	Asp	His	Phe	Gly	Arg	Ile	Thr	Tyr
			450				455					460				
	Ile	Lys	Lys	Tyr	Asn	Gln	Pro	Leu	Ala	Pro	Asp	Phe	Glu	Tyr	Tyr	Arg
		465				470					475					480
50	Asn	Arg	Ala	Asp	Lys	Arg	Glu	Gly	Ala	Ala	Phe	Ala	Lys	Ala	Asn	Trp
				485						490					495	
	Gln	Ile	Thr	Pro	Glu	Leu	Asn	Met	Tyr	Ala	Asp	Leu	Gln	Tyr	Arg	Thr
				500					505					510		
	Ile	Gly	Tyr	Thr	Ile	Asn	Gly	Ile	Thr	Asp	Glu	Tyr	Asp	Glu	Val	Gln
			515				520						525			
55	Gly	Ser	Met	Gln	His	Ile	Asp	Leu	Asp	Lys	Thr	Phe	Arg	Phe	Leu	Asn
			530				535					540				
	Pro	Lys	Ala	Gly	Leu	Thr	Ser	Phe	Asp	Asp	Ala	His	Thr	Ala	Tyr	
			545			550				555					560	
60	Ala	Ser	Val	Ala	Val	Ala	His	Arg	Glu	Pro	Asn	Arg	Thr	Asn	Tyr	Thr
				565						570					575	
	Glu	Ala	Gly	Ile	Gly	Gln	Tyr	Pro	Thr	Pro	Glu	Arg	Leu	Ile	Asp	Tyr
				580					585					590		
	Glu	Leu	Gly	Tyr	Arg	Tyr	Ala	Ser	Pro	Leu	Leu	Ser	Ala	Gly	Val	Gly
			595					600					605			
65	Leu	Tyr	Tyr	Met	Gln	Tyr	Lys	Asp	Gln	Leu	Val	Leu	Asp	Gly	Arg	Leu
			610				615						620			
	Ser	Asp	Val	Gly	Gln	Met	Leu	Thr	Ser	Asn	Val	Pro	Asp	Ser	Tyr	Arg
		625				630					635					640
70	Met	Gly	Leu	Glu	Leu	Thr	Leu	Gly	Trp	Gln	Ile	Leu	Pro	Arg	Leu	Leu
				645						650					655	
	Arg	Trp	Asp	Ala	Ser	Phe	Thr	Met	Ser	Arg	Asn	Lys	Ile	Asp	Arg	Tyr
				660					665					670		
	Val	Gln	Tyr	Thr	Ser	Val	Tyr	Asp	Ala	Asp	Tyr	Asn	Trp	Leu	Glu	Leu
			675					680					685			
75	Lys	Glu	Glu	Thr	Leu	Glu	Ser	Thr	Asp	Ile	Ala	Tyr	Ser	Pro	Asn	Val

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5                   690                                   695                                   700  
 Ile Ala Gly Ser Met Leu Thr Leu Ser His Ala Gly Phe Glu Met Ala  
 705                   710                   715                   720  
 Trp Thr Ser Arg Phe Val Ser Lys Gln Tyr Leu Asp Asn Thr Gln Arg  
 725                   730                   735  
 Ser Asp Arg Met Leu Ser Ser Tyr Trp Val Asn Asp Leu Arg Leu Gly  
 740                   745                   750  
 Tyr Val Leu Pro Val His Phe Val Lys Arg Val Ala Leu Gly Val Gln  
 755                   760                   765  
 10   Leu Asn Asn Leu Phe Asn Leu Met Tyr Ala Ser Asn Ala Tyr Ile Tyr  
 770                   775                   780  
 Asp Ala Gly Tyr Val Gln Ala Ser Gly Glu Leu Ser Ala Tyr Ala Asp  
 785                   790                   795                   800  
 15   Leu Arg Tyr Tyr Pro Gln Ala Gly Phe Asn Ala Leu Gly Ser Leu Thr  
 805                   810                   815  
 Ile Asp Phe

20   (2) INFORMATION FOR SEQ ID NO:345

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 532 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

(A) NAME/KEY: misc\_feature

(B) LOCATION 1...532

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:345

40   Tyr Arg Arg Ser Gly Arg Val Cys Pro Arg Ile Leu Arg Asn Lys Arg  
 1                   5                   10                   15  
 Ser Tyr Ala Asp Thr Arg Leu Gln Pro Arg Arg Ala Val Arg Leu Arg  
 20                   25                   30  
 Ala Gly Thr Arg Thr Lys Met Lys Arg Arg Phe Leu Ser Leu Leu Leu  
 35                   40                   45  
 45   Leu Tyr Ile Leu Ser Ser Ile Ser Leu Ser Ala Gln Arg Phe Pro Met  
 50                   55                   60  
 Val Gln Gly Ile Glu Leu Asp Thr Asp Ser Leu Phe Ser Leu Pro Lys  
 65                   70                   75                   80  
 Arg Pro Trp Arg Ala Ile Gly Lys Thr Ile Gly Val Asn Leu Ala Val  
 85                   90                   95  
 50   Trp Gly Phe Asp His Phe Ile Met Asn Glu Asp Phe Ala Asp Ile Ser  
 100                   105                   110  
 Trp Gln Thr Ile Lys Ser Asn Phe Gln Thr Gly Phe Gly Trp Asp Asn  
 115                   120                   125  
 55   Asp Lys Phe Val Thr Asn Leu Phe Ala His Pro Tyr His Gly Ser Leu  
 130                   135                   140  
 Tyr Phe Asn Ala Ala Arg Ser Asn Gly Leu Ser Phe Arg His Ser Ala  
 145                   150                   155                   160  
 60   Pro Phe Ala Phe Phe Gly Ser Leu Met Trp Glu Leu Leu Met Glu Asn  
 165                   170                   175  
 Glu Pro Pro Ser Ile Asn Asp Leu Cys Ala Thr Thr Ile Gly Gly Ile  
 180                   185                   190  
 Ala Leu Gly Glu Met Gly His Arg Leu Ser Asp Leu Leu Ile Asp Asn  
 195                   200                   205  
 65   Arg Thr Thr Gly Trp Glu Arg Met Gly Arg Glu Val Ala Ile Ala Leu  
 210                   215                   220  
 Ile Asn Pro Met Arg Phe Leu Asn Arg Leu Thr Ala Gly Glu Val Thr  
 225                   230                   235                   240  
 Ser Val Gly Ser Arg Ser Gly Gln Ile Phe Gln Ser Val Pro Ile Asn  
 245                   250                   255  
 70   Ile Val Val Asp Ala Gly Phe Arg Phe Leu Ala Asp Lys Arg His Ala  
 260                   265                   270  
 Arg Thr Gly Ala Thr Ala Leu Thr Leu Asn Leu Arg Phe Asp Tyr Gly  
 275                   280                   285  
 75   Asp Pro Phe Arg Ser Glu Thr Phe Ser Pro Tyr Asp Phe Phe Gln Phe

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      290      295      300
Lys Ala Gly Leu Ser Phe Ser Glu Ser Gln Pro Leu Leu Ser Gln Ile
305      310      315      320
5  Asn Leu Ile Gly Ile Leu Ser Gly Cys Gln Leu Leu Ala His Glu Arg
      325      330      335
    Thr Val Leu Val Gly Gly Leu Phe Gln His Phe Asp Tyr Tyr Asn Ser
      340      345      350
    Glu Lys Arg Ile Ser Lys Asn Ser Glu Glu Val Leu Val Thr Pro Tyr
      355      360      365
10  Arg Ile Ser Gln Val Ala Ala Leu Gly Gly Gly Leu Ile Phe Gln His
      370      375      380
    His Gly Lys Phe Arg Arg Arg Pro Leu Glu Leu Tyr Ala Glu Thr Tyr
      385      390      395      400
15  Leu Asn Val Val Pro Met Gly Ala Ser Leu Ser Asp His Tyr Asn Val
      405      410      415
    Asp Asn Arg Asp Tyr Asn Leu Gly Ser Gly Leu Ser Gly Lys Leu Tyr
      420      425      430
    Leu Gly Ala Thr Tyr Asn Asp Leu Trp Ser Trp Leu Leu Gly Val Glu
      435      440      445
20  Ser Tyr Arg Leu Tyr Thr Trp Ile Gly Tyr Glu Glu Pro His Gln Lys
      450      455      460
    Asn Thr Asp Val Ser Ser Phe Met Val Gln Gly Asp Glu Ser Lys Ala
      465      470      475      480
25  Arg Leu Leu Val Thr Ser Ser Glu Phe Ala Phe His Pro Gly Pro Trp
      485      490      495
    His Val Ala Ile Val Ala Arg Arg Phe Ile Arg Lys Thr Ala Tyr Gln
      500      505      510
    Phe Tyr Pro Asn Val Ser Phe Asp Thr Gly Asp Ile Gln Leu Arg Val
      515      520      525
30  Gly Phe His Phe
      530

```

(2) INFORMATION FOR SEQ ID NO:346

- 35 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 300 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear
- 40 (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- 45 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Porphyromonas gingivalis
- (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...300
- 50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:346

```

Lys Arg Arg Lys Lys Gln Met Lys Arg Leu Ile Val Phe Leu Ala Met
1 5 10 15
55 Gly Gly Leu Leu Phe Thr Leu Ala Asn Ala Gln Glu Ala Asn Thr Ala
      20 25 30
    Ser Asp Thr Pro Lys Lys Asp Trp Thr Ile Lys Gly Val Thr Gly Leu
      35 40 45
60 Asn Ala Ser Gln Thr Ser Leu Thr Asn Trp Ala Ala Gly Gly Glu Asn
      50 55 60
    Thr Val Ala Gly Asn Leu Tyr Leu Asn Ile Asp Ala Asn Tyr Leu Lys
      65 70 75 80
    Asp Lys Trp Ser Trp Asp Asn Gly Leu Arg Thr Asp Phe Gly Leu Thr
      85 90 95
65 Tyr Thr Thr Ala Asn Lys Trp Asn Lys Ser Val Asp Lys Ile Glu Leu
      100 105 110
    Phe Thr Lys Ala Gly Tyr Glu Ile Gly Lys His Trp Tyr Gly Ser Ala
      115 120 125
70 Leu Phe Thr Phe Leu Ser Gln Tyr Ala Lys Gly Tyr Glu Lys Pro Ser
      130 135 140
    Asp His Leu Thr Gly Val Lys His Ile Ser Asn Phe Phe Ala Pro Ala
      145 150 155 160
    Tyr Leu Thr Leu Gly Ile Gly Ala Asp Tyr Lys Pro Asn Glu Lys Phe
      165 170 175
75 Ser Leu Tyr Leu Ser Pro Thr Thr Gly Lys Leu Thr Val Val Ala Asp

```

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180 185 190  
 Asp Tyr Leu Ser Ser Leu Gly Ala Phe Gly Val Lys Val Gly Glu Lys  
 195 200 205  
 5 Thr Met Phe Glu Leu Gly Ala Leu Val Val Gly Ser Ala Asn Ile Asn  
 210 215 220  
 Leu Met Glu Asn Val Asn Leu Ile Thr Lys Ala Ser Phe Phe Ser Ala  
 225 230 235 240  
 Tyr Thr His Asp Phe Gly Asn Ile Asp Ile Asn Trp Glu Ala Met Leu  
 245 250 255  
 10 Ala Met Lys Ile Asn Lys Phe Leu Thr Ala Thr Ile Ala Thr Asn Leu  
 260 265 270  
 Ile Tyr Asp Asp Asp Val Lys Ile Asn Asp Gly Pro Lys Ile Gln Phe  
 275 280 285  
 15 Lys Glu Val Val Gly Val Gly Val Ala Tyr Thr Phe  
 290 295 300

(2) INFORMATION FOR SEQ ID NO:347

- 20 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 221 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
 25 (ii) MOLECULE TYPE: protein  
 (iii) HYPOTHETICAL: YES  
 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Porphyromonas gingivalis  
 30 (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...221  
 35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:347

Thr Arg Glu Ser Val Leu His Cys Arg Thr Lys Leu Lys Lys Glu Arg  
 1 5 10 15  
 40 Lys Met Lys Lys Met Ile Leu Ala Ala Thr Met Leu Leu Ala Thr Ile  
 20 25 30  
 Gly Phe Ala Asn Ala Gln Ser Arg Pro Ala Leu Arg Leu Asp Ala Asn  
 35 40 45  
 Phe Val Gly Ser Asn Leu Met Gln Lys Val Ala Asn Thr Ser Val Asn  
 50 55 60  
 45 Asn Lys Met Ile Val Gly Leu Arg Val Gly Ala Ala Glu Phe Ala  
 65 70 75 80  
 Leu Ser Asn Asp Gly Phe Tyr Leu Ala Pro Gly Leu Ala Tyr Thr Met  
 85 90 95  
 50 Arg Gly Ala Lys Met Glu Ser Leu Ser Glu Thr Thr Thr Arg Leu His  
 100 105 110  
 Tyr Leu Gln Ile Pro Val Asn Ala Gly Met Arg Phe Ser Phe Ala Asp  
 115 120 125  
 Asn Met Ala Ile Ser Leu Glu Ala Gly Pro Tyr Phe Ala Tyr Gly Val  
 130 135 140  
 55 Ala Gly Thr Ile Lys Thr Lys Val Ala Gly Val Thr Ala Ser Val Asp  
 145 150 155 160  
 Ala Phe Gly Asp Asn Gly Tyr Asn Arg Phe Asp Leu Gly Leu Gly Leu  
 165 170 175  
 60 Ser Ala Ala Leu Ser Tyr Asp Arg Tyr Tyr Val Gln Ile Gly Tyr Glu  
 180 185 190  
 His Gly Leu Leu Asn Met Leu Lys Asp Ala Pro Asp Lys Thr Ser Leu  
 195 200 205  
 Arg Asn His Asp Phe Phe Val Gly Leu Gly Val Arg Phe  
 210 215 220

(2) INFORMATION FOR SEQ ID NO:348

- 70 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 248 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
 (ii) MOLECULE TYPE: protein  
 75 (iii) HYPOTHETICAL: YES

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(vi) ORIGINAL SOURCE:

(A) ORGANISM: Porphyromonas gingivalis

5

(ix) FEATURE:

(A) NAME/KEY: misc\_feature

(B) LOCATION 1...248

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:348

10

```

Ile Lys Arg Ile Glu Met Lys Arg Ile Phe Thr Val Ala Leu Val Leu
1      5      10      15
Leu Ala Ser Val Thr Met Ala Ile Gly Gln Ser Arg Pro Ala Leu Arg
20      25      30
15 Val Asp Ala Asn Phe Val Gly Ser Asn Gln Ser Met Lys Arg Asp Gly
35      40      45
Tyr Val Trp Asp Thr Lys Met Asn Val Gly Leu Arg Val Gly Ala Ala
50      55      60
20 Ala Glu Phe Met Ile Gly Ser Arg Gly Phe Tyr Leu Ala Pro Gly Leu
65      70      75      80
Asn Tyr Thr Met Lys Gly Ser Lys Thr Glu Trp Asp Ile Pro Glu Met
85      90      95
Val Pro Gly Thr Tyr Ile Thr Met Val Ser Thr Arg Leu His Tyr Leu
100      105      110
25 Gln Leu Pro Ile Asn Ala Gly Met Arg Phe Asp Leu Met Asn Asp Met
115      120      125
Ala Val Ser Ile Glu Ala Gly Pro Phe Leu Ala Tyr Gly Ile Tyr Gly
130      135      140
30 Thr Tyr Arg Gln Lys Leu Glu Gly Trp Lys Pro Asn Asn Tyr Ser Thr
145      150      155      160
Glu Phe Phe Gly Pro Thr Leu Gly Gly Pro Thr Asn Ile Arg Trp Asp
165      170      175
Ile Gly Ala Asn Ile Ile Ala Ala Phe His Tyr Lys Arg Tyr Tyr Ile
180      185      190
35 Gln Ile Gly Tyr Glu His Gly Phe Val Asp Ile Val Ser Gly Gly Gly
195      200      205
Ser Asp Ile Pro Arg Leu Asn Asp Asn Arg Gln Ser Ser Ser Thr Thr
210      215      220
40 Ala Leu Arg Glu Lys Gly Asn Asn Glu Tyr Ala Tyr Asn Arg Asp Phe
225      230      235      240
Phe Val Gly Ile Gly Tyr Arg Phe
245

```

(2) INFORMATION FOR SEQ ID NO:349

45

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 211 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

50

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

55

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

(A) NAME/KEY: misc\_feature

(B) LOCATION 1...211

60

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:349

65

```

Lys Arg Lys Ser Met Lys Arg Met Leu Leu Leu Val Val Leu Leu
1      5      10      15
Tyr Gly Ile Ala Gly Arg Leu Ala Ala Gln Asp Val Ile Arg Pro Trp
20      25      30
Ser Leu Gln Val Gly Ala Gly Tyr Ser Asp Thr Glu Asn Ile Pro Gly
35      40      45
70 Gly Phe Thr Tyr Gly Phe Tyr Leu Gly Lys Arg Met Gly Ser Phe Leu
50      55      60
Glu Val Gly Leu Ser Met Tyr Asn Ser Thr Arg Gln Thr Ala Asn Asn
65      70      75      80
75 Ala Asp Ser Phe Ala Ser Asn Glu Gly Asp Gly Ser Phe Gln Val Asn
85      90      95

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Met Ser Ser Pro Asn Glu Lys Trp Ser Phe Phe Asp Ala Gly Ser Ala  
 100 105 110  
 Asn Cys Tyr Met Ile Val Val Gly Val Asn Pro Leu His Leu Phe Trp  
 115 120 125  
 5 Gln Asn Ser Arg His Asn Leu Phe Leu Ala Val Gln Ala Gly Leu Ser  
 130 135 140  
 Asn Lys His Asn Ile His Phe Ile Tyr Gly Asp Lys Gly Ala Lys Val  
 145 150 155 160  
 10 Ser Ile Tyr Thr Asn Ser Asn Thr Tyr Ile Gly Tyr Gly Ala Arg Val  
 165 170 175  
 Ala Tyr Glu Tyr Gln Ile His Lys Asn Val Gly Ala Gly Ala Ala Val  
 180 185 190  
 Met Tyr Asp His Gly Asn Lys Met Leu Thr Ala Met Ala Thr Leu Ser  
 195 200 205  
 15 Thr His Phe  
 210

(2) INFORMATION FOR SEQ ID NO:350

- 20 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 953 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear
- 25 (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- 30 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Porphyromonas gingivalis
- (ix) FEATURE:  
 (A) NAME/KEY: misc feature  
 (B) LOCATION 1...953
- 35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:350

Ile Arg Met Arg Val Ser Asp Leu Cys Ser Arg Leu Ser Trp Leu Leu  
 1 5 10 15  
 40 Pro Val Ile Leu Val Gly Leu Leu Cys Ala Thr Leu Val Ala Ala Glu  
 20 25 30  
 Arg Pro Met Ala Gly Ala Val Gly Leu His His Arg Arg His Ala Ala  
 35 40 45  
 45 Leu Ser Asp Ser Thr Ala Lys Asp Thr Val Pro Leu Ala Lys Pro Ile  
 50 55 60  
 Pro Asp Ser Ala Phe Arg Asp Ser Leu Pro Ala Asp Ser Thr Gly Ser  
 65 70 75 80  
 Met Arg Gln Asp Ser Val Tyr Asp Asp Glu Phe Glu Leu Glu Asp Ile  
 85 90 95  
 50 Val Glu Tyr Glu Ala Ala Asp Ser Ile Val Leu Leu Gly Gln Asn Arg  
 100 105 110  
 Ala Tyr Leu Phe Gly Lys Ser Tyr Val Ser Tyr Gln Lys Ser Arg Leu  
 115 120 125  
 55 Glu Ala Asn Phe Met Tyr Leu Asn Thr Asp Ser Ser Thr Val Tyr Thr  
 130 135 140  
 Arg Tyr Val Leu Asp Thr Ala Gly Tyr Pro Met Ala Phe Pro Val Phe  
 145 150 155 160  
 Lys Asp Gly Glu Gln Ser Phe Glu Ala Lys Asn Phe Thr Tyr Asn Phe  
 165 170 175  
 60 Arg Thr Glu Lys Gly Ile Ile Ser Gly Val Ile Thr Gln Gln Gly Glu  
 180 185 190  
 Gly Tyr Leu Thr Ala Gly Lys Thr Lys Lys Met Pro Asp Asn Ile Met  
 195 200 205  
 Phe Met Gln Gly Gly Arg Tyr Thr Cys Asp Asn His Asp His Pro  
 210 215 220  
 65 His Phe Tyr Ile Asn Leu Ser Lys Ala Lys Val His Pro Glu Lys Asp  
 225 230 235 240  
 Ile Val Thr Gly Pro Val Asn Leu Val Ile Ala Asp Met Pro Leu Pro  
 245 250 255  
 70 Ile Gly Leu Pro Phe Gly Tyr Phe Pro Phe Ser Asn Lys Tyr Ser Ser  
 260 265 270  
 Gly Ile Leu Met Pro Thr Tyr Gly Glu Asp Asn Arg Tyr Gly Phe Tyr  
 275 280 285  
 75 Leu Arg Asn Gly Gly Tyr Tyr Phe Ala Phe Ser Asp Tyr Ile Asp Leu  
 290 295 300

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	Ala	Leu	Arg	Gly	Glu	Ile	Phe	Ser	Lys	Gly	Ser	Trp	Gly	Ile	Ser	Ala
	305					310					315					320
	Gln	Ser	Lys	Tyr	Lys	Lys	Arg	Tyr	Lys	Tyr	Asn	Gly	Ser	Phe	Glu	Ala
					325					330					335	
5	Asn	Tyr	Leu	Val	Ser	Lys	Ser	Gly	Asp	Lys	Tyr	Val	Pro	Gly	Asp	Tyr
				340					345					350		
	Ser	Lys	Thr	Thr	Ser	Leu	Asn	Ile	Arg	Trp	Thr	His	Ser	Gln	Asp	Pro
				355				360					365			
10	Lys	Ala	Asn	Pro	Leu	Gln	Thr	Leu	Ser	Ala	Asn	Val	Asn	Phe	Ala	Thr
		370					375					380				
	Gly	Ser	Tyr	Phe	Gln	Asn	Ser	Leu	Asn	Thr	Thr	Tyr	Asp	Val	Asn	Ala
		385				390					395					400
	Arg	Thr	Ala	Thr	Thr	Arg	Ser	Ser	Ala	Val	Ser	Tyr	Ser	Arg	Lys	Phe
					405					410					415	
15	Pro	Gly	Thr	Pro	Phe	Ser	Ile	Thr	Gly	Ser	Met	Asp	Ile	Ser	Gln	Asn
				420					425					430		
	Met	Arg	Asp	Thr	Thr	Val	Ser	Leu	Thr	Leu	Pro	Asn	Leu	Ser	Ile	Asn
			435					440					445			
20	Met	Ser	Thr	Arg	Tyr	Pro	Phe	Lys	Arg	Lys	Thr	Arg	Val	Gly	Pro	Glu
		450					455					460				
	Arg	Trp	Tyr	Glu	Lys	Leu	Ser	Val	Gly	Tyr	Ser	Gly	Gln	Leu	Arg	Asn
		465				470				475						480
	Ser	Ile	Leu	Thr	Lys	Glu	Lys	Asp	Leu	Leu	Gln	Ser	Asn	Leu	Val	Arg
					485					490					495	
25	Asp	Trp	Lys	Asn	Gly	Met	Arg	His	Ser	Val	Pro	Ile	Ser	Leu	Thr	Val
				500					505					510		
	Pro	Leu	Leu	Asp	Tyr	Ile	Asn	Leu	Thr	Met	Gly	Val	Asn	Tyr	Asn	Glu
			515					520					525			
30	Trp	Trp	Tyr	Thr	Lys	Gly	Ile	Arg	Lys	Ser	Trp	Asn	Glu	Asp	Lys	Lys
		530					535						540			
	Thr	Phe	Leu	Pro	Ser	Asp	Thr	Thr	Tyr	Lys	Phe	Arg	Arg	Leu	Tyr	Asp
		545				550					555					560
	Tyr	Ser	Leu	Ser	Ala	Gly	Leu	Ser	Thr	Thr	Leu	Tyr	Gly	Met	Phe	Lys
					565					570					575	
35	Pro	Trp	Lys	Pro	Phe	Ser	Phe	Gly	Gly	Asn	Leu	Ile	Met	Ile	Arg	His
				580					585					590		
	Arg	Phe	Thr	Pro	Thr	Val	Ser	Phe	Ser	Tyr	Met	Pro	Asp	Phe	Thr	Lys
			595					600					605			
40	Arg	Arg	Tyr	Gly	Phe	Trp	Glu	Leu	Leu	Glu	His	Thr	Asp	Gln	Asn	Gly
		610					615					620				
	Lys	Leu	His	Thr	Leu	Leu	Tyr	Ser	Pro	Tyr	Phe	Glu	Gln	Ile	Phe	Gly
		625				630					635					640
	Ala	Pro	Ser	Met	Gly	Asn	Ala	Gly	Ser	Val	Asn	Phe	Ser	Phe	Asp	Asn
					645					650					655	
45	Asn	Leu	Glu	Ala	Lys	Ile	Lys	Ser	Lys	Ser	Asp	Ser	Thr	Gly	Ile	Lys
				660					665					670		
	Lys	Ile	Ser	Leu	Ile	Asp	Gln	Phe	Thr	Trp	Ser	Thr	Ser	Tyr	Asn	Met
			675					680					685			
50	Phe	Ala	Asp	Ser	Ile	Arg	Trp	Ser	Asn	Ile	Ser	Ala	Ser	Leu	Ala	Leu
		690					695					700				
	Arg	Leu	Ser	Lys	Ser	Phe	Thr	Leu	Arg	Leu	Ser	Gly	Leu	Phe	Asp	Pro
		705				710					715					720
	Tyr	Leu	Thr	Lys	Tyr	Tyr	Glu	Gly	Glu	Asp	Gly	Lys	Ile	Ile	Pro	Tyr
				725						730					735	
55	Lys	Ser	Asn	Asp	Leu	Arg	Ile	Phe	Asn	Gly	Lys	Gly	Leu	Ala	Arg	Leu
				740					745					750		
	Ile	Ser	Thr	Gly	Thr	Ser	Phe	Ser	Tyr	Thr	Leu	Asn	Lys	Glu	Ser	Leu
			755				760						765			
60	Ser	Gly	Leu	Ile	Ala	Leu	Phe	Ser	Gly	Lys	Lys	Glu	Arg	Arg	Asp	Glu
		770					775						780			
	Lys	Lys	Asn	Thr	Gly	Ala	Thr	Pro	His	Glu	Gly	Asp	Asp	Ala	Ala	Asp
		785				790				795						800
	Ile	Leu	Glu	Gly	Gly	Arg	Pro	Gln	Asn	Glu	Ser	Gly	Gly	Ser	Leu	Leu
					805					810					815	
65	Glu	Arg	Asn	Arg	Gln	Gly	Gly	Ala	Val	Asp	Gln	Asp	Gly	Tyr	Phe	Ala
				820					825					830		
	Tyr	Ser	Ile	Pro	Trp	Ser	Leu	Ser	Phe	Asp	Tyr	Ser	Trp	Asn	Ile	Ala
			835				840						845			
70	Thr	Asp	Tyr	Asn	Arg	Tyr	Asn	Val	Asn	Lys	Met	Glu	His	Tyr	Tyr	Arg
		850					855					860				
	Val	Thr	Gln	Asn	Leu	Ser	Phe	Arg	Gly	Asn	Ile	Gln	Pro	Thr	Pro	Asn
		865				870					875					880
	Trp	Ser	Phe	Gly	Phe	Asn	Ala	Asn	Tyr	Asn	Phe	Asp	Leu	Lys	Lys	Ile
					885					890					895	
75	Thr	Ser	Leu	Thr	Cys	Asn	Val	Thr	Arg	Asp	Met	His	Cys	Trp	Ala	Ile

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900 905 910  
 Ser Ala Ser Phe Ile Pro Ile Gly Ala Tyr Lys Ser Tyr Asn Phe Val  
 915 920 925  
 Ile Ser Val Lys Ser Ser Leu Gln Asp Leu Lys Tyr Gln Gln Ser  
 930 935 940  
 Asn Arg Pro Ile Thr Asn Thr Trp Tyr  
 945 950

(2) INFORMATION FOR SEQ ID NO:351

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1251 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

(A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...1251

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:351

Lys Trp Lys Leu Ala Cys Ala Phe Asp Cys Ala Cys Cys Phe Asp Pro  
 1 5 10 15  
 Phe Val Val Thr Asn Glu Val Ile Ile Met Met Lys Arg Tyr Thr Ile  
 20 25 30  
 Ile Leu Ala Val Phe Leu Leu Phe Cys Thr Val Phe Thr Phe Gln Ile  
 35 40 45  
 Lys Ala Arg Pro Tyr Glu Arg Phe Ala Asp Val Glu Lys Pro Trp Ile  
 50 55 60  
 Gln Lys His Ser Met Asp Ser Lys Leu Val Pro Ala Asn Lys Gly Asn  
 65 70 75 80  
 Leu Ile Gln Ala Glu Ile Val Tyr Gln Ser Val Ser Glu His Ser Asp  
 40 85 90 95  
 Leu Val Ile Ser Pro Val Asn Glu Ile Arg Pro Ala Asn Arg Phe Pro  
 100 105 110  
 Ser His Arg Lys Ser Phe Phe Ala Glu Asn Leu Arg Ala Ser Pro Pro  
 115 120 125  
 Val Val Pro Val Ala Val Asp Lys Tyr Ala Val Pro Val Ala Asn Pro  
 45 130 135 140  
 Met Asp Pro Glu Asn Pro Asn Ala Trp Asp Val Thr Leu Lys Ile Thr  
 145 150 155 160  
 Thr Lys Ala Val Thr Val Pro Val Asp Val Val Met Val Ile Asp Gln  
 50 165 170 175  
 Ser Ser Ser Met Gly Gly Gln Asn Ile Ala Arg Leu Lys Ser Ala Ile  
 180 185 190  
 Ala Ser Gly Gln Arg Phe Val Lys Lys Met Leu Pro Lys Gly Thr Ala  
 195 200 205  
 Thr Glu Gly Val Arg Ile Ala Leu Val Ser Tyr Asp His Glu Pro His  
 55 210 215 220  
 Arg Leu Ser Asp Phe Thr Lys Asp Thr Ala Phe Leu Cys Gln Lys Ile  
 225 230 235 240  
 Arg Ala Leu Thr Pro Ile Trp Gly Thr His Thr Gln Gly Gly Leu Lys  
 60 245 250 255  
 Met Ala Arg Asn Ile Met Ala Thr Ser Thr Ala Val Asp Lys His Ile  
 260 265 270  
 Ile Leu Met Ser Asp Gly Leu Ala Thr Glu Gln Tyr Pro Val Lys Asn  
 275 280 285  
 Val Thr Thr Ala Asp Phe Ile Gly Lys Thr Gly Asn Ala Asn Asp Pro  
 65 290 295 300  
 Ile Asp Leu Val Ile Gln Gly Ala Ile Asn Phe Pro Thr Asn Tyr Val  
 305 310 315 320  
 Ser Asn Asn Pro Ser Thr Pro Leu Thr Pro Asn Tyr Pro Thr His Ser  
 70 325 330 335  
 Ser Lys Val Gly Arg Arg Asn Leu Pro Glu Ser Lys Phe Asp Tyr Ser  
 340 345 350  
 Asn Leu Ser Ala Arg Ile Thr Phe Asp Gly Val Ala Gly Ala Leu Val  
 355 360 365  
 Tyr Glu Pro Arg Phe Pro His Pro Tyr Tyr Tyr Tyr Phe Pro Cys Asn

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[illegible]

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Lys Asn Thr Ala Gly Gln Asp Asn Leu Pro Asp Arg Ile Pro Ser Met  
 980 985 990  
 His Ser Phe Leu Val Lys Met Gln Asn Gly Ala Ser Cys Thr Leu Unk  
 995 1000 1005  
 5 Ile Leu Tyr Asp Lys Leu Leu Lys Asn Thr Thr Val Asn Asn Gly Asn  
 1010 1015 1020  
 Gly Thr Gln Ile Thr Trp Arg Ser Gly Asn Ser Gly Ser Ala Asn Met  
 1025 1030 1035 1040  
 10 Pro Ser Leu Val Met Asp Val Leu Gly Asn Glu Ser Ala Asp Arg Leu  
 1045 1050 1055  
 Trp Ile Phe Thr Asp Gly Gly Leu Ser Phe Gly Phe Asp Asn Gly Trp  
 1060 1065 1070  
 Asp Gly Arg Lys Leu Thr Glu Lys Gly Leu Ser Gln Leu Tyr Ala Met  
 1075 1080 1085  
 15 Ser Asp Ile Gly Asn Asp Lys Phe Gln Val Ala Gly Val Pro Glu Leu  
 1090 1095 1100  
 Asn Asn Leu Leu Ile Gly Phe Asp Ala Asp Lys Asp Gly Gln Tyr Thr  
 1105 1110 1115 1120  
 20 Leu Glu Phe Ala Leu Ser Asp His Phe Ala Lys Gly Ala Val Tyr Leu  
 1125 1130 1135  
 His Asp Leu Gln Ser Gly Ala Lys His Arg Ile Thr Asn Ser Thr Ser  
 1140 1145 1150  
 Tyr Ser Phe Asp Ala Lys Arg Gly Asp Ser Gly Ala Arg Phe Arg Leu  
 1155 1160 1165  
 25 Ser Tyr Gly Cys Asp Glu Asn Val Asp Asp Ser His Val Val Ser Thr  
 1170 1175 1180  
 Asn Gly Arg Glu Ile Ile Ile Leu Asn Gln Asp Ala Leu Asp Cys Thr  
 1185 1190 1195 1200  
 30 Val Thr Leu Phe Thr Ile Glu Gly Lys Leu Leu Arg Arg Leu Lys Val  
 1205 1210 1215  
 Leu Ala Gly His Arg Glu Val Met Lys Val Gln Thr Gly Gly Ala Tyr  
 1220 1225 1230  
 Ile Val His Leu Gln Asn Ala Phe Thr Asn Asp Val His Lys Val Leu  
 1235 1240 1245  
 35 Val Glu Tyr  
 1250

(2) INFORMATION FOR SEQ ID NO:352

- 40 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 426 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
 45 (ii) MOLECULE TYPE: protein  
 (iii) HYPOTHETICAL: YES  
 (vi) ORIGINAL SOURCE:  
 50 (A) ORGANISM: Porphyromonas gingivalis  
 (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...426  
 55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:352

Thr Met Glu Val Lys Lys Asn Thr Val Val Leu Arg Leu Leu Ile Trp  
 1 5 10 15  
 60 Phe Val Ala Ile Leu Leu Phe His Ser Ser Arg Leu Trp Gly Gln Glu  
 20 25 30  
 Gly Glu Gly Ser Ala Arg Tyr Arg Phe Lys Gly Phe Val Asp Thr Tyr  
 35 40 45  
 65 His Ala Val Arg Ser Ser Ser Pro Phe Asp Phe Met Ser Ser Arg Thr  
 50 55 60  
 Arg Val Arg Gly Glu Leu Glu Arg Ser Phe Gly Asn Ser Lys Val Ala  
 65 70 75 80  
 Val Ser Val Asn Ala Thr Tyr Asn Ala Leu Leu Lys Asp Glu Thr Gly  
 85 90 95  
 70 Leu Arg Leu Arg Glu Ala Phe Phe Glu His Gln Glu Glu His Trp Gly  
 100 105 110  
 Leu Arg Leu Gly Arg Gln Ile Val Ile Trp Gly Ala Ala Asp Gly Val  
 115 120 125  
 75 Arg Ile Thr Asp Leu Ile Ser Pro Met Asp Met Thr Glu Phe Leu Ala  
 130 135 140

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5	Gln 145	Asp	Tyr	Asp	Asp	Ile 150	Arg	Met	Pro	Val	Asn 155	Ala	Leu	Arg	Phe	Ser 160
	Val	Phe	Asn	Glu	Ser 165	Met	Lys	Val	Glu	Val	Val	Val	Leu	Pro	Val	Phe
	Glu	Gly	Tyr	Arg 180	Leu	Pro	Val	Asp	Pro 185	Arg	Asn	Pro	Trp	Asn 190	Ile	Phe
	Ser	Leu	Ser	Pro	Ile	Ala	Gln	Gly 200	Met	Asn	Ile	Val	Trp 205	Lys	Glu	Glu
10	Ala 210	Gly	Lys	Pro	Ala	Phe	Lys 215	Val	Ala	Asn	Ile	Glu 220	Tyr	Gly	Ala	Arg
	Trp 225	Ser	Thr	Thr	Leu	Ser 230	Gly	Ile	Asp	Phe	Ala 235	Leu	Ala	Ala	Leu	His
	Thr	Trp	Asn	Lys	Met 245	Pro	Val	Ile	Glu	Val 250	Gln	Gly	Ile	Val	Pro 255	Thr
	Glu	Ile	Ile	Val 260	Ser	Pro	Arg	Tyr	Tyr 265	Arg	Met	Gly	Phe	Val 270	Gly	Gly
15	Asp	Leu	Ser 275	Val	Pro	Val	Gly	Gln 280	Phe	Val	Phe	Arg	Gly 285	Glu	Ala	Ala
	Phe	Asn 290	Ile	Asp	Lys	His	Phe 295	Thr	Tyr	Lys	Ser	His 300	Ala	Glu	Gln	Glu
	Gly 305	Phe	Gln	Thr	Ile	Asn 310	Trp	Leu	Ala	Gly	Ala 315	Asp	Trp	Tyr	Ala	Pro
	Gly	Glu	Trp	Met	Ile 325	Ser	Gly	Gln	Phe	Ser 330	Met	Glu	Ser	Ile	Phe 335	Arg
20	Tyr	Arg	Asp	Phe 340	Ile	Ser	Gln	Arg	Gln 345	His	Ser	Thr	Leu	Ile 350	Thr	Leu
	Asn	Val	Ser 355	Lys	Lys	Phe	Phe	Gly 360	Ser	Thr	Leu	Gln 365	Leu	Ser	Asp	Phe
	Thr 370	Tyr	Tyr	Asp	Leu	Thr	Gly 375	Lys	Gly	Trp	Phe	Ser 380	Arg	Phe	Ala	Ala
	Asp 385	Tyr	Ala	Leu	Asn	Asp 390	Gln	Ile	His	Leu	Met 395	Ala	Gly	Tyr	Asp	Trp
25	Phe	Ser	Ser	Lys	Gly 405	Ser	Gly	Ile	Phe	Asp 410	Arg	Tyr	Lys	Asp	Asn 415	Ser
	Glu	Leu	Trp	Phe 420	Lys	Ala	Arg	Tyr	Ser 425	Phe						

## (2) INFORMATION FOR SEO ID NO:353

```

40      (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 464 amino acids
          (B) TYPE: amino acid
          (D) TOPOLOGY: linear

45      (ii) MOLECULE TYPE: protein

      (iii) HYPOTHETICAL: YES

50      (vi) ORIGINAL SOURCE:
          (A) ORGANISM: Porphyromonas gingivalis

      (ix) FEATURE:
          (A) NAME/KEY: misc_feature
          (B) LOCATION 1...464

55      (xi) SEQUENCE DESCRIPTION: SEO ID NO:353

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	Tyr	Gly	Lys	Arg	Arg	Lys	Leu	Gly	Thr	Ser	Val	Arg	Pro	Ser	Val	Leu
60	1				5					10					15	
	Thr	Gln	Ile	Arg	Phe	Ile	Leu	Asp	Leu	His	Leu	Ile	Thr	Asp	Phe	Phe
				20					25					30		
	Glu	Gly	Leu	Arg	Val	Asn	Pro	Ile	Gly	Ala	Ala	Ala	Ile	Val	Ala	Phe
			35					40					45			
65	Ile	Ile	Asp	Leu	Leu	Leu	Leu	Cys	Cys	Ser	Ala	Phe	Met	Ser	Ser	Cys
	50					55						60				
	Glu	Val	Ala	Tyr	Phe	Ser	Leu	Lys	Pro	Ile	Asp	Leu	Gln	Asn	Ile	Arg
	65					70					75				80	
	Glu	Arg	Asn	His	Ser	Ser	Asp	Ile	Ala	Leu	Ser	Asn	Leu	Leu	Asp	Asn
					85					90				95		
70	Ser	Asn	Gln	Leu	Leu	Ala	Thr	Ile	Leu	Ile	Gly	Asn	Asn	Val	Ile	Asn
				100					105					110		
	Val	Ala	Ile	Val	Ile	Leu	Ser	Asn	Tyr	Ala	Ile	Glu	Gln	Thr	Phe	Val
			115					120					125			
75	Phe	Ser	Ser	Pro	Ile	Ile	Gly	Phe	Leu	Ile	Gln	Thr	Ile	Leu	Leu	Thr
	130						135					140				

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Thr Val Leu Leu Leu Phe Gly Glu Ile Leu Pro Lys Val Tyr Ala Arg  
 145 150 155 160  
 Lys Asn Pro Leu Gln Tyr Ser Arg Phe Ser Ala Ala Ala Met Ser Val  
 165 170 175  
 5 Ile Tyr Lys Ile Leu Ser Pro Phe Ser Lys Leu Leu Val Lys Ser Thr  
 180 185 190  
 Gly Ile Val Thr Arg Gly Ile Ser Lys Lys Lys Tyr Asp Met Ser Val  
 195 200 205  
 10 Asp Glu Leu Ser Lys Ala Val Ala Leu Thr Thr Thr Glu Gly Glu Pro  
 210 215 220  
 Glu Glu Lys Glu Met Ile Asn Glu Ile Ile Lys Phe Tyr Asn Lys Thr  
 225 230 235 240  
 Ala Cys Glu Ile Met Val Pro Arg Ile Asp Ile Val Asp Val Asp Leu  
 245 250 255  
 15 Ser Trp Pro Phe Arg Lys Met Leu Asp Phe Val Val Ser Ser Gly Tyr  
 260 265 270  
 Ser Arg Leu Pro Val Ser Glu Gly Ser Glu Asp Asn Ile Lys Gly Val  
 275 280 285  
 20 Ile Tyr Ile Lys Asp Leu Ile Pro His Met Asp Lys Gly Asp Glu Phe  
 290 295 300  
 Asp Trp His Pro Leu Ile Arg Lys Ala Tyr Phe Val Pro Glu Asn Lys  
 305 310 315 320  
 Arg Ile Asp Asp Leu Leu Glu Glu Phe Arg Ala Asn Lys Val His Val  
 325 330 335  
 25 Ser Ile Val Val Asp Glu Phe Gly Gly Thr Cys Gly Leu Ile Thr Met  
 340 345 350  
 Glu Asp Ile Leu Glu Glu Ile Val Gly Glu Ile Thr Asp Glu Tyr Asp  
 355 360 365  
 30 Glu Glu Glu Leu Pro Phe Lys Val Leu Gly Asp Gly Ser Tyr Leu Phe  
 370 375 380  
 Glu Gly Lys Thr Ser Leu Ser Asp Val Arg His Tyr Leu Asp Leu Pro  
 385 390 395 400  
 Glu Asn Ala Phe Gly Glu Leu Gly Asp Glu Val Asp Thr Leu Ser Gly  
 405 410 415  
 35 Leu Phe Leu Glu Ile Lys Gln Glu Leu Pro His Val Gly Asp Thr Ala  
 420 425 430  
 Val Tyr Glu Pro Phe Arg Phe Gln Val Thr Gln Met Asp Lys Arg Arg  
 435 440 445  
 40 Ile Ile Glu Ile Lys Ile Phe Pro Phe Glu Arg Thr Trp Glu Val Glu  
 450 455 460

## (2) INFORMATION FOR SEQ ID NO:354

- 45 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 266 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
 50 (ii) MOLECULE TYPE: protein  
 (iii) HYPOTHETICAL: YES  
 (vi) ORIGINAL SOURCE:  
 55 (A) ORGANISM: Porphyromonas gingivalis  
 (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...266  
 60 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:354

Ile Ile Tyr Arg Ser Thr Met Lys Leu Leu Leu Tyr Leu Leu Leu Val  
 1 5 10 15  
 65 Leu Ser Thr Leu Ser Pro Met Tyr Ser Gln Met Leu Phe Ser Glu Asn  
 20 25 30  
 Leu Thr Met Asn Ile Asp Ser Thr Lys Thr Ile Gln Gly Thr Ile Leu  
 35 40 45  
 Pro Val Leu Asp Phe Lys Thr Glu Lys Glu Asn Val Phe Thr Phe Lys  
 50 55 60  
 70 Asn Thr Ala Asn Leu Asn Leu Leu Ile Lys His Gly Gln Val Ile Asn  
 65 70 75 80  
 Leu Ile Asn Lys Leu Glu Phe Ser Thr Tyr Gly Asn Lys Val Thr Val  
 85 90 95  
 75 Ser Gly Gly Tyr Val His Thr Glu Tyr Arg Tyr Leu Leu His His Val  
 100 105 110



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Phe Glu Val Tyr Pro Tyr Val Glu Ser Gln Trp Ala Glu Ser Arg Gly  
 115 120 125  
 Met Lys Tyr Lys Val Ser Thr Gly Leu Gln Ser Arg Tyr Arg Leu Val  
 130 135 140  
 5 Asn Ser Asp Asn Cys Leu Met Phe Ala Thr Leu Gly Val Phe Phe Glu  
 145 150 155 160  
 Phe Glu Lys Trp Glu Gln Pro Ala Thr Ser Leu Phe Ala Gly Thr Tyr  
 165 170 175  
 10 Ala Tyr Ser Arg Ser Ile Lys Ser His Leu Ser Ile Ser Phe Arg His  
 180 185 190  
 Arg Leu Gly Glu His Trp Glu Phe Thr Thr Thr Ala Ile His Gln Gly  
 195 200 205  
 Lys Pro Asp Ser Tyr Phe Lys Lys Ala Arg Phe Gly Gly Ala Ile Asp  
 210 215 220  
 15 Leu Lys Tyr His Ile Thr Pro Thr Ile Gly Ile Arg Gly Ala Tyr Arg  
 225 230 235 240  
 Ile Ile Tyr Asp Thr Ala Pro Ile Val Pro Val Arg Lys Asp Tyr Asn  
 245 250 255  
 20 Thr Val Asp Val Gly Ile Asp Ile Ser Phe  
 260 265

## (2) INFORMATION FOR SEQ ID NO:355

- 25 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 907 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
 30 (ii) MOLECULE TYPE: protein  
 (iii) HYPOTHETICAL: YES  
 (vi) ORIGINAL SOURCE:  
 35 (A) ORGANISM: Porphyromonas gingivalis  
 (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...907  
 40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:355

Thr Ile Cys Val Ala Phe Leu Ser Ala Pro Val Ala Ala Leu Arg Glu  
 1 5 10 15  
 45 Ser Pro Pro Met Gly Ala Glu Arg Lys Thr Pro Ser Leu Leu Pro Leu  
 20 25 30  
 Leu Phe Glu His Ser Asp Lys Gly Lys Gly Phe Asp Tyr Arg Leu Phe  
 35 40 45  
 Thr Ser Asn Lys Leu Lys Val Phe Ala Thr Gly Asn Ser Arg Tyr Ile  
 50 55 60  
 His Asn Lys Pro Thr Ile Ile Gln Ala Met Lys Arg Ile Val Leu Ser  
 65 70 75 80  
 Ser Phe Leu Phe Val Leu Ser Ile Leu Ser Leu Met Ala Gln Asn Asn  
 85 90 95  
 55 Thr Leu Asp Val His Ile Ser Gly Thr Ile Lys Asp Ala Ser Ser Gly  
 100 105 110  
 Glu Pro Val Pro Tyr Ala Thr Val Ser Ile Arg Leu Thr Gly Ala Asp  
 115 120 125  
 60 Thr Thr Gln Val Phe Arg Gln Val Thr Asp Gly Asn Gly Tyr Phe Val  
 130 135 140  
 Ile Gly Leu Pro Ala Ala Pro Ser Tyr His Leu Thr Ala Ser Phe Val  
 145 150 155 160  
 Gly Met Lys Thr His Thr Met Gln Ile Ser Arg Gly Asn Gly Gln His  
 165 170 175  
 65 Asp Ile Lys Ser Ile Asp Ile Ser Leu Glu Ser Glu Asp Lys Gln Leu  
 180 185 190  
 Ser Thr Val Thr Val Ser Ala Ala Arg Pro Leu Val Lys Met Glu Ile  
 195 200 205  
 Asp Arg Leu Ser Tyr Asn Met Lys Asp Asp Pro Ala Lys Thr Asn  
 210 215 220  
 70 Asn Leu Leu Glu Met Leu Arg Asn Val Pro Leu Val Thr Val Asp Gly  
 225 230 235 240  
 Gln Gly Asn Ile Gln Val Lys Gly Ser Ser Asn Phe Lys Ile His Leu  
 245 250 255  
 75 Asn Gly Arg Pro Ser Thr Met Val Ser Ser Asn Pro Lys Glu Val Phe  
 260 265 270

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	Arg	Ser	Ile	Pro	Ala	His	Thr	Ile	Lys	Arg	Val	Glu	Val	Ile	Thr	Asp
			275					280					285			
	Pro	Gly	Val	Lys	Tyr	Asp	Ala	Glu	Gly	Thr	Ser	Ala	Ile	Leu	Asp	Ile
		290					295					300				
5	Val	Thr	Glu	Glu	Gly	Lys	Lys	Leu	Glu	Gly	Tyr	Ser	Gly	Ser	Ile	Thr
	305					310					315				320	
	Ala	Ser	Val	Ser	Asn	Asn	Pro	Thr	Ala	Asn	Gly	Ser	Ile	Phe	Leu	Thr
					325					330					335	
10	Ala	Lys	Ser	Gly	Lys	Val	Gly	Leu	Thr	Thr	Asn	Tyr	Asn	Tyr	Tyr	Gly
			340						345					350		
	Gly	Lys	Asn	Lys	Gly	Ser	Arg	Tyr	Phe	Thr	Glu	Arg	Thr	Thr	Ser	Met
			355					360					365			
	Leu	Gln	Thr	Ile	Glu	Glu	Gly	Lys	Gly	Gln	Glu	Thr	Phe	Gly	Gly	His
		370					375					380				
15	Phe	Gly	Asn	Ala	Leu	Leu	Ser	Phe	Glu	Ile	Asp	Ser	Leu	Asn	Leu	Phe
	385						390				395					400
	Thr	Val	Gly	Gly	Asn	Val	Arg	Leu	Trp	Glu	Met	Thr	Thr	Asp	Arg	Asn
					405					410					415	
20	Ser	Val	Glu	Lys	Ser	Phe	Ala	Gly	Ser	Asn	Leu	Met	Ser	Tyr	Ile	Asp
					420				425					430		
	Arg	Lys	Leu	Lys	Thr	Gln	Met	Asp	Ala	Gly	Ser	Tyr	Glu	Leu	Asn	Ala
			435					440					445			
	Asp	Tyr	Gln	His	Ser	Thr	Arg	Leu	Pro	Gly	Glu	Leu	Leu	Thr	Val	Ser
		450					455					460				
25	Tyr	Arg	Phe	Thr	His	Asn	Pro	Asn	Asn	Ser	Glu	Thr	Phe	Ile	Asp	Gln
		465				470					475					480
	Trp	Lys	Arg	Asp	Pro	Leu	Asn	Thr	Ala	Asn	Thr	Ile	Gln	Tyr	Ala	Gly
					485					490					495	
30	Gln	His	Ser	Lys	Ser	Asp	Ala	Gly	Met	Asp	Glu	His	Thr	Ala	Gln	Val
			500						505					510		
	Asp	Tyr	Thr	Arg	Pro	Leu	Gly	Gln	Ala	His	Ser	Leu	Glu	Ala	Gly	Leu
			515					520					525			
	Lys	Tyr	Ile	Tyr	Arg	His	Ala	Thr	Ser	Asp	Pro	Leu	Tyr	Glu	Ile	Arg
		530					535						540			
35	Pro	Ser	Glu	Asp	Ala	Pro	Trp	Gln	Pro	Gly	Ser	Leu	Tyr	Ala	Gln	Asn
		545				550					555					560
	Pro	Ser	Asn	Gly	Lys	Phe	Arg	His	Asp	Gln	Tyr	Ile	Gly	Ala	Ala	Tyr
					565					570				575		
40	Ala	Gly	Tyr	Asn	Tyr	Arg	Lys	Asp	Gln	Tyr	Ser	Leu	Gln	Thr	Gly	Leu
				580					585					590		
	Arg	Val	Glu	Ser	Ser	Arg	Leu	Lys	Ala	Leu	Phe	Pro	Glu	Asn	Ala	Ala
		595						600					605			
	Ala	Asp	Phe	Ser	His	Asn	Ser	Phe	Asp	Trp	Val	Pro	Gln	Leu	Thr	Leu
		610				615						620				
45	Gly	Tyr	Thr	Pro	Ser	Pro	Met	Lys	Gln	Leu	Lys	Leu	Ala	Tyr	Asn	Phe
		625				630					635					640
	Arg	Ile	Gln	Arg	Pro	Ala	Ile	Gly	Gln	Leu	Asn	Pro	Tyr	Arg	Leu	Gln
					645					650					655	
50	Thr	Asn	Asp	Tyr	Gln	Val	Gln	Tyr	Gly	Asn	Pro	Asp	Leu	Lys	Ser	Glu
			660						665					670		
	Lys	Arg	His	His	Val	Gly	Leu	Ser	Tyr	Asn	Gln	Tyr	Gly	Ala	Lys	Val
			675					680					685			
	Met	Leu	Thr	Ala	Ser	Leu	Asp	Tyr	Asp	Phe	Cys	Asn	Asn	Ala	Ile	Gln
		690					695					700				
55	Asn	Tyr	Thr	Phe	Ser	Asp	Pro	Ala	Asn	Pro	Asn	Leu	Phe	His	Gln	Thr
		705				710					715					720
	Tyr	Gly	Asn	Ile	Gly	Arg	Glu	His	Ser	Phe	Ser	Leu	Asn	Thr	Tyr	Ala
					725					730					735	
60	Met	Tyr	Thr	Pro	Ala	Val	Trp	Val	Arg	Ile	Met	Leu	Asn	Gly	Asn	Ile
			740						745					750		
	Asp	Arg	Thr	Phe	Gln	Lys	Ser	Glu	Ala	Leu	Gly	Ile	Asp	Val	Asn	Ser
			755					760					765			
	Trp	Ser	Gly	Met	Val	Tyr	Ser	Gly	Leu	Met	Phe	Thr	Leu	Pro	Lys	Asp
		770					775					780				
65	Trp	Thr	Val	Asn	Leu	Phe	Gly	Gly	Tyr	Tyr	His	Gly	Gly	Arg	Ser	Tyr
		785				790					795					800
	Gln	Thr	Lys	Tyr	Asp	Gly	Asn	Val	Phe	Asn	Asn	Ile	Gly	Ile	Ala	Lys
					805					810					815	
70	Gln	Leu	Phe	Asp	Lys	Lys	Leu	Arg	Val	Ser	Leu	Ser	Ala	Asn	Asn	Ile
			820						825					830		
	His	Ala	Lys	Tyr	Ser	Thr	Trp	Lys	Ser	Arg	Thr	Ile	Gly	Asn	Gly	Phe
			835					840					845			
	Thr	Ile	Tyr	Ser	Glu	Asn	Ala	Gly	Ile	Gln	Arg	Ser	Val	Ser	Leu	Ser
		850					855					860				
75	Leu	Thr	Tyr	Ser	Phe	Gly	Lys	Met	Asn	Thr	Gln	Val	Arg	Lys	Val	Glu



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355 360 365  
 Gln Val Asn Leu Phe Leu Lys Gly Met Tyr Glu Asn Gly Tyr Ala Pro  
 370 375 380  
 5 Ala Gln Tyr Gly Glu Ser Ser His Thr Arg His Ser Tyr Gly Tyr Met  
 385 390 395 400  
 Gly Gly Val Glu Tyr Tyr Pro Thr Glu Thr Asn Phe Arg Leu Phe Val  
 405 410 415  
 Thr Tyr Ile Gly Arg His Tyr Arg Tyr Ser Ala Thr Glu Thr Glu Ser  
 420 425 430  
 10 Thr Asn Ala Leu Arg Ala Gly Leu Ile Tyr Gln Ile Pro Phe Leu  
 435 440 445

(2) INFORMATION FOR SEQ ID NO:358

- 15 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 227 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
 20 (ii) MOLECULE TYPE: protein  
 (iii) HYPOTHETICAL: YES  
 25 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Porphyromonas gingivalis  
 (ix) FEATURE:  
 (A) NAME/KEY: misc feature  
 (B) LOCATION 1...227  
 30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:358

Tyr Lys Gln Ala Ile Met Lys His Leu Phe Lys Ser Thr Leu Val Leu  
 1 5 10 15  
 35 Leu Cys Ala Leu Ser Phe Ser Gly Thr Tyr Thr Phe Ala Gln Glu Asn  
 20 25 30  
 Asn Thr Glu Lys Ser Arg Phe Asp Phe Ser Val Arg Leu Gly Gln Gly  
 35 40 45  
 40 Tyr Ile Ala Gly Ser Thr Thr Asn Leu Met Tyr Gly Tyr Thr Ser Ala  
 50 55 60  
 Asn Asp Arg Leu Leu Ser Gly Ala Ile Tyr Leu Gly Leu Thr Pro Ser  
 65 70 75 80  
 Lys Lys Glu Asn Ala Thr Gly Val Ala Phe Arg Phe Leu Ser Pro Ser  
 85 90 95  
 45 Pro Gly Tyr Tyr Val Asp Ile Ser Gly Lys Glu Asn Thr Leu Asn Tyr  
 100 105 110  
 Ala Phe Tyr Val Val Gly Ala Tyr Asn Arg Ile Ala Ile Pro Ile Arg  
 115 120 125  
 50 Pro Ile Lys Asn Phe Asn Phe Ile Phe Ser Thr Glu Val Gly Met Ala  
 130 135 140  
 Trp Met Ser Arg His Glu Gln Ile Tyr Asn Ser Thr Ser Gln Thr Trp  
 145 150 155 160  
 Asp Lys Gln Arg Lys Ser Arg Ser Gly Leu Asp Phe Gly Leu Gly Met  
 165 170 175  
 55 His Leu Gln Unk His Ile Asn Lys Thr Val Tyr Phe Met Ala Gly Thr  
 180 185 190  
 Asp Leu Thr Ser Cys Met Phe Gly Lys Arg Ile Asn Asp Tyr Gln Gln  
 195 200 205  
 60 Lys Asp Arg Thr Phe Ile Ala Leu Ile Asp Asn Ser Ile Gly Ile Gly  
 210 215 220  
 Leu Asn Leu  
 225

(2) INFORMATION FOR SEQ ID NO:359

- 65 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 406 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
 70 (ii) MOLECULE TYPE: protein  
 (iii) HYPOTHETICAL: YES  
 75 (vi) ORIGINAL SOURCE:

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(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

(A) NAME/KEY: misc\_feature

(B) LOCATION 1...406

((i) SEQUENCE DESCRIPTION: SEQ ID NO:359

10 Ile Phe Ile Asp Pro Asp Lys Asn Thr Lys Gln Asn Glu Arg Asn Met  
 1 5 10 15  
 Ile Ile Lys Lys Met Leu Lys Asn Lys Leu Ala Pro Leu Ala Ile Leu  
 20 25 30  
 Phe Leu Phe Ala Pro Lys Ala Met Lys Ala Gln Glu Gln Leu Asn Val  
 35 40 45  
 15 Val His Thr Ser Val Pro Ser Leu Asn Ile Ser Pro Asp Ala Arg Ala  
 50 55 60  
 Ala Gly Met Gly Asp Ile Gly Val Ala Thr Thr Pro Asp Ala Tyr Ser  
 65 70 75 80  
 20 Gln Tyr Trp Asn Pro Ser Lys Tyr Ala Phe Met Asp Thr Lys Ala Gly  
 85 90 95  
 Ile Ser Phe Ser Tyr Thr Pro Trp Leu Ser Lys Leu Val Asn Asp Ile  
 100 105 110  
 Ala Leu Met Gln Met Thr Gly Phe Tyr Lys Leu Gly Thr Asp Glu Asn  
 115 120 125  
 25 Gln Ala Ile Ser Ala Ser Leu Arg Tyr Phe Thr Leu Gly Lys Leu Glu  
 130 135 140  
 Thr Phe Asp Glu Leu Gly Glu Ser Met Gly Glu Ala His Pro Asn Glu  
 145 150 155 160  
 30 Phe Ala Val Asp Leu Gly Tyr Ser Arg Gln Leu Ser Glu Asn Phe Ser  
 165 170 175  
 Met Ala Val Ala Leu Arg Tyr Ile Arg Ser Asp Gln Ser Thr His Asn  
 180 185 190  
 Thr Gly Glu Asn Gln Ala Gly Asn Ala Phe Ala Ala Asp Ile Ala Gly  
 195 200 205  
 35 Tyr Leu Gln Lys Tyr Val Leu Leu Gly Asn Ala Glu Ser Leu Trp Ser  
 210 215 220  
 Leu Gly Phe Asn Val Lys Asn Ile Gly Thr Lys Ile Ser Tyr Asp Gly  
 225 230 235 240  
 40 Gly Val Thr Ser Phe Phe Ile Pro Thr Ser Leu Asn Leu Gly Thr Gly  
 245 250 255  
 Leu Leu Tyr Pro Ile Asp Asp Tyr Asn Ser Ile Asn Phe Asn Leu Glu  
 260 265 270  
 Leu Ser Lys Leu Leu Val Pro Thr Pro Pro Ile Met Asp Gln Asn Asp  
 275 280 285  
 45 Gln Ala Gly Tyr Glu Ala Ala Leu Lys Lys Tyr Gln Glu Thr Ser Ser  
 290 295 300  
 Ile Ser Gly Ile Phe Ser Ser Phe Gly Asp Ala Pro Gly Gly Leu Lys  
 305 310 315 320  
 50 Glu Glu Phe Arg Glu Ile Thr Trp Gly Leu Gly Ala Glu Tyr Ser Tyr  
 325 330 335  
 Asp Asp Lys Phe Phe Val Arg Ala Gly Tyr Ser Tyr Leu His Pro Thr  
 340 345 350  
 Lys Gly Asn Leu Gln Tyr Phe Thr Ala Gly Ala Gly Phe Lys Met Asn  
 355 360 365  
 55 Ile Phe Arg Ile Asp Ala Ser Tyr Leu Leu Ser Thr Ile Gln Ser Asn  
 370 375 380  
 Pro Leu Asp Gln Thr Leu Arg Phe Thr Leu Ala Phe Asp Met Asp Gly  
 385 390 395 400  
 60 Leu Arg Asn Leu Phe His  
 405

(2) INFORMATION FOR SEQ ID NO:360

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 452 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Porphyromonas gingivalis

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## (ix) FEATURE:

(A) NAME/KEY: misc\_feature  
(B) LOCATION 1...452

## 5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:360

Leu Ile Ile Glu Lys Glu Met Lys Thr Thr Val Gln Gln Ile Ile Leu  
1 5 10 15  
Cys Leu Ala Leu Met Met Ser Gly Val Leu Gly Gly Asn Ala Gln Ser  
10 20 25 30  
Phe Trp Glu Glu Ile Ala Pro Pro Phe Ile Ser Asn Glu Pro Asn Val  
35 40 45  
Lys Tyr Ile Ile Pro Asn Met Gly Ile Asp Ser Lys Gly Thr Ile Tyr  
50 55 60  
15 Val Thr Val Thr Lys Arg Ile Gln Gln Gly Ala Asn Tyr Thr Ser Glu  
65 70 75 80  
Gln Leu Gly Met Tyr Tyr Arg Pro Leu Gly Asp Asn Glu Gln Trp Trp  
85 90 95  
20 Lys His Asp Pro Tyr Phe Asp Asp Lys Ile Val Ala Asp Ile Gln Thr  
100 105 110  
Asp Ala Tyr Gly Arg Val Tyr Val Cys Thr Thr Ser Ser Arg Asp Gln  
115 120 125  
Glu Tyr Gln Leu Tyr Ile Asn Glu Gln Asn Glu Trp Arg Cys Ile Phe  
130 135 140  
25 Lys Thr Ser Val Ser Thr Tyr Glu His Gly Met Ala Val Phe Arg Ser  
145 150 155 160  
Ser Thr Gly Val Thr Tyr Ile Gly Thr Arg His His Ile Phe Ala Ser  
165 170 175  
30 Gly Val Asn Asp Phe Glu Phe Asn Thr Ile Tyr Glu Asp Ser Thr Pro  
180 185 190  
Met Ser Cys Arg Phe Ala Glu Ala Thr Asn Ser Gly Thr Ile Tyr Leu  
195 200 205  
Ala Leu Met His Glu Thr Thr Met Ser Thr Thr Ile Leu Thr Tyr Gln  
210 215 220  
35 Asn Gly Glu Phe Val Asp Ile Ser Glu Ser Glu Leu Ser Asn Ser Ile  
225 230 235 240  
Ile Ala Ser Met Cys Ser Asn Lys Glu Gly Asp Ile Ile Ala Leu Val  
245 250 255  
40 Thr Ser Tyr Thr Gly Phe Met Ser Gly Thr Leu Ala Ile Arg Lys Ala  
260 265 270  
Asp Glu Gly Lys Trp Gln Leu Val Gly Gly Asp Ile Gln Asn Ala Ile  
275 280 285  
Val Gln Asn Ile Cys Met Met Asp Asp Asn Lys Ile Ala Cys Glu Val  
290 295 300  
45 Phe Gly Thr Pro Asn Gly Val Asp Gly Arg Thr Arg Val Cys Val Ser  
305 310 315 320  
Asp Ala Ser Val Phe Asp Phe Glu Trp Tyr Glu Asp Glu Ile Tyr Gly  
325 330 335  
50 Gly Leu Ile Phe Asp Thr Phe Phe Tyr Ser Pro Trp Asp Lys Leu Leu  
340 345 350  
Tyr Ala Lys Phe Gly Gly Ile Met Leu Arg Ser Lys Glu Ser Phe Ile  
355 360 365  
Thr Ser Phe Ile Ser Pro Thr Val Val Gln Gly Val Asp Val Tyr Thr  
370 375 380  
55 Leu Ala Gly Lys Ile Arg Ile Glu Ser Glu Thr Pro Val Ser Glu Val  
385 390 395 400  
Leu Leu Phe Asp Leu Ala Gly Arg Met Val Leu Arg Gln Thr Ile Asp  
405 410 415  
Asn Lys Ile Tyr Ser Asp Ile Asp Thr Asn Gly Leu Lys Arg Ser Gly  
420 425 430  
60 Ile Tyr Val Val Ser Val Arg Leu Ser Ser Gly Gln Val Phe Ser His  
435 440 445  
Lys Val Gln Val  
450

65

## (2) INFORMATION FOR SEQ ID NO:361

## (i) SEQUENCE CHARACTERISTICS:

70

(A) LENGTH: 331 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

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## (iii) HYPOTHETICAL: YES

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(vi) ORIGINAL SOURCE:

(A) ORGANISM: Porphyromonas gingivalis

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(ix) FEATURE:

(A) NAME/KEY: misc\_feature

(B) LOCATION 1...331

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:361

10

Gly Leu Tyr Gly Met Ser Val Val Pro Ile Ile Ile Tyr Leu Cys Gly  
 1 5 10 15  
 Ile Ser Asn Tyr Ala Arg Leu Met Ile Ile Arg Cys Leu Ile Arg Arg  
 20 25 30  
 15 Pro Arg Thr Val Leu Phe Gly Leu Ile Phe Val Val Gly Leu Phe Ser  
 35 40 45  
 Ala Met Ala Gln Glu Lys Lys Asp Ser Leu Ser Thr Val Gln Pro Val  
 50 55 60  
 20 Pro Asn Ser Ser Met Val Glu Gln Thr Pro Leu Ser Ile Asp His  
 65 70 75 80  
 Pro Val Leu Pro Ala Ser Phe Gln Asn Thr Arg Thr Leu Lys Arg Phe  
 85 90 95  
 Arg Asp Lys His Leu Ser Asp Ala Leu Leu Asn Gly Leu Lys Pro His  
 100 105 110  
 25 Arg Ser Ser Leu Gln Leu Asn Glu Leu Asn Phe Ala Ala Glu Arg  
 115 120 125  
 Arg Asp Phe Val Ser Pro Leu Leu Gln Thr Arg His Ala Ala Gly Val  
 130 135 140  
 30 Leu Ser Trp Arg Pro Thr Asp Arg Met His Phe Tyr Thr Ser Gly Asn  
 145 150 155 160  
 Ile Gly Leu Gly His Asp Leu Leu Thr Gly Val Arg Lys Asp Phe Gly  
 165 170 175  
 Trp Asn Ala Gly Ala Asp Phe Leu Leu Ser Gln Asn Leu Thr Ala His  
 180 185 190  
 35 Val Gln Gly Gly Trp Gln Gln Asn Phe Gly Phe Ile Pro Met Thr Ala  
 195 200 205  
 Val Asn Gly Gln Leu Arg Trp Gln Ala Thr Glu Arg Leu Ser Phe Thr  
 210 215 220  
 40 Thr Gly Ile Asp Tyr Arg Gln Val Gln Trp Asn Ala Phe Asp Asn Arg  
 225 230 235 240  
 Thr Phe Ser Leu Lys Gly Ser Ala Arg Tyr Glu Val Met Asp Asn Val  
 245 250 255  
 Phe Val Asn Gly Phe Gly Ser Tyr Pro Leu Tyr Ser Ser Thr Arg Ser  
 260 265 270  
 45 Gly Leu Asn Met Ala Val Pro Met His Gly Phe Gly Pro Gln Tyr Gly  
 275 280 285  
 Gly Ser Leu Glu Leu Lys Val Ser Glu Arg Phe Gly Phe Ala Val Gly  
 290 295 300  
 50 Met Glu Arg Glu Tyr Asn Ile Trp Thr Arg Arg Trp Glu Thr His Tyr  
 305 310 315 320  
 Phe Ala Tyr Pro Val Phe Tyr Gly Asp Lys Lys  
 325 330

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(2) INFORMATION FOR SEQ ID NO:362

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 329 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

60

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

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(vi) ORIGINAL SOURCE:

(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

(A) NAME/KEY: misc\_feature

(B) LOCATION 1...329

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:362

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Glu Thr Asn Ser Trp Val Ser Ser Asp Cys Asn Ser Thr Thr Met Lys  
 1 5 10 15



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Thr Asn Arg Arg Tyr Ala Phe Val Leu Pro Leu Leu Leu Leu Thr Gly  
 20 25 30  
 Leu Leu Ala Trp Gly Gln Asp Ser Ser His Gly Ser Asn Thr Ala Phe  
 35 40 45  
 5 Ala Thr Asp Ser Ser Ser Arg Glu Leu Pro Thr Glu Gln Ser Ala Tyr  
 50 55 60  
 Arg Ile His Ser Ala Tyr Met Val Gly Gly Gly Gly Ser Ile Thr Arg  
 65 70 75 80  
 10 Asp Thr Tyr Leu Ser Pro Leu Arg Tyr Gly Gly Trp Thr Leu Asn Leu  
 85 90 95  
 Leu Gly Glu Lys Thr Phe Pro Leu Lys Ala Ser Asp Ser Arg Tip Met  
 100 105 110  
 Ile Arg Thr Gly His Glu Leu Asp Phe Ala Leu Met Asp Asn Pro Ala  
 115 120 125  
 15 Asn Asn Ala His Phe Tyr Ser Leu Leu Tyr Asn Gly Ser Ala Ala Ala  
 130 135 140  
 Leu Tyr Arg Leu Gly Ala Lys His Leu Arg Ala Ala Trp Met Asp Asn  
 145 150 155 160  
 20 Leu Arg Leu Ala Phe Gly Pro Gly Leu Glu Ile Gly Leu Gly Gly Ile  
 165 170 175  
 Tyr Ser Thr Arg Asn Gly Asn Asn Pro Ala Thr Leu Lys Leu Tyr Thr  
 180 185 190  
 Asn Ala Ile Ala Gln Ala Ser Ile Gly Tyr Tyr Val Pro Ser Glu Thr  
 195 200 205  
 25 Phe Pro Leu Tyr Phe Arg Leu Leu Ser Gln Ile Asn Leu Phe Gly Ile  
 210 215 220  
 Ala Tyr Gly Asn Gly Phe Gly Glu Ser Tyr Tyr Glu Asn Phe Leu Leu  
 225 230 235 240  
 30 Asn Asn Gly Ile Ala Gly Ser Leu His Phe Thr Tyr Pro Gly Lys Phe  
 245 250 255  
 Thr Arg Phe Thr Thr Leu Ile Thr Ala Asp Ile Pro Ile Arg Asn Phe  
 260 265 270  
 Cys Thr Leu Arg Val Gly Tyr Arg Tyr Ser His Leu Gly Ser Ser Leu  
 275 280 285  
 35 Asn Ala Leu Asp Thr Arg Ile His Ser His Thr Ala Phe Ile Gly Phe  
 290 295 300  
 Val Thr Glu Phe Tyr Arg Phe Arg Gly Arg Lys Ala Met Asn Thr Gly  
 305 310 315 320  
 40 Arg Arg Thr Ser Leu Tyr Tyr His Asp  
 325

## (2) INFORMATION FOR SEQ ID NO:363

- 45 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 319 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
 50 (ii) MOLECULE TYPE: protein  
 (iii) HYPOTHETICAL: YES  
 (vi) ORIGINAL SOURCE:  
 55 (A) ORGANISM: Porphyromonas gingivalis  
 (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...319  
 60 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:363

Phe Thr Ser Gly Thr Ile Phe Val Arg Ile Ala Ile Ser Gly Arg Val  
 1 5 10 15  
 65 Val Cys Arg Glu Val Glu Asp Asn Gly Arg Arg Glu Ala Val Arg His  
 20 25 30  
 Asp Gly Met Val Val Thr Leu Leu Val Ile Val Gly Ile Val Val Val  
 35 40 45  
 Val Arg Tyr Ser Leu Arg Val His Val His Lys Thr Gly Thr Val Val  
 50 55 60  
 70 Ser Ala Ala Ile Phe Gly Phe Ile Leu Leu Gly Lys Thr Val Pro Cys  
 65 70 75 80  
 Asp Thr Arg Asn Phe Phe Ser Ser Glu Ser Asp Glu Pro Glu Ser Arg  
 85 90 95  
 75 Val Ala Thr Glu Ile Ala His Leu Cys Glu Ile Gly Phe Gln Ile His  
 100 105 110

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Ala Ser Ser Ile His Val Ala Val Arg Thr Asp Phe Gly Gln Ala Gly  
 115 120 125  
 Ile His Cys Pro Met Ala Thr Asp Ala Ser Ala Thr Glu Phe Asp Arg  
 130 135 140  
 5 Ser Ala Glu Cys Ala Glu Arg Thr Ser Ala Gln Ile Asp Thr Ala Ile  
 145 150 155 160  
 Arg Ser Gln Ser Gln Ile Ile Arg Thr His Ile Asp Thr Cys Pro Lys  
 165 170 175  
 10 Ser Ser Gly Thr Ile Gly Gly Ser Thr His Thr Ser Leu His Leu Lys  
 180 185 190  
 Val Phe Asp Gly Arg Gly Glu Val Gly His Ile His Pro Lys Asp Gly  
 195 200 205  
 Leu Arg Phe Gly Val Val Glu Gly Tyr Ser Ile Gly Ser Tyr Val Asp  
 210 215 220  
 15 Ala Ile Gly Ile Gly Ala Thr His Ala Lys Ala Gly Ile Ser Asp Thr  
 225 230 235 240  
 Arg Thr Gly Ile Ala Gly Tyr His Gly Gly Ser Gln His Gln Gln  
 245 250 255  
 20 Ile Gly Asp Val Thr Thr Ile Ile Gly Leu Gly Lys Phe Gly Leu Ala  
 260 265 270  
 Asn Val Gly Val Ser Asp Arg Gly Phe Arg Arg Gly Ala Ser Ser Tyr  
 275 280 285  
 Asp Leu Tyr Gly Leu Glu Leu His Ile Ala Lys Thr Ile Tyr Leu Ala  
 290 295 300  
 25 Val Gly Asp Gly Cys Leu Cys Arg Gln Ala Glu Arg Gln Asp Gly  
 305 310 315

(2) INFORMATION FOR SEQ ID NO:364

- 30 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 614 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear
- 35 (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- 40 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Porphyromonas gingivalis
- (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...614
- 45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:364

Pro Tyr Asn Val Gln Ser Ile Ser Asn Lys Thr Ile Lys Lys Gln Met  
 1 5 10 15  
 50 Glu Asn Leu Lys Asn Ile Gln Pro Arg Glu Asp Phe Asn Trp Glu Glu  
 20 25 30  
 Phe Glu Ala Gly Gly Val His Ala Ala Val Ser Arg Gln Glu Gln Glu  
 35 40 45  
 55 Ala Ala Tyr Asp Lys Thr Leu Asn Thr Ile Lys Glu Lys Glu Val Val  
 50 55 60  
 Met Gly Arg Val Thr Ala Ile Asn Lys Arg Glu Val Val Ile Asn Val  
 65 70 75 80  
 Gly Tyr Lys Ser Glu Gly Val Val Pro Ala Thr Glu Phe Arg Tyr Asn  
 85 90 95  
 60 Pro Glu Leu Lys Val Gly Asp Glu Val Glu Val Tyr Ile Glu Asn Gln  
 100 105 110  
 Glu Asp Lys Lys Gly Gln Leu Val Leu Ser His Arg Lys Gly Arg Ala  
 115 120 125  
 65 Ala Arg Ser Trp Glu Arg Val Asn Glu Ala Leu Glu Lys Asp Glu Ile  
 130 135 140  
 Val Lys Gly Tyr Val Lys Cys Arg Thr Lys Gly Gly Met Ile Val Asp  
 145 150 155 160  
 Val Phe Gly Ile Glu Ala Phe Leu Pro Gly Ser Gln Ile Asp Val Arg  
 165 170 175  
 70 Pro Ile Arg Asp Tyr Asp Ala Phe Val Glu Lys Thr Met Glu Phe Lys  
 180 185 190  
 Ile Val Lys Ile Asn Gln Glu Tyr Lys Asn Val Val Val Ser His Lys  
 195 200 205  
 75 Val Leu Ile Glu Ala Glu Leu Glu Gln Gln Lys Lys Glu Ile Ile Gly  
 210 215 220

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Lys Leu Glu Lys Gly Gln Val Leu Glu Gly Ile Val Lys Asn Ile Thr  
 225 230 235 240  
 Ser Tyr Gly Val Phe Ile Asp Leu Gly Gly Val Asp Gly Leu Ile His  
 245 250 255  
 5 Ile Thr Asp Leu Ser Trp Gly Arg Val Ala His Pro Glu Glu Ile Val  
 260 265 270  
 Gln Leu Asp Gln Lys Ile Asn Val Val Ile Leu Asp Phe Asp Glu Asp  
 275 280 285  
 10 Arg Lys Arg Ile Ala Leu Gly Leu Lys Gln Leu Met Pro His Pro Trp  
 290 295 300  
 Asp Ala Leu Asp Ser Glu Leu Lys Val Gly Asp Lys Val Lys Gly Lys  
 305 310 315 320  
 Val Val Val Met Ala Asp Tyr Gly Ala Phe Val Glu Ile Ala Gln Gly  
 325 330 335  
 15 Val Glu Gly Leu Ile His Val Ser Glu Met Ser Trp Thr Gln His Leu  
 340 345 350  
 Arg Ser Ala Gln Asp Phe Leu His Val Gly Asp Glu Val Glu Ala Val  
 355 360 365  
 20 Ile Leu Thr Leu Asp Arg Glu Arg Lys Met Ser Leu Gly Leu Lys  
 370 375 380  
 Gln Leu Lys Pro Asp Pro Trp Ala Asp Ile Glu Thr Arg Phe Pro Val  
 385 390 395 400  
 Gly Ser Arg His His Ala Arg Val Arg Asn Phe Thr Asn Phe Gly Val  
 405 410 415  
 25 Phe Val Glu Ile Glu Glu Gly Val Asp Gly Leu Ile His Ile Ser Asp  
 420 425 430  
 Leu Ser Trp Thr Lys Lys Ile Lys His Pro Ser Glu Phe Thr Glu Val  
 435 440 445  
 30 Gly Ala Asp Ile Glu Val Gln Val Ile Glu Ile Asp Lys Glu Asn Arg  
 450 455 460  
 Arg Leu Ser Leu Gly His Lys Gln Leu Glu Glu Asn Pro Trp Asp Val  
 465 470 475 480  
 Phe Glu Thr Val Phe Thr Val Gly Ser Ile His Glu Gly Thr Val Ile  
 485 490 495  
 35 Glu Val Met Asp Lys Gly Ala Val Val Ser Leu Pro Tyr Gly Val Glu  
 500 505 510  
 Gly Phe Ala Thr Pro Lys His Met Val Lys Glu Asp Gly Ser Gln Ala  
 515 520 525  
 40 Val Leu Glu Glu Lys Leu Pro Phe Lys Val Ile Glu Phe Asn Lys Asp  
 530 535 540  
 Ala Lys Arg Ile Ile Val Ser His Ser Arg Val Phe Glu Asp Glu Gln  
 545 550 555 560  
 Lys Met Ala Gln Arg Glu Ala Asn Ala Glu Arg Lys Ala Glu Ala Lys  
 565 570 575  
 45 Ala Ala Gln Lys Glu Ala Ala Ala Glu Ala Ala Asn Pro Ala Gln Ala  
 580 585 590  
 Val Glu Lys Ala Thr Leu Gly Asp Leu Gly Glu Leu Ala Ala Leu Lys  
 595 600 605  
 50 Glu Lys Leu Ser Glu Asn  
 610

(2) INFORMATION FOR SEQ ID NO:365

55 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 243 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

60 (ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

65 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...243

70 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:365

Ser Thr Ile Met Lys Lys Ala Ile Leu Ser Gly Ala Ala Leu Leu Leu  
 1 5 10 15  
 75 Gly Leu Cys Ala Asn Ala Gln Asn Val Gln Leu His Tyr Asp Phe Gly  
 20 25 30

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His Ser Ile Tyr Asp Glu Leu Asp Gly Arg Pro Lys Leu Thr Thr Thr  
 35 40 45  
 Val Glu Asn Phe Thr Pro Asp Lys Trp Gly Ser Thr Phe Phe Phe Ile  
 50 55 60  
 5 Asp Met Asp Tyr Thr Gly Lys Gly Ile Gln Ser Ala Tyr Trp Glu Ile  
 65 70 75 80  
 Ser Arg Glu Leu Lys Phe Trp Gln Ala Pro Val Ser Ile His Leu Glu  
 85 90 95  
 10 Tyr Asn Gly Gly Leu Ser Thr Ser Phe Thr Phe Gly His Asp Ala Leu  
 100 105 110  
 Ile Gly Ala Thr Tyr Thr Tyr Asn Asn Pro Ser Phe Thr Arg Gly Phe  
 115 120 125  
 Thr Ile Thr Pro Met Tyr Lys His Leu Gly Ala His Asp Phe His Thr  
 130 135 140  
 15 Tyr Gln Ile Thr Gly Thr Trp Tyr Met His Phe Leu Asp Gly Leu Leu  
 145 150 155 160  
 Thr Phe Asn Gly Phe Leu Asp Leu Trp Gly Phe Pro Gln Glu Asn Pro  
 165 170 175  
 20 Ile Gly Gly Pro Val Leu Lys Glu Gly Asp Lys Phe Val Phe Leu Ser  
 180 185 190  
 Glu Pro Gln Phe Trp Ile Asn Leu Asn Arg Ile Lys Gly Ile Asp Lys  
 195 200 205  
 Asp Phe Asn Leu Ser Ile Gly Thr Glu Met Glu Ile Ser Arg Asn Phe  
 210 215 220  
 25 Ala Arg Met Asp Lys Phe Ser Cys Ile Pro Thr Leu Ala Val Lys Trp  
 225 230 235 240  
 Thr Phe Asn

30 (2) INFORMATION FOR SEQ ID NO:366  
 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 235 amino acids  
 (B) TYPE: amino acid  
 35 (D) TOPOLOGY: linear  
 (ii) MOLECULE TYPE: protein  
 (iii) HYPOTHETICAL: YES  
 40 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Porphyromonas gingivalis  
 (ix) FEATURE:  
 45 (A) NAME/KEY: misc feature  
 (B) LOCATION 1...235  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:366

50 Met Lys Thr Ile Ser Lys Asn His Ala Ala Arg Ile Cys Ala Ala Ile  
 1 5 10 15  
 Ala Leu Phe Ala Val Cys Asn Gly Arg Ile Ala Ala Gln Asp Phe Leu  
 20 25 30  
 55 Tyr Glu Ile Gly Gly Gly Phe Gly Ala Ala Gln Tyr Phe Gly Asp Ala  
 35 40 45  
 Asn Arg Gly Leu Phe Gly Ser Ser Gly Val Gly Leu Leu Val Gly  
 50 55 60  
 Arg Tyr Asn Tyr Asn Phe Arg Trp Ala Phe Ser Thr Met Leu Asp Trp  
 65 70 75 80  
 60 Arg Thr Leu Arg Gly Asp Thr Asp Lys Ser Gly Asn Val Phe Pro Asp  
 85 90 95  
 Phe Ala Gln Ala Asp Phe Lys Val Gly Leu Thr Gln Leu His Val Arg  
 100 105 110  
 65 Ser Glu Phe Asn Phe Leu Pro Tyr Ser Asp Gly Tyr Lys Tyr Leu Gly  
 115 120 125  
 Thr Ala Arg Leu Ser Pro Tyr Val Ala Ala Gly Leu Ser Leu Gly Phe  
 130 135 140  
 Ala Ser Gly Ala Lys Gly Ser Ala Phe Ala Pro Gly Ile Thr Ala Gly  
 145 150 155 160  
 70 Met Gly Val Lys Tyr Lys Leu Lys Pro Arg Ile Asn Val Gly Ile Glu  
 165 170 175  
 Tyr Ser Phe Thr Gly Leu Leu Thr Asp Ala Leu Asp Ala Leu Thr Asp  
 180 185 190  
 75 Lys Ser Val Trp Leu Glu Asp Pro Tyr Lys Ile Asn Asp Ser Trp Val  
 195 200 205

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Lys Asn Lys Asp Ala Thr Gly Ala Leu Val Leu Arg Ile Thr Tyr Asp  
 210 215 220  
 Phe Gly Leu Arg Lys Thr Phe Cys Asn Lys Gln  
 225 230 235

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(2) INFORMATION FOR SEQ ID NO:367

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 436 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

10

(ii) MOLECULE TYPE: protein

15

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Porphyromonas gingivalis

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(ix) FEATURE:

(A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...436

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:367

Asn Ile Met Tyr Lys Asp Tyr Lys Gly Leu Tyr Ala Ser Leu Arg Trp  
 1 5 10 15  
 Tyr Ala Leu Ile Ile Gly Leu Leu Phe Ala Ala Asp Gly Ile Gln Ala  
 20 25 30  
 Gln Asn Asn Asn Phe Thr Glu Ser Pro Tyr Thr Arg Phe Gly Leu Gly  
 35 40 45  
 Arg Leu Gly Glu Arg Thr Thr Ile Ser Gly His Ser Met Gly Gly Leu  
 50 55 60  
 Gly Val Gly Leu Arg Gln Gly Thr Tyr Val Asn Ala Val Asn Pro Ala  
 65 70 75 80  
 Ser Tyr Ser Ala Val Asp Ser Met Thr Phe Ile Phe Asp Phe Gly Ala  
 85 90 95  
 Ser Thr Gly Ile Thr Trp Tyr Ala Glu Asn Gly Lys Lys Asp Asn Arg  
 100 105 110  
 Lys Met Gly Asn Ile Glu Tyr Phe Ala Met Leu Phe Pro Ile Ser Lys  
 115 120 125  
 Ser Ile Ala Met Ser Ala Gly Val Leu Pro Tyr Ser Ala Ser Gly Tyr  
 130 135 140  
 Gln Phe Gly Ser Val Asp Gln Val Glu Gly Gly Ser Val Gln Tyr Thr  
 145 150 155 160  
 Arg Lys Tyr Leu Gly Thr Gly Asn Leu Asn Asp Leu Tyr Val Gly Ile  
 165 170 175  
 Gly Ala Thr Pro Phe Lys Asn Phe Ser Ile Gly Ala Asn Ala Ser Ser  
 180 185 190  
 Leu Phe Gly Arg Phe Thr His Ser Arg Gln Val Ile Phe Ser Thr Glu  
 195 200 205  
 Ala Pro Tyr Asn Pro Val His Leu Ser Thr Leu Tyr Leu Lys Ala Ala  
 210 215 220  
 Lys Phe Asp Phe Gly Met Gln Tyr His Leu Leu Leu Lys Ser Asp Arg  
 225 230 235 240  
 Ser Leu Val Ile Gly Ala Val Tyr Ser Pro Arg Val Lys Met His Ser  
 245 250 255  
 Glu Leu Thr Gln Ile Lys Asn Gln Val Gln Asn Gly Val Val Val Glu  
 260 265 270  
 Ser Glu Thr Gln Glu Tyr Ile Lys Gly Met Asp Tyr Tyr Thr Leu Pro  
 275 280 285  
 His Thr Leu Gly Ile Gly Phe Ser Tyr Glu Lys Lys Asp Lys Leu Leu  
 290 295 300  
 Leu Gly Ala Asp Val Gln Tyr Ser Lys Trp Lys Gly Glu Lys Phe Tyr  
 305 310 315 320  
 Lys Ser Asp Cys Lys Phe Gln Asp Arg Ile Arg Val Ser Leu Gly Gly  
 325 330 335  
 Glu Ile Ile Pro Asp Ile Asn Ala Val Gly Met Trp Pro Lys Val Arg  
 340 345 350  
 Tyr Arg Phe Gly Leu His Gly Glu Asn Ser Tyr Leu Lys Val Pro Thr  
 355 360 365  
 Lys Gly Gly Val Tyr Gln Gly Tyr His Ile Val Gly Ala Val Phe Gly  
 370 375 380  
 Ile Gly Ile Pro Leu Asn Asp Arg Arg Ser Phe Val Asn Val Ser Leu  
 385 390 395 400

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Glu Tyr Asp Arg Leu Ile Pro Lys Glu Gly Met Ile Lys Glu Asn Ala  
 405 410 415  
 Leu Lys Leu Thr Phe Gly Leu Thr Phe Asn Glu Ser Trp Phe Lys Lys  
 420 425 430  
 5 Leu Lys Leu Asn  
 435

(2) INFORMATION FOR SEQ ID NO:368

10

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 945 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

15

(ii) MOLECULE TYPE: protein  
 (iii) HYPOTHETICAL: YES

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(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Porphyromonas gingivalis

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(ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...945

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:368

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Asn Thr Ile Ser Glu Asn Gly Asn Asp Ser Thr Tyr Phe Ser Phe Gln  
 1 5 10 15  
 Thr Phe Leu Met Arg Ser Ile Tyr Gln Leu Leu Leu Ser Ile Leu Leu  
 20 25 30  
 Ala Ser Leu Gly Phe Val Gly Leu Glu Ala Gln Gln Ala Gly Val Ala  
 35 40 45  
 Gly Arg Val Leu Asp Glu Glu Gly Asn Pro Met Ile Gln Ala Asn Val  
 50 55 60  
 Gln Leu Val Gln Ser Thr Gly Gln Val Ala Val Ala Ala Gly Ala Thr  
 65 70 75 80  
 Asn Glu Lys Gly Leu Phe Ser Leu Lys Thr Ser Gln Glu Gly Asp Tyr  
 85 90 95  
 Ile Leu Arg Val Ser Tyr Val Gly Tyr Thr Thr His Asp Glu Lys Ile  
 100 105 110  
 Ser Leu Arg Asn Gly Gln Thr Ile Thr Leu Lys Asp Ile Ser Met Asn  
 115 120 125  
 Glu Asp Ala Arg Leu Leu Gln Ser Val Thr Val Gln Ala Lys Ala Ala  
 130 135 140  
 Glu Val Val Val Arg Asn Asp Thr Leu Glu Phe Asn Ala Gly Ser Tyr  
 145 150 155 160  
 Thr Val Ala Gln Gly Ala Ser Ile Glu Glu Leu Ile Lys Lys Leu Pro  
 165 170 175  
 Gly Ala Glu Ile Gly Ser Asp Gly Lys Ile Thr Ile Asn Gly Lys Asp  
 180 185 190  
 Ile Ser Lys Ile Leu Val Asp Gly Lys Glu Phe Phe Ser Lys Asp Pro  
 195 200 205  
 Gln Val Ala Ile Lys Asn Leu Pro Ala Asp Met Val Asn Lys Val Gln  
 210 215 220  
 Val Leu Asn Lys Leu Ser Glu Leu Ser Arg Met Ser Gly Phe Asp Asp  
 225 230 235 240  
 Gly Glu Glu Glu Thr Val Ile Asn Leu Thr Val Lys Pro Glu Lys Lys  
 245 250 255  
 Lys Gly Leu Phe Gly Thr Leu Gln Ala Gly Tyr Gly Thr Asp Gln Arg  
 260 265 270  
 Tyr Met Ala Gly Gly Asn Val Asn Arg Phe Asp Gly Asn Lys Gln Trp  
 275 280 285  
 Thr Leu Ile Gly Ser Ala Asn Asn Thr Asn Asn Met Gly Phe Ser Glu  
 290 295 300  
 Met Asp Ser Glu Met Gly Ser Met Thr Phe Phe Ser Pro Gln Gly Gly  
 305 310 315 320  
 Gly Arg Arg Gly Phe Gly Asn Ser Gly Gly Val Thr Ser Ser Met  
 325 330 335  
 Leu Gly Gly Asn Phe Ser Val Glu Phe Ser Ser Ala Leu Asn Thr Gly  
 340 345 350  
 Gly Asp Ala Arg Tyr Gly Tyr Asn Asp Lys Ala Ile Glu Thr Thr Lys  
 355 360 365  
 Arg Val Glu Asn Ile Leu Ala Glu Gly Asn Thr Tyr Met Asp Glu Asn  
 370 375 380

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Ile Leu Glu Arg Ser Phe Ser His Asn Gly Gln Ala Arg Phe Arg Met  
 385 390 395 400  
 Gln Trp Lys Pro Ser Glu Arg Thr Glu Val Val Phe Glu Pro Asp Leu  
 405 410 415  
 5 Ser Ile Ser Lys Ile Asp Gly Phe Phe Asn Asp Thr Tyr Glu Thr Lys  
 420 425 430  
 Asp Ala Thr Gly Ile Ser Ile Asn Lys Gly Ser Ile His Gln Thr Thr  
 435 440 445  
 10 Gln Gly Asn Asn Phe Arg Leu Asn Gly Glu Leu Asp Ile Ser His Lys  
 450 455 460  
 Leu Asn Asp Glu Gly Arg Thr Ile Ser Ala Ser Val Ser Gly Gly Leu  
 465 470 475 480  
 Thr Asp Glu Asp Gly Asp Gly Ile Tyr Gln Ala Val Leu Gln Ser Val  
 485 490 495  
 15 Glu Thr Asn Gln Lys Gln Phe Asn Asp Asn Ser Asn Leu Gln Tyr Arg  
 500 505 510  
 Leu Arg Leu Ser Tyr Val Glu Pro Leu Gly Lys Asn Tyr Phe Ala Gln  
 515 520 525  
 20 Ala Ile Leu Asn Arg Arg Phe Ser Arg Arg Asn Ser Asp Arg Glu Val  
 530 535 540  
 Tyr Arg Leu Gly Asp Asp Gly Gln Tyr Ser Ile Leu Asp Ser Gln Tyr  
 545 550 555 560  
 Gly Leu Ser Tyr Ser Asn Glu Phe Thr Gln Tyr Arg Ile Gly Leu Asn  
 565 570 575  
 25 Leu Lys Lys Ile Ala Lys Thr Trp Asp Tyr Thr Val Gly Phe Asn Val  
 580 585 590  
 Asp Pro Asn Arg Thr Val Ser Tyr Arg Ser Val Ala Gly Val Glu Gln  
 595 600 605  
 30 Asp Lys Leu Ala Phe Asn Arg Val Asn Leu Ser Pro Met Leu Arg Ile  
 610 615 620  
 Asn Tyr Lys Pro Ser Arg Thr Thr Asn Leu Arg Val Asp Tyr Arg Gly  
 625 630 635 640  
 Arg Thr Thr Gln Pro Ser Ile Asn Gln Ile Ala Pro Val Gln Asp Ile  
 645 650 655  
 35 Thr Asn Pro Leu Phe Val Thr Glu Gly Asn Pro Gly Leu Lys Pro Ser  
 660 665 670  
 Tyr Ser Asn Asn Val Met Ala Met Phe Ser Asp Phe Asp Ala Lys Ser  
 675 680 685  
 40 Gln Arg Ala Phe Asn Ile Val Phe Phe Gly Asn Tyr Thr Phe Asp Asp  
 690 695 700  
 Ile Val Pro Asn Thr His Tyr Asp Pro Ser Thr Gly Ile Arg Thr Thr  
 705 710 715 720  
 Arg Tyr Glu Asn Ala Ser Gly Thr Trp Gln Ala Asn Leu His Gly Thr  
 725 730 735  
 45 Leu Ser Leu Pro Leu Lys Asn Arg Ala Phe Ser Phe Arg Met Ser Leu  
 740 745 750  
 Phe Asn Arg Leu Ala Glu Gly Gln Ser Phe Ile Asn Asp Asp Lys Asn  
 755 760 765  
 50 Lys Ala Leu Ser Phe Arg Thr Arg Glu Arg Leu Thr Leu Thr Tyr Arg  
 770 775 780  
 Asn Asn Trp Ile Asp Thr Ser Ile Gly Gly Asn Ile Gly Phe Tyr Met  
 785 790 795 800  
 Ala Asn Asn Ser Leu Ser Gly Gln Lys Asp Ser Arg Thr Tyr Asp Phe  
 805 810 815  
 55 Gly Gly Asn Tyr Gln Val Ala Leu Thr Leu Pro Tyr Gly Phe Arg Ile  
 820 825 830  
 Asp Ser Asp Val Glu Tyr Asn Thr Asn Ser Gly Tyr Ser Gly Gly Phe  
 835 840 845  
 60 Ser Leu Asp Glu Trp Leu Trp Asn Ala Ser Leu Ser Tyr Ser Phe Leu  
 850 855 860  
 Arg Asp Lys Ala Gly Thr Leu Arg Val Asn Gly Tyr Asp Ile Leu Gly  
 865 870 875 880  
 Gln Arg Ser Ser Ile Ser Arg Ser Ala Ser Ala Ile Asn Ile Glu Glu  
 885 890 895  
 65 Ser Met Ser Asn Thr Ile Gly Arg Tyr Val Met Val Asp Phe Ile Tyr  
 900 905 910  
 Arg Phe Asn Ala Phe Ser Gly Gly Gly Ser Arg Ser Asp His Gln Arg  
 915 920 925  
 70 Gly Asn Met Asn Arg Pro Gly Pro Pro Phe Gly Gly Gly Arg Arg Pro  
 930 935 940  
 Ser  
 945

(2) INFORMATION FOR SEQ ID NO:369

75

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(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 412 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...412

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:369

20	Gly	Glu	Tyr	Pro	Ala	Asn	Ser	Asn	Asp	Lys	Lys	Glu	Met	Val	Met	Lys
	1				5					10				15		
	Leu	Ile	Lys	Arg	Ser	Leu	Leu	Leu	Leu	Gly	Ala	Val	Leu	Leu	Ile	Thr
				20					25					30		
	Leu	Pro	Ala	Tyr	Ser	Gln	Asn	Asp	Asp	Ile	Phe	Glu	Asp	Asp	Ile	Tyr
		35					40					45				
25	Thr	Ser	Arg	Lys	Glu	Ile	Arg	Lys	Gln	Asn	Gln	Val	Lys	Asp	Trp	Gln
		50				55					60					
	Asn	Gln	Glu	Asp	Gly	Tyr	Gly	Asp	Asp	Thr	Glu	Tyr	Thr	Val	Ala	Ser
	65				70					75				80		
	Asp	Arg	Asp	Ile	Asp	Ala	Tyr	Asn	Arg	Arg	Asp	Gly	Gln	Ser	Tyr	Asp
30				85					90					95		
	Gly	Lys	Lys	Leu	Ser	Lys	Asp	Lys	Lys	Arg	Asp	Ser	Thr	Arg	Ser	Ser
				100				105						110		
	Val	Pro	Gly	Arg	Tyr	Ser	Arg	Arg	Leu	Ala	Arg	Phe	Tyr	Lys	Pro	Asn
		115					120					125				
35	Thr	Ile	Val	Ile	Ser	Gly	Ala	Asp	Asn	Val	Tyr	Val	Thr	Asp	Asp	Gly
		130				135						140				
	Glu	Tyr	Phe	Val	Tyr	Gly	Asp	Glu	Tyr	Tyr	Asp	Ala	Ser	Ser	Val	
	145					150				155				160		
	Asn	Ile	Tyr	Ile	Asn	Ser	Pro	Trp	Cys	Asp	Pro	Phe	Pro	Tyr	Thr	Ser
40				165					170					175		
	Trp	Tyr	Pro	Ser	Phe	Ser	Gly	Trp	Tyr	Asn	Tyr	Thr	Trp	Asn	Tyr	Pro
			180					185						190		
	Trp	Phe	Tyr	Tyr	Gly	Ser	His	Ile	Gly	Trp	Gly	Gly	Tyr	Tyr	Pro	Gly
		195					200					205				
45	Tyr	Asn	Trp	Tyr	Trp	Ser	Tyr	Tyr	Tyr	Asp	Pro	Phe	Tyr	Asn	Pro	Tyr
		210				215					220					
	Gly	Ile	Gly	Met	Gly	Trp	Gly	Tyr	Pro	Tyr	Gly	Trp	Gly	Ser	Tyr	Tyr
	225					230					235				240	
	Gly	Trp	Gly	Gly	Tyr	Pro	Gly	Val	Ile	His	His	Tyr	His	His	Tyr	Pro
50				245					250					255		
	Lys	Lys	Thr	Tyr	Ser	Asn	Gly	Gln	His	Ser	Gly	Ala	Tyr	Tyr	Ser	Tyr
			260				265							270		
	Gly	Arg	Pro	Asn	Arg	Ile	Lys	Gly	Gly	Thr	Ser	Gly	Ala	Lys	Leu	Gly
		275					280						285			
55	Thr	Gly	Arg	Tyr	Asp	Arg	Ile	Gln	Asn	Ser	Ser	Ser	Gln	Lys	Asn	Lys
		290					295					300				
	Phe	Gly	Leu	Gln	Ser	Asn	Lys	Pro	Asn	Asn	Asn	Leu	Gln	Asn	Val	Lys
		305				310					315				320	
	Ser	Gly	Arg	Thr	Gly	Arg	Ala	Asn	Arg	Asp	Arg	Asn	Ile	Glu	Thr	Val
60				325						330					335	
	Thr	Pro	Asn	Asn	Gly	Gln	Lys	Gln	Asn	Arg	Pro	Val	Phe	Gln	Gln	Asn
			340					345						350		
	Gln	Ser	Gly	Asn	Asp	Arg	Pro	Thr	Gly	Arg	Asn	Ile	Arg	Ser	Glu	Arg
		355					360					365				
65	Gln	Gly	Glu	Asn	Asn	Asp	Arg	Thr	Phe	Ser	Thr	Pro	Ser	Arg	Ser	Asn
		370				375						380				
	Ser	Asn	Gly	Gly	Phe	Ser	Thr	Pro	Ser	Arg	Ser	Ser	Ser	Gly	Ser	Met
		385				390					395					400
	Ser	Gly	Gly	Gly	Gly	Arg	Ser	Gly	Arg	Gly	Arg	Asn				
70				405								410				

(2) INFORMATION FOR SEQ ID NO:370

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 601 amino acids



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(B) TYPE: amino acid  
(D) TOPOLOGY: linear

5 (ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

10 (A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

(A) NAME/KEY: misc\_feature

(B) LOCATION: 1...601

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:370

	Ser	Asn	Ser	Ser	Ser	His	Lys	Trp	Leu	Ile	Tyr	Tyr	His	Ile	Glu	Lys
	1				5					10					15	
20	Thr	Lys	Ser	Ile	Met	Ile	Arg	Lys	Leu	Ile	Leu	Leu	Leu	Ala	Leu	Met
			20						25					30		
	Pro	Val	Ala	Ser	Val	Ala	Phe	Ala	Val	Pro	Thr	Asp	Ser	Thr	Glu	Ser
			35					40					45			
	Lys	Asp	Asn	Arg	Ile	Leu	Thr	Ser	Met	Gln	Ser	Ser	Ser	Leu	Asn	Arg
		50				55					60					
25	Asp	Asp	Ala	Pro	Asp	Lys	Trp	Gln	Pro	Met	His	Ala	Asn	Phe	Ser	Ile
	65					70					75					80
	Gln	Ser	Asp	Met	Leu	Leu	Ser	Thr	Ala	Gln	Lys	Ser	Lys	Asn	Thr	Trp
					85					90					95	
30	Phe	Gly	Asn	Ser	Tyr	Ile	Met	Gly	Ile	Ile	Lys	Asn	Asn	Tyr	Leu	Glu
					100				105					110		
	Phe	Gly	Ala	Arg	Phe	Glu	Asp	Leu	Tyr	Lys	Pro	Leu	Pro	Gly	His	Glu
			115					120					125			
	Pro	Glu	Met	Gly	Arg	Gly	Val	Pro	His	Met	Tyr	Val	Lys	Gly	Ser	Tyr
		130					135					140				
35	His	Trp	Ala	Glu	Leu	Thr	Met	Gly	Asp	Phe	Tyr	Asp	Gln	Phe	Gly	Ser
					150						155					160
	Gly	Met	Val	Phe	Arg	Thr	Tyr	Glu	Glu	Arg	Asn	Leu	Gly	Ile	Asp	Asn
					165					170					175	
40	Ala	Val	Arg	Gly	Gly	Arg	Ile	Val	Leu	Thr	Pro	Phe	Asp	Gly	Val	Arg
					180					185				190		
	Val	Lys	Gly	Ile	Ala	Gly	Gln	Gln	Arg	Asn	Tyr	Phe	Asp	Arg	Thr	Gly
			195				200					205				
	Lys	Val	Phe	Asn	Ser	Gly	Arg	Gly	Tyr	Leu	Leu	Gly	Ser	Asp	Leu	Glu
		210				215						220				
45	Leu	Asn	Val	Glu	Arg	Trp	Ser	Ser	Ala	Met	Arg	Asp	Asn	Asp	Tyr	His
					230						235					240
	Leu	Ala	Ile	Gly	Gly	Ser	Phe	Val	Ser	Lys	His	Glu	Ala	Asp	Glu	Asp
					245					250					255	
50	Ile	Phe	Val	Gly	Val	Gly	Glu	Asp	Arg	Lys	Arg	Leu	Asn	Leu	Pro	Leu
					260				265					270		
	Asn	Val	Pro	Ile	Met	Gly	Leu	Arg	Thr	Asn	Phe	Gln	Lys	Gly	Gly	Leu
			275				280						285			
	Ala	Leu	Tyr	Ala	Glu	Tyr	Gly	Tyr	Lys	Tyr	Asn	Asp	Pro	Ser	Ala	Asp
		290					295					300				
55	Asn	Asp	Tyr	Ile	Tyr	His	Asp	Gly	Gln	Ala	Ala	Leu	Leu	Ser	Ala	Ser
						310					315					320
	Tyr	Ser	Lys	Lys	Gly	Met	Ser	Ile	Leu	Leu	Gln	Ala	Lys	Arg	Cys	Glu
					325					330					335	
60	Asn	Phe	Ala	Phe	Arg	Ser	Lys	Arg	Ser	Ala	Gln	Leu	Thr	Pro	Leu	Met
					340					345				350		
	Ile	Asn	Tyr	Met	Pro	Ala	Phe	Thr	Gln	Ala	His	Thr	Tyr	Thr	Leu	Ala
					355				360					365		
	Ala	Ile	Tyr	Pro	Tyr	Ala	Thr	Gln	Pro	Gln	Gly	Glu	Trp	Ala	Phe	Gln
					370			375				380				
65	Gly	Glu	Leu	Arg	Tyr	Asn	Phe	Ala	Arg	Arg	Thr	Ala	Leu	Gly	Gly	Arg
						390					395					400
	Tyr	Gly	Thr	Gly	Leu	Arg	Ile	Asn	Val	Ser	His	Val	Arg	Gly	Leu	Asp
					405					410					415	
70	Lys	Lys	Met	Leu	Lys	Glu	Asn	Pro	Asp	Glu	Leu	Ile	Gly	Thr	Asp	Gly
					420				425					430		
	Tyr	Thr	Val	Ser	Phe	Phe	Gly	Met	Gly	Asp	Leu	Tyr	Tyr	Ser	Asp	Ile
					435			440					445			
	Asp	Val	Glu	Ile	Thr	Lys	Lys	Val	Ser	Pro	Gly	Phe	Asn	Phe	Thr	Leu
					450			455				460				
75	Thr	Tyr	Leu	Asn	Gln	Ile	Tyr	Asn	Asn	Lys	Val	Leu	His	Gly	Ala	Ala

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465                      470                      475                      480  
 Gly Glu Lys Pro Glu Lys Ile Tyr Ala Asn Ile Phe Val Tyr Asp Gly  
                                  485                      490                      495  
 5    Lys Tyr Lys Leu Ser Asn Lys Val Ala Leu Arg Thr Glu Leu Gln Tyr  
                                  500                      505                      510  
 Leu His Thr Lys Gln Asp Gln Gly Asp Trp Ile Tyr Gly Met Ala Glu  
                                  515                      520                      525  
 Leu Ser Ile Leu Pro Ser Leu Met Leu Ser Leu Ser Glu Gln Tyr Asn  
                                  530                      535                      540  
 10   Ile Gly Glu Thr Lys Lys His Tyr Val Met Gly Ser Val Thr Tyr Thr  
                                  545                      550                      555                      560  
 His Gly Ala His Arg Val Ala Phe Ser Ala Gly Lys Thr Arg Ala Gly  
                                  565                      570                      575  
 15   Met Asn Cys Ser Gly Val Cys Arg Val Val Pro Glu Thr Gln Gly  
                                  580                      585                      590  
 Phe Tyr Leu Ser Tyr Ser Thr Asn Leu  
                                  595                      600

20    (2) INFORMATION FOR SEQ ID NO:371

(i) SEQUENCE CHARACTERISTICS:  
       (A) LENGTH: 252 amino acids  
       (B) TYPE: amino acid  
       (D) TOPOLOGY: linear

25    (ii) MOLECULE TYPE: protein

      (iii) HYPOTHETICAL: YES

30    (vi) ORIGINAL SOURCE:  
       (A) ORGANISM: Porphyromonas gingivalis

35    (ix) FEATURE:  
       (A) NAME/KEY: misc\_feature  
       (B) LOCATION 1...252

      (xi) SEQUENCE DESCRIPTION: SEQ ID NO:371

40    Arg Gly Ser Ser Ser Gly Ile Ser Ala Arg Gly Arg Asp Met Arg Ser  
       1                      5                      10                      15  
 Leu Phe Leu Ser Ala Leu Arg Ser Ser Ser Leu His Gly Ser Glu Arg  
                                  20                      25                      30  
 Arg Ser Arg Ile Ser Ser Ser Val Val Met Ser Ile Arg Gln Lys Ile  
                                  35                      40                      45  
 45   Arg Leu Phe His Leu Ser Val Cys Ala Gln Thr His Asp His Leu Ile  
                                  50                      55                      60  
 Glu Ile His Leu Val Cys Ile Glu Phe Gly Ala Ile Asp Thr Asp Glu  
                                  65                      70                      75                      80  
 50   Phe Arg Leu Ser Ser His Ala Tyr Thr Thr Ser Pro Thr His Thr Gly  
                                  85                      90                      95  
 Ala Ile His His Asn Cys Ile Glu Arg Ser Tyr Gly Arg Tyr Leu Val  
                                  100                      105                      110  
 Thr Phe Gly Gln Glu Arg Asn Glu Leu His His His Ser Arg Pro Asp  
                                  115                      120                      125  
 55   Arg Asn Ala Glu Val Tyr Arg Phe Pro Phe Asp Asn Ala Phe His Ser  
                                  130                      135                      140  
 Ile Arg Tyr Glu Ala Phe Arg Pro Ile Arg Pro Ile Val Cys His Asp  
                                  145                      150                      155                      160  
 60   Asp His Phe Ile Ala Ile Gly Ser His Leu Phe Phe Lys Asp Asn Gln  
                                  165                      170                      175  
 Ile Phe Ser Ser Gly Ser Gln Tyr Asp Asn Tyr Thr Val Ala Cys Phe  
                                  180                      185                      190  
 Val Glu Ser Leu His Asp Arg Glu Gln Arg Ser His Thr His Thr Ala  
                                  195                      200                      205  
 65   Ser Gly Thr Asn His Cys Ala Asp Leu Phe Asp Met Arg Thr Leu Ser  
                                  210                      215                      220  
 Gln Arg Thr Tyr His Ile Arg Asp Ile Val Ala Asp Phe Glu Phe Gly  
                                  225                      230                      235                      240  
 70   Gln Phe Leu Gly Arg Phe Ala His Gly Leu Asn His  
                                  245                      250

75    (2) INFORMATION FOR SEQ ID NO:372

(i) SEQUENCE CHARACTERISTICS:  
       (A) LENGTH: 790 amino acids

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(B) TYPE: amino acid  
(D) TOPOLOGY: linear

5 (ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

10 (A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

(A) NAME/KEY: misc\_feature

(B) LOCATION 1...790

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:372

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Leu Leu Phe Ser Ser Pro Leu Pro Arg Met Asp Arg Pro Lys Pro Ser
1      5      10      15
Tyr Ile Val Arg Ile Ala Ala Ile Leu Cys Leu Phe Val Gly Arg Pro
20      25      30
Leu Phe Ala Gln Ser Tyr Val Asp Tyr Val Asp Pro Leu Ile Gly Thr
35      40      45
Leu Ser Ser Phe Glu Leu Ser Ala Gly Asn Thr Tyr Pro Val Ile Gly
50      55      60
25 Leu Pro Trp Gly Met Asn Ser Trp Thr Pro Met Thr Gly Val Pro Gly
65      70      75
Asp Gly Trp Gln Tyr Thr Tyr Ser Ala His Lys Ile Arg Gly Phe Lys
85      90      95
30 Gln Thr His Gln Pro Ser Pro Trp Ile Asn Asp Tyr Gly Gln Phe Ser
100      105      110
Leu Leu Pro Leu Thr Ala Pro Gln Lys Pro Ser Ser Asn Asp Ser Ile
115      120      125
Ala Leu Thr Lys Trp Cys Lys Gln Leu Phe Ser Asp Glu Gln Thr Ser
130      135      140
35 Trp Phe Ser His Lys Ala Glu Thr Ala Thr Pro Tyr Tyr Tyr Ser Val
145      150      155
Tyr Leu Ala Asp Tyr Asp Thr Arg Val Glu Met Ala Pro Thr Glu Arg
165      170      175
40 Ala Ala Ile Phe Arg Ile Arg Tyr Ser Gly Asn Thr Glu Ser Gly Ser
180      185      190
Gly Arg Trp Leu Arg Leu Asp Ala Phe Thr Gly Gly Ser Glu Ile Ser
195      200      205
Ile Val Asp Pro His Thr Val Val Gly Ile Ser Arg Lys Asn Ser Gly
210      215      220
45 Gly Val Pro Ala Asn Phe Ala Cys Tyr Phe Ile Leu Gln Ser Asp Thr
225      230      235
Pro Met Ala Asp Val Leu Leu Glu Thr Asp Thr Gly Lys Ser Asp Glu
245      250      255
50 Gly Thr Arg Ala Trp Ala Ala Cys Arg Phe Asp Ser Gln Glu Val Thr
260      265      270
Val Arg Val Ala Ser Ser Phe Ile Ser Val Glu Gln Ala Glu Arg Asn
275      280      285
Leu Ala Glu Val Lys Gly Gln Ser Phe Asp Arg Ile Arg Leu Ala Gly
290      295      300
55 Arg Glu Ala Trp Asn Lys Val Leu Gly Arg Ile His Val Glu Gly Gly
305      310      315
Thr Lys Asp Glu Arg Thr Thr Phe Tyr Ser Ala Leu Tyr Arg Cys Leu
325      330      335
60 Leu Phe Pro Arg Arg Phe Tyr Glu Glu Asp Ala Ser Gly Asn Phe Val
340      345      350
His Tyr Ser Pro Tyr Asn Gly Glu Val Leu Pro Gly Tyr Leu Tyr Thr
355      360      365
Asp Thr Gly Phe Trp Asp Thr Phe Arg Ala Leu Phe Pro Leu Leu Asn
370      375      380
65 Leu Leu Tyr Pro Asp Glu Asn Ile Lys Ile Gln Glu Gly Leu Leu Asn
385      390      395
Val Tyr Arg Glu Ser Gly Phe Phe Pro Glu Trp Ala Ser Pro Gly His
405      410      415
70 Arg Asp Cys Met Ile Gly Asn Asn Ser Ala Ser Val Leu Ala Asp Ala
420      425      430
Tyr Leu Lys Gly Val Arg Val Glu Asp Thr Arg Thr Leu Met Asn Gly
435      440      445
Leu Leu His Ala Thr Lys Ala Val His Pro Lys Ile Ser Ser Thr Gly
450      455      460
75 Arg Lys Gly Trp Glu Trp Tyr Asn Ser Leu Gly Tyr Val Pro Ala Asp

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465 470 475 480  
 Ala Gly Ile Asp Glu Ser Ala Ala Arg Thr Leu Glu Tyr Ala Tyr Asn  
 485 490 495  
 5 Asp Trp Cys Ile Leu Arg Leu Gly Arg Thr Leu Gly Trp Asp Arg Ala  
 500 505 510  
 Ala Leu Asp Thr Leu Ala His Arg Ser Met Asn Tyr Arg His Leu Phe  
 515 520 525  
 Asp Pro Glu Thr Lys Leu Met Arg Gly Arg Asn Gln Asp Gly Ser Phe  
 530 535 540  
 10 Arg Thr Pro Phe Ser Pro Phe Lys Trp Gly Asp Val Phe Thr Glu Gly  
 545 550 555 560  
 Asn Ala Trp His Tyr Thr Trp Ser Val Phe His Asp Val Gln Gly Leu  
 565 570 575  
 15 Ile Asp Leu Met Gly Gly Asp Arg Pro Phe Val Ser Met Leu Asp Ser  
 580 585 590  
 Val Phe Asn Thr Pro Pro Met Phe Asp Glu Ser Tyr Tyr Gly Phe Val  
 595 600 605  
 Ile His Glu Ile Arg Glu Met Gln Ile Ala Asp Met Gly Asn Tyr Ala  
 610 615 620  
 20 His Gly Asn Gln Pro Ile Gln His Met Ile Tyr Leu Tyr Asn His Ala  
 625 630 635 640  
 Gly His Pro Trp Lys Ala Gln Glu Arg Leu Arg Glu Val Met Gly Arg  
 645 650 655  
 25 Leu Tyr Arg Pro Thr Pro Asp Gly Tyr Cys Gly Asp Glu Asp Asn Gly  
 660 665 670  
 Gln Thr Ser Ala Trp Tyr Val Phe Ser Ala Leu Gly Phe Tyr Pro Val  
 675 680 685  
 Thr Pro Ala Thr Asp Gln Tyr Val Leu Gly Ser Pro Ile Phe Ser Lys  
 690 695 700  
 30 Val Ile Leu Ser Phe Pro Asp Gly His Lys Thr Val Leu His Ala Pro  
 705 710 715 720  
 Ala Asn Ser Ala Asp Thr Pro Tyr Ile Arg Ser Ile Ser Val Glu Gly  
 725 730 735  
 35 Lys Glu Trp Ser Cys Asn Tyr Leu Thr His Glu Gln Leu Arg Ser Ser  
 740 745 750  
 Ala Ser Ile Gln Trp Met Met Asp Thr Lys Pro Asn Tyr Asn Arg Gly  
 755 760 765  
 Met Lys Glu Ser Asp Arg Pro Tyr Ser Phe Ser Thr Glu Gln Gln Arg  
 770 775 780  
 40 Arg Ala Asn His Ser Asn  
 785 790

(2) INFORMATION FOR SEQ ID NO:373

- 45 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 286 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
 50 (ii) MOLECULE TYPE: protein  
 (iii) HYPOTHETICAL: YES  
 (vi) ORIGINAL SOURCE:  
 55 (A) ORGANISM: Porphyromonas gingivalis  
 (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...286  
 60 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:373

Ile Cys Gly Ser Lys Met Asn Leu Ser Gly Leu Gln Ser Phe Thr Met  
 1 5 10 15  
 65 Met Lys Ser Met Arg Ser Val Leu Leu Leu Leu Phe Pro Leu Ser Leu  
 20 25 30  
 Ile Thr Ala Leu Gly Cys Ser Asn Asn Lys Ala Ala Glu Ser Lys Ser  
 35 40 45  
 70 Val Ser Phe Asp Ser Ala Tyr Leu Glu Arg Tyr Ile Pro Leu Arg Ala  
 50 55 60  
 Asp Ile Asp Thr Pro Ser Leu His Val Met Ile Ser Tyr Val Tyr Pro  
 65 70 75 80  
 Ser Gly Asp Asp Met Leu Thr Glu Ile Phe Asn Gly Leu Leu Phe Gly  
 85 90 95  
 75 Asp Ser Leu Met Asp Ser Ser Ser Pro Glu Asn Ala Met Glu Gly Tyr

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5                   100                   105                   110  
       Ala Gln Met Leu Gly Glu Asp Tyr Arg Ser Asn Asn Ala Glu Ala Asn  
           115                   120                   125  
       Leu Gln Gly Leu Pro Ser Asp Leu Leu Asp Tyr Ile Tyr Lys Gln Glu  
           130                   135                   140  
       Asn Thr Ile Ala Tyr Cys Asp Thr Gly Leu Ile Ser Thr Arg Ile Asn  
           145                   150                   155                   160  
       Thr Tyr Thr Tyr Glu Gly Gly Ala His Thr Glu Asn Thr Val Arg Phe  
                   165                   170                   175  
 10       Ala Asn Ile Leu Arg Thr Thr Gly Lys Val Leu Glu Glu Arg Asp Ile  
                   180                   185                   190  
       Phe Lys Ile Asp Tyr Ala Glu Arg Leu Ser Ala Leu Ile Ile Gly Gln  
           195                   200                   205  
 15       Leu Val His Asp Phe Gly Lys Thr Thr Pro Ala Glu Leu Asp Ala Ile  
           210                   215                   220  
       Gly Phe Phe Asn Ala Glu Glu Ile Gln Pro Asn Gly Asn Phe Met Ile  
           225                   230                   235                   240  
       Asp Asp Lys Gly Leu Thr Tyr Cys Phe Asn Glu Tyr Gln Ile Ala Ala  
                   245                   250                   255  
 20       Tyr Ala Arg Gly Ala Val Tyr Val Arg Leu Gly Tyr Asp Val Leu Ala  
                   260                   265                   270  
       Pro Leu Leu Arg Asp Asp Ser Pro Leu Lys Arg Tyr Leu Pro  
                   275                   280                   285

25       (2) INFORMATION FOR SEQ ID NO:374  
           (i) SEQUENCE CHARACTERISTICS:  
               (A) LENGTH: 378 amino acids  
               (B) TYPE: amino acid  
               (D) TOPOLOGY: linear  
 30           (ii) MOLECULE TYPE: protein  
           (iii) HYPOTHETICAL: YES  
 35           (vi) ORIGINAL SOURCE:  
               (A) ORGANISM: Porphyromonas gingivalis  
           (ix) FEATURE:  
               (A) NAME/KEY: misc feature  
               (B) LOCATION 1...378  
 40           (xi) SEQUENCE DESCRIPTION: SEQ ID NO:374  
 45       Gly Ile Ile Ser Val Leu Ser His Val Val Asp Arg Pro Gln Trp Gly  
           1                   5                   10                   15  
       Ala Ser Pro Glu Ala Ala Gly Thr His Ser Val Tyr Ser Ile Leu His  
           20                   25                   30  
 50       Pro Ser Ala Gly Ile Ile Arg Ile Arg Ser Met Gly Ile Ile Ser Ala  
           35                   40                   45  
       Cys Arg Ile Ala Ile Leu Ala Gly Lys His Pro Arg Ser Gly Leu Ser  
           50                   55                   60  
       Arg Ala Asn Val Gly Ile Leu Ser Tyr Asn Pro Glu Asn Thr Pro Glu  
           65                   70                   75                   80  
 55       Lys Lys Arg Lys Leu Gln Glu Lys Asn Val Phe Leu Gln Ile Arg Leu  
           85                   90                   95  
       Arg Gln Ser Phe Asn Asn Leu Ile Pro Ser Leu Pro Phe Arg Ile Asp  
           100                   105                   110  
 60       Asn Thr Lys Lys Ile Thr Glu Met Lys Lys Thr Thr Leu Thr Gly Ser  
           115                   120                   125  
       Ile Cys Ala Leu Leu Leu Phe Leu Gly Leu Ser Ala Asn Ala Gln Ser  
           130                   135                   140  
       Lys Leu Lys Ile Lys Ser Ile Glu Ala Ala Thr Thr Phe Ser Ser Ala  
           145                   150                   155                   160  
 65       Thr Ala Gly Asn Gly Phe Gly Gly Asn Ile Phe Gly Met Asp Met Ser  
           165                   170                   175  
       Ile Arg Met Arg Val His His Ser Ile Leu Pro Glu Gly Leu Asp Phe  
           180                   185                   190  
 70       Ser Val Gly Ile His Glu Arg Arg Ala His Trp Glu Glu Ala Gly Ser  
           195                   200                   205  
       Pro Lys Leu Met Tyr Thr Asn Val Pro Ser Ile Ile Gly Ile Val Glu  
           210                   215                   220  
       Lys Val Ile Val Phe Glu Asp Ala Glu Asp Phe Phe Asp Lys Lys Ala  
           225                   230                   235                   240  
 75       Leu Gly Arg Phe Leu Ile Ser Leu Gly Ile Ser Tyr Thr Lys His Leu

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5 Gly Ala Tyr Trp 245 Gly Trp Thr Asn Asp 250 Ala His Ile Leu Phe Ser Pro 255  
 Ile Pro Lys Ser 260 Lys Val His Tyr Asp 265 Thr Tyr Thr Arg Ala Gly Ser 270  
 Asp Leu Val Leu Gln Ser Glu Asp Val Ala Thr Val Ser Asn Gly Phe 285  
 Ser Pro Gly Ile Gly Leu Lys Ser Ser Ile Trp Trp Lys Met Pro Ile 300  
 10 Lys Ser Lys Tyr Asp Phe Arg Leu Gly Phe Ser Leu Gly Tyr Glu Tyr 315  
 Leu Asn Leu Leu Tyr Pro Tyr Arg Asn Phe Lys Leu Asp Gly Asn Lys 320  
 Pro Leu Ser Ala Leu Ser Pro Arg Met Asn His Ile Gly His Val Gly 335  
 15 Phe Asn Phe Thr Val Gly Leu Trp Thr Asn 345  
 20 (2) INFORMATION FOR SEQ ID NO:375  
 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1269 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
 25 (ii) MOLECULE TYPE: protein  
 (iii) HYPOTHETICAL: YES  
 30 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Porphyromonas gingivalis  
 (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 35 (B) LOCATION 1...1269  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:375  
 40 Val Lys Cys Met Gly Lys Tyr Lys Arg Ala Lys Tyr Arg Tyr Trp Leu  
 1 5 10 15  
 Phe Pro Phe Cys Ser Asp Tyr Tyr Thr Phe Glu Gly Val Thr Phe Leu  
 20 25 30  
 Cys Ala Ser Asp Asp Met Thr Thr Lys Lys Pro Gln Ala Ile Leu Asp  
 35 40 45  
 45 Leu Glu Lys Ala Tyr Asn Ile Glu Ile Pro Asp Leu Ser Ser Gln Glu  
 50 55 60  
 Gly Ile Ser Trp Ser Val Asn Arg Tyr Phe Lys Gln Asp Ser Ser Gly  
 65 70 75 80  
 50 Ala Val Val Glu Leu Cys Leu Arg Glu Cys Gln Ile Glu Ser Met Thr  
 85 90 95  
 Trp Leu Ile Asp Phe Pro Ala Leu Lys Lys Leu Asp Leu Ser Tyr Asn  
 100 105 110  
 Gln Ile Ser Lys Leu Glu Gly Leu Glu Arg Leu Thr Ser Leu Thr Lys  
 115 120 125  
 55 Leu Arg Leu Arg Ser Asn Gln Ile Arg Lys Leu Glu Gly Leu Asp Ser  
 130 135 140  
 Leu Thr Ser Leu Thr Lys Leu Ser Leu Ser Asp Asn Gln Ile Ser Lys  
 145 150 155 160  
 60 Leu Glu Gly Leu Glu Arg Leu Thr Ser Leu Ala Glu Leu Tyr Leu Leu  
 165 170 175  
 Asp Asn Gln Ile Ser Lys Leu Glu Gly Leu Glu Arg Leu Thr Ser Leu  
 180 185 190  
 Ala Thr Leu Glu Leu Ser Gly Asn Gln Ile Arg Lys Leu Glu Gly Leu  
 195 200 205  
 65 Glu Arg Leu Thr Ser Leu Ala Thr Leu Glu Leu Ser Gly Asn Gln Ile  
 210 215 220  
 Arg Lys Leu Glu Gly Leu Glu Arg Leu Thr Ser Leu Thr Lys Leu Arg  
 225 230 235 240  
 70 Leu Arg Ser Asn Gln Ile Ser Lys Leu Glu Gly Leu Glu Arg Leu Thr  
 245 250 255  
 Ser Leu Ala Thr Leu Glu Leu Ser Gly Asn Gln Ile Arg Lys Leu Glu  
 260 265 270  
 Gly Leu Glu Arg Leu Thr Ser Leu Ala Thr Leu Glu Leu Ser Gly Asn  
 275 280 285  
 75 Gln Ile Ser Lys Leu Glu Gly Leu Glu Arg Leu Ser Ser Leu Thr Lys

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5	290	Leu	Arg	Leu	Arg	Ser	Asn	Gln	Ile	Ser	Lys	Leu	Glu	Gly	Leu	Glu	Arg
	305	Leu	Thr	Ser	Leu	Thr	310	Lys	Leu	Ser	Leu	Ser	315	Asn	Gln	Ile	Ser
						325						330					335
		Leu	Glu	Gly	Leu	Glu	Arg	Leu	Thr	Ser	Leu	Ala	Glu	Leu	Tyr	Leu	Leu
10		Asp	Asn	Gln	Ile	Arg	Lys	Leu	Glu	Gly	Leu	Glu	Arg	Leu	Thr	Ser	Leu
		Thr	Lys	Leu	Arg	Leu	Arg	Ser	375	Asn	Gln	Ile	Ser	Lys	Leu	Glu	Gly
		Asp	Ser	Leu	Thr	Ser	Leu	Thr	Lys	Leu	Ser	Leu	Ser	Asp	Asn	Gln	Ile
15	385	Ser	Lys	Leu	Glu	Gly	Leu	Glu	Arg	Leu	Thr	Ser	Leu	Ala	Glu	Leu	Tyr
						405											415
		Leu	Leu	Asp	Asn	Gln	Ile	Arg	Lys	Leu	Glu	Gly	Leu	Asp	Gly	Leu	Ala
						420											430
20		Ser	Leu	Thr	Arg	Leu	Ser	Leu	Arg	Arg	Asn	Gln	Ile	Ser	Lys	Leu	Glu
		Gly	Leu	Asp	Arg	Leu	Lys	Val	Leu	Arg	Lys	Leu	Asp	Val	Ser	Gly	Asn
25		Asp	Ile	Gln	Ser	Ile	Asp	Asp	Ile	Lys	Leu	Leu	Ala	Pro	Ile	Leu	Glu
		Gln	Thr	Leu	Glu	Lys	Leu	Arg	Ile	His	Asp	Asn	Pro	Phe	Val	Ala	Ser
30		Ser	Gly	Leu	Ile	Leu	Ser	Pro	Tyr	Asp	Asn	His	Leu	Pro	Glu	Ile	Lys
		Ala	Leu	Leu	Glu	Lys	Glu	Lys	Glu	Lys	Gln	Lys	Lys	Thr	Ser	Val	Glu
35		Tyr	His	Pro	Phe	Cys	Lys	Val	Met	Leu	Leu	Gly	Asn	His	Ser	Ser	Gly
		Lys	Thr	Thr	Phe	Leu	Ser	Gln	Tyr	Asp	Thr	Asn	Tyr	Thr	Tyr	Gln	Lys
40		Asn	Thr	His	Val	Leu	Ser	Ile	His	Arg	Ser	Asn	Asn	Pro	Asn	Ala	Ile
		Phe	Tyr	Asp	Phe	Gly	Gly	Gln	Asp	Tyr	Tyr	His	Gly	Ile	Tyr	Gln	Ala
45		Phe	Phe	Thr	Thr	Gln	Ser	Leu	Tyr	Leu	Phe	Trp	Asp	Ala	Lys	Lys	
		Asp	Arg	Asn	Phe	Val	Ser	Val	Asp	Asp	Lys	Glu	Tyr	Gln	Thr	Leu	Asn
50		Phe	Asn	Arg	Pro	Tyr	Trp	Leu	Gly	Gln	Ile	Ala	Tyr	Ala	Cys	Asn	Arg
		Cys	Met	Ser	Val	Gly	Gly	Asn	Pro	Asp	Gly	Lys	Asp	Thr	Pro	Gln	Thr
55		Thr	Asp	Asp	Thr	Ile	Ile	Ile	Gln	Thr	His	Ala	Asp	Glu	Thr	Gly	Ala
		Lys	Gln	Gln	Thr	Leu	Gly	Cys	Ala	Al							

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Leu Lys Phe Glu Arg Phe Ile Pro Phe Gly Leu Ile Asn Gln Ile Ile  
 900 905 910  
 Ala Tyr Tyr Gly Arg Glu Glu Gly Ala Leu Lys Arg Tyr Trp Arg Asp  
 915 920 925  
 5 Gln Val Ile Phe Thr Ala Gly Arg Glu Met Asp Arg Gln Thr Leu Glu  
 930 935 940  
 Gln Glu Glu Glu Lys Glu Gly Leu Pro Lys Thr Asn Ala Glu Asp Tyr  
 945 950 955 960  
 10 Gln Ile Trp Ile Lys Leu Asp Phe Thr Asp Leu Ala Ile Ser Val Phe  
 965 970 975  
 Ile Lys Glu Gln Arg Lys Thr Ser Ala Lys Asp Met Gln Arg Lys Glu  
 980 985 990  
 Ala Thr Ile Leu Ser Asp Met Leu Asp Met Tyr Trp Asn Asn Ile Pro  
 995 1000 1005  
 15 Pro Arg Glu Gln Ile Gly Asp Lys Asp Thr Glu Gln Thr Arg Ser Thr  
 1010 1015 1020  
 Ile Arg Glu Thr Asn Arg Lys Lys Arg Pro Ile Gln Asp Leu Tyr Leu  
 1025 1030 1035 1040  
 20 Ser Cys Ala Gln Ala Asp Lys Asp Leu Thr Glu Ser His Tyr Ile His  
 1045 1050 1055  
 Leu Gly Thr Leu Asp Asp Glu Ser Lys Thr Thr Ala Arg Ile Ala Ala  
 1060 1065 1070  
 Tyr Pro Leu Lys Asn Gly Val Ile Asp Lys Glu Arg Val Arg Glu Val  
 1075 1080 1085  
 25 Ser Thr Arg Pro Tyr Lys His Leu Ser Val Asn Lys Asn Leu Ala Thr  
 1090 1095 1100  
 Ala Lys Gln Ile Phe Ile Ser Tyr Ser Lys Glu Asp Gln Thr Glu Leu  
 1105 1110 1115 1120  
 30 Glu Thr Cys Leu Gln Phe Phe Lys Pro Leu Glu Lys Asn Gly Gln Ile  
 1125 1130 1135  
 Glu Ile Tyr Tyr Asp Lys Leu Thr Lys Phe Glu Thr Pro Ile His Pro  
 1140 1145 1150  
 Glu Ile Arg Lys Arg Ile Val Glu Ala Asp Cys Ile Ile Ala Leu Ile  
 1155 1160 1165  
 35 Ser Gln Arg Tyr Leu Ala Thr Asp Tyr Ile Leu Asp His Glu Leu Pro  
 1170 1175 1180  
 Val Phe Arg Glu Tyr Asn Lys Thr Ile Val Pro Ile Leu Ile Lys Pro  
 1185 1190 1195 1200  
 40 Cys Thr Phe Glu Asp Asp Glu Phe Leu Arg Glu Lys Tyr Phe Ala Gln  
 1205 1210 1215  
 Lys Ala Gln Ile Ile Asn Leu Gly Lys Glu Gly Lys Thr Ile Lys Ala  
 1220 1225 1230  
 Tyr Asp Ser Ile Thr Ala Ser Ala His Arg Asp Glu Asn Trp Val Ala  
 1235 1240 1245  
 45 Val Val Arg Glu Phe Lys Glu Lys Ile Leu Arg Ile Thr Lys Gln Glu  
 1250 1255 1260  
 Val Asn Thr Asp Glu  
 1265

50 (2) INFORMATION FOR SEQ ID NO:376

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 231 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
 55  
 (ii) MOLECULE TYPE: protein  
 (iii) HYPOTHETICAL: YES  
 60  
 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Porphyromonas gingivalis  
 (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...231  
 65  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:376

70 Lys Phe Met Met Lys Lys Ala Phe Val Phe Val Leu Leu Val Cys Leu  
 1 5 10 15  
 Phe Ser Ser Phe Ser Ser Ser Ala Gln Thr Thr Asn Ser Ser Arg  
 20 25 30  
 75 Ser Tyr Phe Thr Gly Arg Ile Glu Lys Val Ser Leu Asn Leu Gly Val  
 35 40 45



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5 Pro Pro Val Ser Thr Glu Val Trp Gly Met Thr His Asp Ala Asn Gly  
 50 55 60  
 Leu Pro Phe Glu Ile Pro Ile Ser Phe Ser Arg Phe Asn Ser Gln Gly  
 65 70 75 80  
 Asp Ile Ala Thr Thr Tyr Tyr Ile Ala Asn Ser Glu Ala Thr Leu Asn  
 85 90 95  
 Glu Trp Cys Asp Tyr Ala His Pro Gly Gly Ile Val Arg Val Glu Gly  
 100 105 110  
 10 Arg Phe Trp Lys Met Thr Tyr Asn Ile Pro Thr Tyr Asn Ala Val Cys  
 115 120 125  
 Thr Arg Ile Thr Phe Glu Asn Gln Glu Ile Glu Gly Thr Ile Val Leu  
 130 135 140  
 Ile Pro Lys Pro Lys Val Ser Leu Pro His Val Ser Glu Ser Val Pro  
 145 150 155 160  
 15 Cys Ile Arg Thr Glu Ala Gly Arg Glu Phe Ile Leu Cys Glu Glu Asp  
 165 170 175  
 Asp Thr Phe Val Ser His Asp Gly Asn Glu Val Thr Ile Gly Gly Lys  
 180 185 190  
 20 Pro Phe Leu Leu Asn Thr Asn Val Lys Ile Val Gly Asp Val Ser Gln  
 195 200 205  
 Lys Tyr Ala Val Gly Val Gly Glu Ile Arg Phe Leu Gln Ile Cys Ala  
 210 215 220  
 Gln Thr Val Ser Gln Gln Lys  
 225 230

(2) INFORMATION FOR SEQ ID NO:377

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 563 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

(A) NAME/KEY: misc\_feature

(B) LOCATION 1...563

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:377

45 Ser Leu Ile Asn Asn Ser Arg Asp Trp Arg Ala Pro Val Arg Leu Ser  
 1 5 10 15  
 Leu Lys Lys Lys Thr Lys Thr Met Lys Thr Lys Val Leu Arg Lys Phe  
 20 25 30  
 50 Val Val Ala Ala Phe Ala Val Ala Thr Leu Cys Pro Leu Ala Gln Ala  
 35 40 45  
 Gln Thr Met Gly Gly Asp Asp Val Lys Val Val Gln Tyr Asn Gln Glu  
 50 55 60  
 55 Lys Leu Val Gln Thr Arg Met Ser Val Ala Asp Asn Gly Trp Ile Tyr  
 65 70 75 80  
 Val Met Thr His Ser Gly Tyr Asp Thr Gly Asn Ser Asn Val Lys Ile  
 85 90 95  
 Phe Arg Ser Lys Asp Gln Gly Ala Thr Tyr Gln Lys Leu Arg Asp Trp  
 100 105 110  
 60 Asp Pro Ser Asp Asp Tyr Gln Phe Gln Asp Phe Asp Ile Val Val Thr  
 115 120 125  
 Gly Lys Asn Glu Ser Asp Ile Lys Ile Trp Ser Val Glu Leu Met Asn  
 130 135 140  
 65 Lys Pro Gly Gly Tyr Lys Ser Arg Val Ala Val Phe Ser Arg Asp Ala  
 145 150 155 160  
 Asn Ala Gln Asn Ala Lys Leu Val Tyr Lys Glu Asp Phe Ser Asn Val  
 165 170 175  
 Gln Leu Tyr Asp Val Asp Ile Ala Ser Asn Tyr Arg Ser Pro Ser Ser  
 180 185 190  
 70 Leu Asn Asn Gly Gly Asn Pro Phe Ala Leu Ala Phe Ala Tyr Thr Gly  
 195 200 205  
 Phe Asn Asn Thr His Lys Ile Ser Phe Val Asp Tyr Val Phe Ser Leu  
 210 215 220  
 75 Asn Gly Gly Gln Asn Phe Asn Lys Asn Leu Leu Phe Ser Gln Asp Gly  
 225 230 235 240

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Glu Lys Lys Ile Asp Lys Val Asp Leu Ser Leu Gly Ser Thr Ser Glu  
 245 250 255  
 Ser Met Gly His Asn Ala Trp Pro Leu Met Gly Val Val Phe Glu Met  
 260 265 270  
 5 Asn Lys Gln Gly Gly Lys Ser Asp Ile Gly Phe Leu Ser Asn Phe Val  
 275 280 285  
 Asp Asn Asp Pro Glu Phe Gln Trp Ser Gly Pro Ile Lys Val Ser Glu  
 290 295 300  
 10 Ser Asp Met Ser Phe Ser Pro Lys Ile Gln Met Leu Leu Asp Glu Asp  
 305 310 315 320  
 Asn Asn Thr Ile Asn Gly Glu Ser Cys His Asn Phe Met Ile Thr Tyr  
 325 330 335  
 Ser Asp Tyr Asp Ser Glu Tyr Ser Asp Trp Asp Ile Arg Tyr Val Tyr  
 340 345 350  
 15 Pro Lys Lys Ser Phe Lys Tyr Glu Lys Gly Lys Thr Pro Thr Met Asp  
 355 360 365  
 Asp Leu Val Glu Ala Phe Leu Thr Ala Ser Tyr Gln Ser Glu Thr Asn  
 370 375 380  
 20 Ser Gly Leu Gly Tyr Asp Lys Asn Ala Asn His Tyr Leu Ile Thr Tyr  
 385 390 395 400  
 Ala Lys Lys Glu Glu Asn Gly Thr Asn Thr Leu Lys Tyr Arg Trp Ala  
 405 410 415  
 Asn Tyr Asp Lys Ile His Asn Lys Asp Leu Trp Ser Asp Thr Phe Thr  
 420 425 430  
 25 Tyr Thr Ser Ser Ala Asn Ala Leu Tyr Thr Pro Gln Val Asp Ile Asn  
 435 440 445  
 Pro Thr Lys Gly Leu Val Cys Trp Ser Trp Val Glu Tyr Leu Pro Gly  
 450 455 460  
 30 Lys Arg Ile Val Trp Ser Asp Thr Gln Trp Thr His Ala Asn Gly Val  
 465 470 475 480  
 Glu Asp Ile Val Met Gln Glu Gly Ser Met Lys Leu Tyr Pro Asn Pro  
 485 490 495  
 Ala Gln Glu Tyr Ala Val Ile Ser Leu Pro Thr Ala Ala Asn Cys Lys  
 500 505 510  
 35 Ala Val Val Tyr Asp Met Gln Gly Arg Val Val Ala Glu Ala Ser Phe  
 515 520 525  
 Ser Gly Asn Glu Tyr Arg Leu Asn Val Gln His Leu Ala Lys Gly Thr  
 530 535 540  
 40 Tyr Ile Leu Lys Val Val Ser Asp Thr Glu Arg Phe Val Glu Lys Leu  
 545 550 555 560  
 Ile Val Glu

- (2) INFORMATION FOR SEQ ID NO:378  
 45 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 786 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
 50 (ii) MOLECULE TYPE: protein  
 (iii) HYPOTHETICAL: YES  
 55 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Porphyromonas gingivalis  
 (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 60 (B) LOCATION 1...786  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:378

65 Ile Val Tyr Leu Cys His Cys Met Asn His Arg Arg Ser Lys Thr Met  
 1 5 10 15  
 Leu Thr Ile Arg Asn Phe Leu Leu Phe Cys Cys Leu Ser Leu Ile Ala  
 20 25 30  
 Phe Ala Ala Asp Ala Gln Ser Ser Val Ser Ser Gly Arg Arg Leu Thr  
 35 40 45  
 70 Glu Tyr Val Asn Pro Phe Ile Gly Thr Ala Asn Tyr Gly Thr Thr Asn  
 50 55 60  
 Pro Gly Ala Val Leu Pro Asn Gly Leu Met Ser Val Thr Pro Phe Asn  
 65 70 75 80  
 75 Val Ser Gly Ser Thr Glu Asn Arg Phe Asp Lys Asp Ser Arg Trp Trp  
 85 90 95

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	Ser	Ala	Pro	Tyr	Ser	Ala	Asp	Asn	Ser	Tyr	Cys	Ile	Gly	Phe	Ser	His
				100					105					110		
	Val	Asn	Leu	Ser	Gly	Val	Gly	Cys	Pro	Glu	Leu	Ser	Gly	Ile	Leu	Leu
			115					120					125			
5	Met	Ala	Thr	Ser	Gly	Thr	Phe	Asp	Pro	Asp	Tyr	Cys	Cys	Tyr	Gly	Ser
		130					135					140				
	Ser	Leu	Ser	Arg	Glu	Tyr	Ala	Arg	Pro	Gly	Glu	Tyr	Lys	Ala	Val	Leu
	145					150					155				160	
10	Asp	Lys	Tyr	Gly	Ile	Asp	Ala	Ala	Val	Thr	Val	Thr	Glu	Arg	Thr	Ala
				165						170					175	
	Leu	Thr	Glu	Phe	Ala	Phe	Pro	Glu	Gly	Glu	Gly	His	Ile	Leu	Leu	Asn
				180					185					190		
	Leu	Gly	Gln	Ala	Leu	Ser	Asn	Glu	Ser	Gly	Ala	Ser	Val	Arg	Phe	Leu
			195					200					205			
15	Asn	Asp	Ser	Thr	Val	Val	Gly	Ser	Arg	Leu	Met	Gly	Thr	Phe	Cys	Tyr
	210						215					220				
	Asn	Pro	Gln	Ala	Val	Phe	Arg	Gln	Tyr	Phe	Val	Leu	Gln	Val	Ser	Arg
	225					230					235				240	
20	Arg	Pro	Ile	Ser	Ala	Gly	Tyr	Trp	Lys	Lys	Gln	Pro	Pro	Met	Thr	Val
				245						250					255	
	Glu	Ala	Gln	Trp	Asp	Ser	Thr	Ala	Gly	Lys	Tyr	Lys	Gln	Tyr	Asp	Gly
				260					265					270		
	Tyr	Lys	Arg	Glu	Met	Ser	Gly	Asp	Asp	Ile	Gly	Val	Arg	Phe	Ser	Phe
			275					280					285			
25	Asn	Cys	Asp	Gln	Gly	Glu	Lys	Ile	Tyr	Val	Arg	Ser	Ala	Val	Ser	Phe
	290						295					300				
	Val	Ser	Glu	Ala	Asn	Ala	Leu	Tyr	Asn	Leu	Glu	Ala	Gln	Glu	Glu	
	305					310					315				320	
30	Val	Phe	Lys	Ser	Val	Gly	Gly	Asn	Pro	Ala	Lys	Ala	Phe	Ser	Ala	Ile
				325						330					335	
	Arg	Ser	Arg	Ala	Ile	Glu	Arg	Trp	Glu	Glu	Ala	Leu	Gly	Thr	Val	Glu
				340					345					350		
	Val	Glu	Gly	Gly	Thr	Pro	Asp	Glu	Lys	Thr	Ile	Phe	Tyr	Thr	Ala	Leu
			355					360					365			
35	Tyr	His	Leu	Leu	Ile	His	Pro	Asn	Ile	Leu	Gln	Asp	Ala	Asn	Gly	Glu
		370				375						380				
	Tyr	Pro	Met	Met	Gly	Ser	Gly	Lys	Thr	Gly	Asn	Thr	Ala	His	Asp	Arg
	385					390					395				400	
40	Tyr	Thr	Val	Phe	Ser	Leu	Trp	Asp	Thr	Tyr	Arg	Asn	Val	His	Pro	Leu
				405						410					415	
	Leu	Cys	Leu	Leu	Tyr	Pro	Glu	Lys	Gln	Leu	Asp	Met	Val	Arg	Thr	Leu
				420					425					430		
	Ile	Asp	Met	Tyr	Arg	Glu	Ser	Gly	Trp	Leu	Pro	Arg	Trp	Glu	Leu	Tyr
		435						440					445			
45	Gly	Gln	Glu	Thr	Leu	Thr	Met	Glu	Gly	Asp	Pro	Ser	Leu	Ile	Val	Ile
		450					455					460				
	Asn	Asp	Thr	Trp	Gln	Arg	Gly	Leu	Arg	Ala	Phe	Asp	Thr	Ala	Thr	Ala
	465					470				475					480	
50	Tyr	Glu	Ala	Met	Lys	Lys	Asn	Ala	Ser	Ser	Ala	Gly	Ala	Thr	His	Pro
				485						490					495	
	Ile	Arg	Pro	Asp	Asn	Asp	Asp	Tyr	Leu	Thr	Leu	Gly	Phe	Val	Pro	Leu
			500						505					510		
	Arg	Glu	Gln	Tyr	Asp	Asn	Ser	Val	Ser	His	Ala	Leu	Glu	Tyr	Tyr	Leu
			515					520					525			
55	Ala	Asp	Trp	Asn	Leu	Ser	Arg	Phe	Ala	His	Ala	Leu	Gly	His	Lys	Glu
		530					535					540				
	Asp	Ala	Ala	Leu	Phe	Gly	Lys	Arg	Ser	Leu	Gly	Tyr	Arg	His	Tyr	Tyr
	545					550					555				560	
60	Asn	Lys	Glu	Tyr	Gly	Met	Leu	Cys	Pro	Leu	Leu	Pro	Asp	Gly	Ser	Phe
				565						570					575	
	Leu	Thr	Pro	Phe	Asp	Pro	Lys	Gln	Gly	Glu	Asn	Phe	Glu	Pro	Asn	Pro
				580					585					590		
	Gly	Phe	His	Glu	Gly	Ser	Ala	Tyr	Asn	Tyr	Ala	Phe	Phe	Val	Pro	His
			595					600					605			
65	Asp	Ile	Gln	Gly	Leu	Ala	Arg	Leu	Met	Gly	Gly	Ala	Lys	Val	Phe	Ser
		610					615					620				
	Glu	Arg	Leu	Gln	Lys	Val	Phe	Asp	Glu	Gly	Tyr	Asp	Pro	Thr	Asn	
	625					630					635				640	
70	Glu	Pro	Asp	Ile	Ala	Tyr	Pro	Tyr	Leu	Phe	Ser	Tyr	Phe	Pro	Lys	Glu
				645						650					655	
	Ala	Trp	Arg	Thr	Gln	Lys	Leu	Thr	Arg	Glu	Leu	Ile	Asp	Lys	His	Phe
				660					665					670		
	Cys	Asn	Ala	Pro	Asn	Gly	Leu	Pro	Gly	Asn	Asp	Asp	Ala	Gly	Thr	Met
			675					680					685			
75	Ser	Ala	Trp	Leu	Val	Tyr	Ser	Met	Leu	Gly	Phe	Tyr	Pro	Asp	Cys	Pro

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690                      695                      700  
 Gly Ser Pro Thr Tyr Thr Leu Thr Ser Pro Val Phe Pro Arg Val Arg  
 705                      710                      715                      720  
 5 Ile Arg Leu Asn Pro Gln Tyr Tyr Pro Gln Gly Glu Leu Ile Ile Thr  
                     725                      730                      735  
 Thr Asn Thr Glu Asn Gln Pro Thr Asp Ser Ile Tyr Ile His Thr Val  
                     740                      745                      750  
 Ser Leu Gly Asn Lys Thr Leu Pro His Gly Thr Arg His Ile Ser His  
                     755                      760                      765  
 10 Ala Asp Leu Val Arg Cys Gly His Leu Arg Tyr Glu Leu Ser Asn Arg  
                     770                      775                      780  
 Pro Arg  
 785

15 (2) INFORMATION FOR SEQ ID NO:379

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 814 amino acids  
 (B) TYPE: amino acid  
 20 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

25 (iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Porphyromonas gingivalis

30 (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...814

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:379

35 Pro Arg Phe His Pro Gly Gly Thr His Ala Gln Leu Cys Arg Asn Gly  
       1                    5                    10                    15  
 Arg Arg Asn Gln Lys Ser Asn Gln Ser Ser Cys Phe Gly Gly Thr  
                     20                    25                    30  
 40 Ala Pro Arg Phe Phe Ile Met Cys Lys Ile Arg Phe Ser Leu Leu Gln  
       35                    40                    45  
 Ala Leu Val Val Cys Leu Leu Phe Thr Ser Phe Ser Leu Gln Ala Gln  
       50                    55                    60  
 Glu Glu Gly Ile Trp Asn Thr Leu Leu Ala Ile His Lys Thr Glu Lys  
       65                    70                    75                    80  
 45 Ala Val Glu Thr Pro Lys Lys Val Phe Ala Val Ala Asn Gly Val Leu  
                     85                    90                    95  
 Tyr Ser Val Gly Lys Glu Ala Pro His Glu Ala Lys Ile Phe Asp Arg  
                     100                    105                    110  
 50 Ile Ser Gly Leu Ser Asp Thr Ser Val Ser Ser Ile Ala Tyr Ser Glu  
                     115                    120                    125  
 Gln Leu Lys Ser Leu Val Ile Tyr Tyr Ala Ser Gly Asn Ile Asp Ile  
                     130                    135                    140  
 Leu Asp Glu Ala Gly Arg Val Thr Asn Val Pro Ala Leu Lys Asp Asn  
                     145                    150                    155                    160  
 55 Ile Asp Leu Ile Asp Lys Thr Leu Asn Arg Leu Leu Ile Val Gly Asn  
                     165                    170                    175  
 Arg Ala Tyr Leu Ala Gly Gly Phe Gly Leu Ser Val Leu Asp Val Ala  
                     180                    185                    190  
 60 Glu Ala Arg Ile Pro Ala Thr Tyr Ala Lys Gly Thr Lys Val Thr Asp  
                     195                    200                    205  
 Val Ala Lys Leu Asp Asn Asp Arg Leu Leu Met Leu Lys Glu Gly Gln  
                     210                    215                    220  
 Leu Phe Ile Gly Lys Glu Thr Asp Asn Leu Gln Asp Pro Ala Ala Trp  
                     225                    230                    235                    240  
 65 Thr Ala Leu Ser Leu Asn Leu Pro Met Gly Ser Val Thr Gly Leu Gly  
                     245                    250                    255  
 Ile Val Gly Glu Asp Ile Cys Phe Leu Leu Ala Asp Gly Arg Val Tyr  
                     260                    265                    270  
 70 Val Ala Ala Asn Gln Ser Phe Glu Pro Glu Leu Leu Leu Ser Ser Ser  
                     275                    280                    285  
 Ala Asp Ser Arg Leu Tyr Val Thr Asp Arg Gly Leu Phe Ile Cys Ala  
                     290                    295                    300  
 Glu Asn Arg Ile Tyr Phe Ile Glu Lys Gly Arg Lys Thr Thr Gln Phe  
                     305                    310                    315                    320  
 75 Pro Ile Ala Asp Val Leu Gly Val Gly Ala Met Asn Glu Ser Asn Thr

5	Ala	Tyr	Ile	Ala	Leu	Gly	Glu	Glu	Gly	Leu	Ala	Ser	Leu	Leu	Leu	Ala
	Glu	Gly	Ser	Thr	Ala	Glu	Ala	Met	Pro	Val	Ala	Phe	Asp	Gly	Pro	Gly
	Asp	Asn	Asp	Phe	Tyr	Glu	Met	Arg	Phe	Ser	His	Gly	Arg	Leu	Tyr	Ala
	Ala	Ser	Gly	Leu	Trp	Gly	Thr	Asn	Leu	Met	Gly	His	Ala	Gly	Met	Val
10	Lys	Leu	Tyr	Asp	Gly	Asn	Arg	Trp	Thr	Asn	Phe	Asp	Lys	Lys	Thr	Val
	Gln	Glu	Gln	Leu	Gly	Gly	Gly	Phe	Ser	Phe	Asn	Asp	Ala	Ile	Asp	Ile
15	Ala	Val	Ser	Asn	Gly	Asp	Pro	Asp	His	Phe	Phe	Val	Gly	Thr	Trp	Gly
	Asn	Gly	Leu	Phe	Glu	Phe	Lys	Asp	Gly	Lys	Ala	Ile	Ala	Arg	Tyr	Ser
20	Gly	Asn	Glu	Thr	Ala	Ile	Ala	Glu	Cys	Asn	Pro	Gly	Asp	Ala	Arg	Val
	Lys	Ala	Ile	Ala	Phe	Asp	Asn	Lys	Gly	Asn	Leu	Trp	Gly	Thr	Leu	Gly
25	Ala	Val	Gly	Lys	Asn	Ile	Phe	Met	Tyr	Asp	Pro	Gln	Ser	Ser	Thr	Trp
	His	Ser	Phe	Ser	Tyr	Pro	Asp	Val	Ala	Asn	Leu	Ala	Ser	Phe	Gly	Asn
30	Met	Ile	Ile	Leu	Pro	Asn	Gly	Asp	Lys	Trp	Val	Asn	Ile	Leu	His	Arg
	Ser	Gly	Gly	Ser	Thr	Arg	Lys	Gly	Val	Leu	Ile	Phe	Asn	Asp	Arg	Gly
35	Thr	Pro	Glu	Thr	Thr	Ser	Asp	Asp	Ser	His	Leu	Tyr	Val	Glu	Gln	Phe
	Val	Asn	Arg	Leu	Gly	Ala	Ala	Ile	Gly	His	Lys	Thr	Ile	Tyr	Ala	Met
40	Ala	Val	Asp	His	Asn	Gly	Ser	Val	Trp	Met	Gly	Ser	Asp	Ile	Gly	Ile
	Phe	Gly	Val	Tyr	Asn	Ala	Ala	Gly	Val	Leu	Ser	Ser	Thr	Ser	Thr	Pro
45	Ile	Ala	Val	Arg	Pro	Val	Gly	Gly	Glu	Glu	Pro	Asn	Leu	Tyr	Tyr	Val
	Leu	Asp	Lys	Val	Thr	Val	Thr	Asp	Ile	Val	Val	Asp	Lys	Leu	Asn	His
50	Lys	Trp	Val	Ala	Thr	Gln	Gly	Thr	Gly	Leu	Tyr	Leu	Leu	Ser	Glu	Asp
	Cys	Ser	Lys	Ile	Leu	Ala	Gln	Phe	Thr	Val	Glu	Asn	Ser	Pro	Leu	Leu
55	Ser	Asn	Asn	Ile	Leu	Ser	Leu	Ala	Leu	Asn	Asp	Asp	Asn	Gly	Leu	Leu
	Tyr	Ile	Gly	Thr	Ala	Asp	Gly	Leu	Met	Thr	Phe	Gln	Thr	Gly	Thr	Gly
60	Ser	Gly	Ser	Ala	Ser	Glu	Leu	Asp	Gly	Val	Tyr	Val	Tyr	Pro	Asn	Pro
	Leu	Arg	Pro	Glu	Tyr	Pro	Asp	Gly	Val	Thr	Ile	Ala	Gly	Leu	Gln	Ala
65	Gly	Cys	Ser	Val	Lys	Ile	Thr	Asp	Thr	Thr	Gly	Arg	Leu	Leu	Tyr	Gln
	Thr	Glu	Ser	Val	Thr	Thr	Glu	Val	Lys	Trp	Asn	Ala	Arg	Gly	Ala	Asp
70	Gly	Asn	Arg	Val	Ala	Ser	Gly	Val	Tyr	Ala	Val	Ala	Val	Tyr	Asp	Pro
	Val	Ser	Lys	Lys	Ser	Lys	Leu	Ile	Arg	Phe	Ala	Val	Ile	Arg		

65 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 1162 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

70 (ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

75 (vi) ORIGINAL SOURCE:  
(A) ORGANISM: *Porphyromonas gingivalis*

BNSDOCID: <WO 9929870A1 | >

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## (ix) FEATURE:

(A) NAME/KEY: misc\_feature  
(B) LOCATION 1...1162

5

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:380

	Ala	Ile	Ser	Gln	Met	Lys	Arg	Ile	Leu	Pro	Ile	Val	Ala	Phe	Leu	Ser
	1				5				10					15		
10	Leu	Phe	Leu	Ala	Leu	Ala	Leu	Pro	Ala	Lys	Ala	Gln	Arg	Ala	Met	Gly
				20					25					30		
	Lys	Thr	Ala	Asp	Arg	Ser	Leu	Met	Ala	Ser	Gly	His	Trp	Val	Lys	Ile
			35					40					45			
15	Arg	Val	Asp	Ala	Ser	Gly	Val	Tyr	Arg	Leu	Thr	Asp	Glu	Gln	Leu	Arg
			50				55					60				
	Ala	Asn	Gly	Phe	Ser	Asp	Pro	Ser	Lys	Val	Gly	Val	Phe	Gly	Tyr	Gly
	65					70					75				80	
	Gly	Gly	Val	Leu	Pro	Glu	Asp	Leu	Ser	Arg	Ile	Thr	Thr	Asp	Asp	Leu
				85						90				95		
20	Pro	Pro	Val	Pro	Val	Leu	Arg	Gln	Gly	Asn	Ala	Leu	Tyr	Phe	Tyr	Ala
				100					105					110		
	Val	Gly	Pro	Val	Thr	Trp	Phe	Tyr	Asn	Pro	Ala	Lys	Thr	Thr	Met	Glu
			115					120					125			
25	His	Thr	Val	Asn	Thr	Tyr	Ser	Thr	His	Gly	Tyr	Tyr	Phe	Leu	Ser	Asp
			130				135					140				
	Ala	Ala	Gly	Ala	Pro	Leu	Gln	Met	Ser	Gln	Tyr	Thr	Gly	Gly	Gly	Ala
	145					150					155				160	
	Ser	Ala	Glu	Ala	Leu	Ile	Asp	Tyr	Tyr	Asp	Glu	Leu	Met	Leu	His	Glu
				165						170				175		
30	Gln	Glu	Leu	Tyr	Ser	Pro	Lys	Glu	Ser	Gly	Arg	Asp	Leu	Tyr	Gly	Glu
			180					185					190			
	Ser	Phe	Ser	Ala	Val	Asn	Thr	Arg	Thr	Val	Lys	Phe	Pro	Leu	Arg	Gly
			195					200					205			
35	Asn	Thr	Arg	Ser	Ser	Gly	Glu	Leu	Gly	Thr	Val	Phe	Ser	Tyr	Ile	Ala
			210				215					220				
	Lys	Ala	Arg	Ser	Ala	Gly	Gly	Gly	Arg	Glu	Met	Ser	Leu	Ser	Ala	Asn
	225					230					235				240	
	Gly	Ile	Leu	Ile	Phe	Ser	Asp	Pro	Phe	Ser	Met	Thr	Ser	Asn	Glu	Val
				245						250				255		
40	Ser	Asn	Ser	Tyr	Leu	Ala	Gly	Lys	Lys	Arg	Arg	Leu	Tyr	His	Ser	Thr
				260					265					270		
	Pro	Met	Asn	Ser	Leu	Val	Asn	Glu	Leu	Arg	Leu	Asp	Ala	Asn	Tyr	Ser
			275					280					285			
45	Met	Thr	Gly	Asp	Ala	Val	Asn	Leu	Asp	Phe	Ile	Glu	Val	Ala	Thr	Gln
			290				295					300				
	Asn	Asp	Leu	Arg	Tyr	Asp	Gly	Ala	Pro	Met	His	Ile	Arg	Arg	Phe	Ser
	305					310				315					320	
	Asn	Leu	Pro	Val	Leu	Gly	Gly	Glu	Ser	Cys	Arg	Phe	Val	Ile	Ser	Glu
				325						330				335		
50	Val	Pro	Glu	Ser	Leu	Val	Val	Leu	Gln	Ala	Asn	Ser	Ser	Leu	Thr	Ala
				340					345					350		
	Ser	Leu	Val	Pro	Val	Lys	Thr	Val	Gly	Asp	Lys	Thr	Ile	Glu	Phe	Val
			355					360					365			
55	Ala	Pro	Pro	Lys	Gly	Gln	Asp	Arg	Arg	Thr	Ile	Asn	Thr	Phe	Tyr	Ala
			370				375					380				
	Val	Asp	Leu	Ser	Gln	Ala	Ser	Ala	Pro	Glu	Ile	Leu	Gly	Ala	Val	Pro
	385					390					395				400	
	Asn	Gln	Asn	Leu	His	Gly	Glu	Glu	Ile	Pro	Asp	Leu	Ile	Ile	Val	Ser
				405						410				415		
60	Thr	Gln	Ala	Leu	Leu	Leu	Glu	Ala	Asp	Arg	Leu	Ala	Thr	Tyr	Arg	Arg
				420					425					430		
	Glu	Lys	Asn	Gly	Leu	Lys	Val	Leu	Val	Val	Leu	Gln	Glu	Gln	Val	Phe
			435					440					445			
65	Asn	Glu	Phe	Ser	Gly	Gly	Thr	Pro	Asp	Ala	Thr	Ala	Tyr	Arg	Leu	Phe
			450				455					460				
	Ala	Lys	Met	Phe	Tyr	Asp	Arg	Trp	Lys	Ala	Asn	Ala	Pro	Val	Gly	Glu
	465					470					475				480	
	Thr	Phe	Pro	Met	Gln	Met	Leu	Leu	Phe	Gly	Asp	Gly	Ala	His	Asp	Asn
				485						490				495		
70	Arg	Lys	Val	Ser	Val	Ala	Trp	Gln	Lys	Pro	Tyr	Leu	Gln	Gln	Thr	Glu
				500					505					510		
	Phe	Leu	Leu	Thr	Phe	Gln	Ala	Val	Asn	Ser	Thr	Asn	Val	Asn	Ser	Tyr
			515					520					525			
75	Val	Thr	Asp	Asp	Tyr	Phe	Gly	Leu	Leu	Asp	Asp	Gln	Pro	Ala	Ser	Val
			530				535					540				

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	Asn	Ile	Gly	Trp	Arg	Asn	Tyr	Asn	Met	Ala	Val	Gly	Arg	Phe	Pro	Val
	545				550					555						560
	Arg	Thr	Pro	Ala	Glu	Ala	Arg	Ile	Ala	Val	Asp	Lys	Thr	Ile	Arg	Tyr
				565						570						575
5	Glu	Glu	Asp	Arg	Glu	Ser	Gly	Ala	Trp	Arg	Ile	Arg	Ala	Cys	Phe	Ala
				580					585					590		
	Ala	Asp	Asn	Gly	Asp	Lys	His	Ala	Thr	Glu	Thr	Ser	Arg	Leu	Ile	Asp
				595				600					605			
10	Thr	Val	Lys	Arg	Tyr	Ala	Pro	Ala	Ile	Met	Pro	Val	Arg	Ala	Phe	Gln
		610					615						620			
	Asp	Val	Tyr	Pro	His	Val	Ile	Glu	Asn	Gly	Leu	His	Ser	Ile	Pro	Gly
		625				630					635					640
	Ala	Lys	Lys	Lys	Met	Leu	Glu	Thr	Leu	Gln	Ser	Gly	Ile	Ile	Leu	Leu
				645						650						655
15	Asn	Tyr	Ala	Gly	His	Gly	Gly	Pro	Ala	Gly	Trp	Ser	Asp	Glu	His	Leu
				660					665					670		
	Leu	Thr	Leu	Asn	Asp	Ile	His	Lys	Phe	Asn	Tyr	Lys	His	Met	Pro	Ile
				675				680					685			
20	Trp	Ile	Thr	Ala	Thr	Cys	Asp	Phe	Ala	Asn	Tyr	Asp	Ser	Gln	Thr	Thr
		690					695					700				
	Ser	Ala	Gly	Glu	Glu	Val	Phe	Leu	His	Glu	Lys	Ser	Gly	Thr	Pro	Ile
		705				710					715					720
	Met	Phe	Ser	Thr	Thr	Arg	Val	Val	Tyr	Asn	Thr	Gln	Asn	Glu	Lys	Ile
					725					730					735	
25	Asn	Gly	Phe	Met	Leu	Arg	Arg	Met	Phe	Glu	Lys	Ala	Lys	Asp	Gly	Arg
				740					745					750		
	Tyr	Arg	Thr	Met	Gly	Glu	Ile	Ile	Arg	Ser	Ala	Lys	Gln	Gly	Met	Leu
				755				760					765			
30	Ser	Thr	Val	Phe	Pro	Asp	Ser	Ile	Asn	Gln	Leu	Ser	Phe	Phe	Leu	Met
		770					775					780				
	Gly	Asp	Pro	Ser	Val	Arg	Met	Asn	Leu	Pro	Thr	His	Lys	Val	Gln	Leu
		785				790					795					800
	Thr	Ala	Ile	Asn	Gly	Gln	Asp	Pro	Glu	Gly	Gln	Tyr	Gly	Thr	Ile	Met
				805						810						815
35	Leu	Lys	Ser	Leu	Glu	Arg	Val	Ala	Leu	Lys	Gly	Lys	Val	Thr	Asp	Glu
				820					825					830		
	Lys	Gly	Thr	Phe	Asp	Glu	Thr	Phe	Ser	Gly	Lys	Val	Phe	Leu	Thr	Val
				835				840					845			
40	Phe	Asp	Gly	Arg	Lys	Lys	Met	Thr	Ala	Leu	Glu	Glu	Glu	Gly	Asn	Asp
		850					855					860				
	Leu	Ser	Leu	Val	Tyr	Tyr	Asp	Tyr	Pro	Asn	Val	Met	Tyr	Ala	Gly	Ile
		865				870					875					880
	Ala	Glu	Val	Lys	Asp	Gly	Leu	Phe	Glu	Thr	Ser	Phe	Ile	Val	Pro	Lys
				885					890						895	
45	Asp	Val	Asn	Tyr	Ser	Glu	His	Glu	Gly	Arg	Ile	Asn	Leu	Tyr	Ala	Tyr
				900					905					910		
	Asn	Glu	Ser	Thr	Lys	Ala	Glu	Ala	Met	Gly	Val	Asp	Phe	Ser	Ile	Arg
				915				920					925			
50	Val	Gln	Pro	Gly	Ile	Pro	Asp	Glu	Val	Thr	Glu	Asp	Asn	Thr	Pro	Pro
		930					935					940				
	Glu	Ile	Ile	Ser	Cys	Phe	Leu	Asn	Asp	Ser	Thr	Phe	Arg	Ser	Gly	Asp
					950						955					960
	Glu	Val	Asn	Pro	Thr	Pro	Leu	Phe	Met	Ala	Glu	Val	Phe	Asp	Leu	Asn
				965						970					975	
55	Gly	Ile	Asn	Ile	Thr	Gly	Ser	Gly	Val	Gly	His	Asp	Ile	Thr	Leu	Cys
				980					985					990		
	Ile	Asp	Gly	Arg	Ala	Asp	Leu	Thr	Tyr	Asn	Leu	Asn	Ala	Tyr	Phe	Thr
				995				1000					1005			
60	Ser	Ser	Ala	Thr	Asp	Ala	Gly	Val	Gly	Thr	Ile	Leu	Phe	Met	Ile	Pro
		1010					1015					1020				
	Ala	Leu	Ala	Glu	Gly	Asp	His	Thr	Ala	Arg	Leu	Thr	Val	Trp	Asp	Ile
		1025				1030						1035				1040
	Phe	Asn	Asn	Ala	Val	His	His	Asp	Phe	Ser	Phe	Arg	Val	Val	Asp	Gly
				1045					1050						1055	
65	Ile	Ala	Pro	Asp	Val	Ala	Asp	Val	Ile	Leu	Phe	Pro	Asn	Pro	Val	Arg
				1060					1065					1070		
	Glu	Ser	Ala	Thr	Phe	Arg	Ile	Phe	His	Asn	Arg	Pro	Gly	Ser	Asp	Leu
				1075				1080					1085			
70	Asn	Val	Ala	Val	Glu	Ile	Tyr	Asp	Phe	Thr	Gly	Arg	Leu	Val	Asn	Ser
		1090					1095					1100				
	Leu	Pro	Val	Lys	Thr	Tyr	Ser	Ser	Ser	Tyr	Gly	Glu	Pro	Ile	Glu	Ile
					1105		1110				1115					1120
	Lys	Trp	Asp	Leu	Thr	Ser	Lys	Tyr	Gly	Val	Lys	Ile	Gly	Asn	Gly	Phe
					1125				1130						1135	
75	Tyr	Leu	Tyr	Arg	Cys	Val	Val	Asn	Ser	Pro	Gly	Gly	Gln	Thr	Ala	Ser

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1140 1145 1150  
Met Ala Lys Lys Met Ile Val Val Gly Gln  
1155 1160

## 5 (2) INFORMATION FOR SEQ ID NO:381

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 973 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

10

(ii) MOLECULE TYPE: protein

15

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:  
(A) ORGANISM: Porphyromonas gingivalis

20

(ix) FEATURE:  
(A) NAME/KEY: misc\_feature  
(B) LOCATION 1...973

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:381

25 Phe Tyr Thr Gly Ile Asp Leu His Ile Glu Ser Gln Met Lys Lys Leu  
1 5 10 15  
Phe Pro Leu Leu Leu Ile Leu Ser Ile Leu Val Gly Cys Gly Lys  
20 25 30  
Lys Glu Lys His Ser Val Thr Glu Ile Ala Arg Glu Lys Lys Arg Ile  
35 40 45  
30 Thr Ala Leu Leu Tyr Glu Lys Glu Leu Pro Thr Asp Ser Val Lys Gln  
50 55 60  
Leu Tyr Glu Asn Ser Val Gln Asn Lys Asn Leu Val Gly Gln Met Leu  
65 70 75 80  
35 Phe Ala Ile Glu Val Gly Lys Arg Met Arg Asn Met Ser Gln Tyr Thr  
85 90 95  
Asp Ala Met Leu Tyr His Gln Lys Gly Leu Asn Ala Ala Leu Asn Leu  
100 105 110  
40 Arg Asp Thr Ile Val Ala Ala Gln Ala Trp Asn His Leu Gly Thr Asp  
115 120 125  
Ser Arg Arg Ile Gly Ala Leu Ala Glu Ala Ser Asp Tyr His Tyr Lys  
130 135 140  
Ala Leu Ser Leu Ile Glu Ser Phe Ser Gly Asn Gln Asn Arg Pro Ala  
145 150 155 160  
45 Ile Lys Ala Arg Ser Ala Ala Leu Asn Gly Ile Gly Asn Ile Asn Leu  
165 170 175  
Glu Leu Gly Tyr His Asp Glu Ala Glu Lys Asn Phe Leu Lys Ala Leu  
180 185 190  
Gln Gly Glu Lys Glu Leu Asp Ser Pro Leu Gly Gln Ala Ile Asn Tyr  
195 200 205  
50 Ala Asn Leu Gly Arg Ile Tyr Arg Gln Arg Lys Glu Tyr Asp Lys Ala  
210 215 220  
Arg Thr Tyr Phe Leu Leu Ser Leu Glu Gln Asn Asn Met Ala Glu Asn  
225 230 235 240  
55 Leu Met Gly Ile Gly Leu Cys Ser Ile Asn Leu Gly Glu Val Asp Glu  
245 250 255  
Glu Lys Gly Asp Tyr Gln Lys Ala Leu Gln Glu Tyr Ala Thr Ala Tyr  
260 265 270  
60 Lys Leu Met Glu Gln Leu Ser Asp Arg Trp His Trp Leu Asn Ser Cys  
275 280 285  
Ile Pro Met Ala Arg Ile Asn Leu Lys Gln Gly Asn Glu Arg Leu Tyr  
290 295 300  
Gln His Phe Ile Ser Leu Ala Glu Gly Thr Ala Lys Glu Ile Asn Ser  
305 310 315 320  
65 Thr Ser His Leu Ile Glu Ile Tyr Asn Leu Gln Tyr Glu Asn Leu Glu  
325 330 335  
Arg Lys Lys Glu Tyr Lys Gln Ala Leu Glu Ala Phe Cys Leu Ser Lys  
340 345 350  
70 Thr Leu Ser Asp Ser Met Ser Ile Ala His Lys Val Ser Ser Ile Gln  
355 360 365  
Glu Thr Arg Phe Asn Tyr Glu Arg Asn Lys Ser Gln Lys Glu Leu Glu  
370 375 380  
Glu Ile Gln Gln Val Ser Lys Ala Lys Gln Glu Lys Ser Lys Phe Ile  
385 390 395 400  
75 Leu Leu Ser Thr Leu Phe Ala Leu Phe Ile Ser Ile Leu Leu Ile Ser



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					405					410					415	
	Val	Leu	Thr	Tyr	Ala	Tyr	Arg	Gln	Gly	Lys	Lys	His	Asn	Lys	Leu	Ile
				420					425					430		
5	Lys	Glu	Thr	Asp	Lys	Leu	Arg	Ser	Gly	Phe	Phe	Thr	Gly	Ile	Thr	His
			435					440					445			
	Glu	Phe	Arg	Thr	Pro	Ile	Thr	Val	Ile	Gln	Gly	Leu	Asn	Glu	Lys	Met
		450					455					460				
10	Ser	Ser	Ser	Pro	Asp	Leu	Gln	Ala	Ser	Asp	Arg	Thr	Glu	Leu	His	Lys
	465					470				475					480	
	Ile	Ile	Asp	Arg	Gln	Ser	Ser	His	Met	Leu	Asn	Leu	Val	Asn	Gln	Leu
			485						490					495		
	Leu	Asp	Ile	Cys	Lys	Ile	Arg	Ser	Gly	Val	Ser	Thr	Pro	Glu	Trp	Arg
			500						505					510		
15	Asn	Gly	Asp	Ile	Val	Ser	Phe	Val	Gln	Ile	Leu	Ile	Asp	Ser	Phe	Ala
		515						520					525			
	Pro	Tyr	Ala	Gln	Ala	Gln	Asp	Ile	Thr	Leu	Glu	Leu	Gln	Pro	Glu	Ser
		530				535						540				
20	Lys	Pro	Ile	Val	Val	Asp	Phe	Val	Pro	Ser	Tyr	Leu	Gln	Lys	Ile	Ile
	545					550				555					560	
	Ser	Asn	Leu	Leu	Ser	Asn	Ala	Ile	Lys	Tyr	Ser	Leu	Ala	Gly	Gly	Arg
			565						570					575		
	Val	Val	Ile	Ser	Leu	Ala	Lys	Thr	Lys	Asn	Glu	Lys	Asn	Leu	Ile	Ile
			580						585					590		
25	Arg	Val	Ala	Asp	Asn	Gly	Ile	Gly	Ile	Asp	Lys	Thr	Asp	Gln	Ala	His
		595						600					605			
	Ile	Phe	Asp	Ile	Phe	Tyr	Arg	Gly	Gln	Ser	Ala	Thr	Glu	Lys	His	Gly
		610				615						620				
30	Ser	Gly	Val	Gly	Leu	Ser	Phe	Thr	Asn	Ile	Leu	Val	Glu	Asn	Leu	Arg
	625					630					635				640	
	Gly	Thr	Ile	Lys	Val	Glu	Ser	Gln	Pro	Gly	Lys	Gly	Ser	Ala	Phe	Thr
			645							650				655		
	Ile	Ser	Ile	Pro	Thr	Gln	Asn	Gln	Ser	Ser	Ser	Ala	Glu	Ile	Leu	Pro
			660						665					670		
35	Trp	Leu	Pro	Ser	Ser	Asp	Asp	Ile	Val	Met	Pro	Val	His	Ile	Ala	Pro
		675						680					685			
	Asp	Asp	Ser	Pro	Thr	Ser	Pro	Met	Val	Ala	Ala	Leu	Asn	His	Arg	Phe
		690					695					700				
40	Glu	Asp	Glu	Arg	Pro	Thr	Ile	Leu	Leu	Val	Glu	Asp	Asn	Lys	Asp	Ile
	705					710					715				720	
	Asn	Leu	Leu	Val	Lys	Leu	Leu	Leu	Cys	Asp	Arg	Tyr	Asn	Val	Leu	Ser
			725							730				735		
	Ala	Ala	Asn	Gly	Lys	Glu	Gly	Ile	Ala	Leu	Ala	Thr	Glu	His	Ile	Pro
			740						745					750		
45	Asp	Ile	Ile	Ile	Thr	Asp	Ile	Met	Met	Pro	Ile	Met	Asp	Gly	Ile	Glu
		755						760					765			
	Met	Thr	Ile	Arg	Met	Lys	Gln	Ser	Pro	Leu	Leu	Cys	His	Ile	Pro	Ile
		770					775					780				
50	Val	Ala	Leu	Thr	Ala	Lys	Ser	Thr	Glu	Gln	Asp	Arg	Leu	Glu	Gly	Ile
		785				790					795				800	
	Lys	Ser	Gly	Val	Val	Ser	Tyr	Leu	Cys	Lys	Pro	Phe	Ser	Pro	Glu	Glu
			805							810				815		
	Leu	Leu	Met	Arg	Ile	Glu	Gln	Leu	Leu	Lys	Asp	Arg	Glu	Leu	Leu	Lys
			820						825					830		
55	Lys	Phe	Tyr	Met	Gln	Lys	Leu	Met	Leu	Asp	Arg	Lys	Pro	Glu	Glu	Glu
		835						840					845			
	Pro	Gln	Pro	Ile	Asp	Asp	Ser	Ser	Met	Gln	Phe	Leu	Leu	Ala	Ala	Lys
		850					855					860				
60	Asp	Ala	Val	Ser	Gly	Gly	Ile	Lys	Gln	Asn	Pro	Asp	Phe	Ser	Ala	Gln
		865				870					875				880	
	Asp	Leu	Ala	Glu	Lys	Met	Cys	Met	Ser	Pro	Ser	Gln	Leu	Asn	Arg	Lys
			885						890					895		
	Leu	Thr	Ser	Val	Val	Gly	Cys	Ser	Thr	Ile	Gly	Tyr	Ile	Gln	Gln	Ile
			900						905					910		
65	Lys	Ile	Lys	Leu	Ala	Cys	Lys	Leu	Leu	Ala	Asp	Glu	Ser	Lys	Asn	Ile
		915						920					925			
	Ser	Asp	Ile	Ser	Ile	Glu	Ala	Gly	Phe	Ser	Asp	Pro	Ala	Tyr	Phe	Ser
		930					935					940				
70	Arg	Thr	Phe	Lys	Arg	Tyr	Met	Asn	Cys	Ser	Pro	Ser	Gln	Tyr	Arg	Gln
		945				950					955				960	
	Lys	Leu	Leu	Ala	Met	Pro	Gly	Ser	Asp	Lys	Glu	Thr	Val			
			965							970						

(2) INFORMATION FOR SEQ ID NO:382

75

(i) SEQUENCE CHARACTERISTICS:

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(A) LENGTH: 563 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

5 (ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

10 (vi) ORIGINAL SOURCE:

(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

(A) NAME/KEY: misc\_feature

(B) LOCATION 1...563

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:382

	His	His	Lys	Thr	Tyr	Gln	Thr	Met	Lys	Lys	Leu	Leu	Gln	Ala	Lys	Ala
	1				5				10					15		
20	Leu	Ile	Leu	Ala	Leu	Gly	Leu	Phe	Gln	Leu	Pro	Ala	Ile	Ala	Gln	Thr
			20						25					30		
	Gln	Met	Gln	Ala	Asp	Arg	Thr	Asn	Gly	Gln	Phe	Ala	Thr	Glu	Glu	Met
			35					40					45			
25	Gln	Arg	Ala	Phe	Gln	Glu	Thr	Asn	Pro	Pro	Ala	Gly	Pro	Val	Arg	Ala
	50						55					60				
	Ile	Ala	Glu	Tyr	Glu	Arg	Ser	Ala	Ala	Val	Leu	Val	Arg	Tyr	Pro	Phe
	65					70				75					80	
	Gly	Ile	Pro	Met	Glu	Leu	Ile	Lys	Glu	Leu	Ala	Lys	Asn	Asp	Lys	Val
				85					90					95		
30	Ile	Thr	Ile	Val	Ala	Ser	Glu	Ser	Gln	Lys	Asn	Thr	Val	Ile	Thr	Gln
				100					105					110		
	Tyr	Thr	Gln	Ser	Gly	Val	Asn	Leu	Ser	Asn	Cys	Asp	Phe	Ile	Ile	Ala
			115					120					125			
35	Lys	Thr	Asp	Ser	Tyr	Trp	Thr	Arg	Asp	Tyr	Thr	Gly	Trp	Phe	Ala	Met
	130						135					140				
	Tyr	Asp	Thr	Asn	Lys	Val	Gly	Leu	Val	Asp	Phe	Ile	Tyr	Asn	Arg	Pro
	145					150				155					160	
	Arg	Pro	Asn	Asp	Asp	Glu	Phe	Pro	Lys	Tyr	Glu	Ala	Gln	Tyr	Leu	Gly
				165					170					175		
40	Ile	Glu	Met	Phe	Gly	Met	Lys	Leu	Lys	Gln	Thr	Gly	Gly	Asn	Tyr	Met
			180					185						190		
	Thr	Asp	Gly	Tyr	Gly	Ser	Ala	Val	Gln	Ser	His	Ile	Ala	Tyr	Thr	Glu
			195					200					205			
45	Asn	Ser	Ser	Leu	Ser	Gln	Ala	Gln	Val	Asn	Gln	Lys	Met	Lys	Asp	Tyr
	210						215					220				
	Leu	Gly	Ile	Thr	His	His	Asp	Val	Val	Gln	Asp	Pro	Asn	Gly	Glu	Tyr
	225					230					235				240	
	Ile	Asn	His	Val	Asp	Cys	Trp	Gly	Lys	Tyr	Leu	Ala	Pro	Asn	Lys	Ile
				245						250				255		
50	Leu	Ile	Arg	Lys	Val	Pro	Asp	Asn	His	Pro	Gln	His	Gln	Ala	Leu	Glu
				260					265					270		
	Asp	Met	Ala	Ala	Tyr	Phe	Ala	Ala	Gln	Thr	Cys	Ala	Trp	Gly	Thr	Lys
			275					280					285			
55	Tyr	Glu	Val	Tyr	Arg	Ala	Leu	Ala	Thr	Asn	Glu	Gln	Pro	Tyr	Thr	Asn
	290						295					300				
	Ser	Leu	Ile	Leu	Asn	Asn	Arg	Val	Phe	Val	Pro	Val	Asn	Gly	Pro	Ala
	305					310				315					320	
	Ser	Val	Asp	Asn	Asp	Ala	Leu	Asn	Val	Tyr	Lys	Thr	Ala	Met	Pro	Gly
				325						330				335		
60	Tyr	Glu	Ile	Ile	Gly	Val	Lys	Gly	Ala	Ser	Gly	Thr	Pro	Trp	Leu	Gly
				340					345					350		
	Thr	Asp	Ala	Leu	His	Cys	Arg	Thr	His	Glu	Val	Ala	Asp	Lys	Gly	Tyr
			355					360					365			
65	Leu	Tyr	Ile	Lys	His	Tyr	Pro	Ile	Leu	Gly	Glu	Gln	Ala	Gly	Pro	Asp
	370						375					380				
	Tyr	Lys	Ile	Glu	Ala	Asp	Val	Val	Ser	Cys	Ala	Asn	Ala	Thr	Ile	Ser
	385					390				395					400	
	Pro	Val	Gln	Cys	Tyr	Tyr	Arg	Ile	Asn	Gly	Ser	Gly	Ser	Phe	Lys	Ala
				405					410					415		
70	Ala	Asp	Met	Thr	Met	Glu	Ser	Thr	Gly	His	Tyr	Thr	Tyr	Ser	Phe	Thr
				420					425					430		
	Gly	Leu	Asn	Lys	Asn	Asp	Lys	Val	Glu	Tyr	Tyr	Ile	Ser	Ala	Ala	Asp
			435					440					445			
75	Asn	Ser	Gly	Arg	Lys	Glu	Thr	Tyr	Pro	Phe	Ile	Gly	Glu	Pro	Asp	Pro
	450						455					460				

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Phe Lys Phe Thr Cys Met Asn Glu Thr Asn Thr Cys Thr Val Thr Gly  
 465 470 475 480  
 Ala Ala Lys Ala Leu Arg Ala Trp Phe Asn Ala Gly Arg Ser Glu Leu  
 485 490 495  
 5 Ala Val Ser Val Ser Leu Asn Ile Ala Gly Thr Tyr Arg Ile Lys Leu  
 500 505 510  
 Tyr Asn Thr Ala Gly Glu Glu Val Ala Ala Met Thr Lys Glu Leu Val  
 515 520 525  
 10 Ala Gly Thr Ser Val Phe Ser Met Asp Val Tyr Ser Gln Ala Pro Gly  
 530 535 540  
 Thr Tyr Val Leu Val Val Glu Gly Asn Gly Ile Arg Glu Thr Met Lys  
 545 550 555 560  
 Ile Leu Lys

15

(2) INFORMATION FOR SEQ ID NO:383

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 437 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

20

(ii) MOLECULE TYPE: protein

25

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Porphyromonas gingivalis

30

(ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...437

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:383

Thr Thr Asn Arg Lys Pro Asn Thr Asn Met Lys Leu Ser Ser Lys Lys  
 1 5 10 15  
 Ile Leu Ala Ile Ile Ala Leu Leu Thr Met Gly His Ala Val Gln Ala  
 20 25 30  
 40 Gln Phe Val Pro Ala Pro Thr Thr Gly Ile Arg Met Ser Val Thr Thr  
 35 40 45  
 Thr Lys Ala Val Gly Glu Lys Ile Glu Leu Leu Val His Ser Ile Glu  
 50 55 60  
 45 Lys Lys Gly Ile Trp Ile Asp Leu Asn Gly Asp Ala Thr Tyr Gln Gln  
 65 70 75 80  
 Gly Glu Glu Ile Thr Val Phe Asp Glu Ala Tyr His Glu Tyr Thr Ile  
 85 90 95  
 Gly Thr Gln Thr Leu Thr Ile Tyr Gly Asn Thr Thr Arg Leu Gly Cys  
 100 105 110  
 50 Arg Ser Thr Gly Ala Thr Ala Val Asp Val Thr Lys Asn Pro Asn Leu  
 115 120 125  
 Thr Tyr Leu Ala Cys Pro Lys Asn Asn Leu Lys Ser Leu Asp Leu Thr  
 130 135 140  
 55 Gln Asn Pro Lys Leu Leu Arg Val Trp Cys Asp Ser Asn Glu Ile Glu  
 145 150 155 160  
 Ser Leu Asp Leu Ser Gly Asn Pro Ala Leu Ile Ile Leu Gly Cys Asp  
 165 170 175  
 Arg Asn Lys Leu Thr Glu Leu Lys Thr Asp Asn Asn Pro Lys Leu Ala  
 180 185 190  
 60 Ser Leu Trp Cys Ser Asp Asn Asn Leu Thr Glu Leu Glu Leu Ser Ala  
 195 200 205  
 Asn Pro Arg Leu Asn Asp Leu Trp Cys Phe Gly Asn Arg Ile Thr Lys  
 210 215 220  
 65 Leu Asp Leu Ser Ala Asn Pro Leu Leu Val Thr Leu Trp Cys Ser Asp  
 225 230 235 240  
 Asn Glu Leu Ser Thr Leu Asp Leu Ser Lys Asn Ser Asp Val Ala Tyr  
 245 250 255  
 Leu Trp Cys Ser Ser Asn Lys Leu Thr Ser Leu Asn Leu Ser Gly Val  
 260 265 270  
 70 Lys Gly Leu Ser Val Leu Val Cys His Ser Asn Gln Ile Ala Gly Glu  
 275 280 285  
 Glu Met Thr Lys Val Val Asn Ala Leu Pro Thr Leu Ser Pro Gly Ala  
 290 295 300  
 75 Gly Ala Gln Ser Lys Phe Val Val Val Asp Leu Lys Asp Thr Asp Glu  
 305 310 315 320

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Lys Asn Ile Cys Thr Val Lys Asp Val Glu Lys Ala Lys Ser Lys Asn  
 325 330 335  
 Trp Arg Val Phe Asp Phe Asn Gly Asp Ser Asp Asn Met Leu Pro Tyr  
 340 345 350  
 5 Glu Gly Ser Pro Thr Ser Asn Leu Ala Val Asp Ala Pro Thr Val Arg  
 355 360 365  
 Ile Tyr Pro Asn Pro Val Gly Arg Tyr Ala Leu Val Glu Ile Pro Glu  
 370 375 380  
 10 Ser Leu Leu Gly Gln Glu Ala Ala Leu Tyr Asp Met Asn Gly Val Lys  
 385 390 395 400  
 Val Tyr Ser Phe Ala Val Glu Ser Leu Arg Gln Asn Ile Asp Leu Thr  
 405 410 415  
 His Leu Pro Asp Gly Thr Tyr Phe Phe Arg Leu Asp Asn Tyr Thr Thr  
 420 425 430  
 15 Lys Leu Ile Lys Gln  
 435

(2) INFORMATION FOR SEQ ID NO:384

- 20 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 318 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
 25 (ii) MOLECULE TYPE: protein  
 (iii) HYPOTHETICAL: YES  
 (vi) ORIGINAL SOURCE:  
 30 (A) ORGANISM: Porphyromonas gingivalis  
 (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...318  
 35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:384

Asn His Leu Lys Thr Asn Ile Lys Met Arg Lys Thr Ile Ile Phe Cys  
 1 5 10 15  
 40 Leu Leu Leu Ala Leu Phe Gly Cys Ser Trp Ala Gln Glu Arg Val Asp  
 20 25 30  
 Glu Lys Val Phe Ser Ala Gly Thr Ser Ile Phe Arg Gly Ile Leu Glu  
 35 40 45  
 45 Lys Val Lys Ala Pro Leu Met Tyr Gly Asp Arg Glu Val Trp Gly Met  
 50 55 60  
 Ala Arg Ala Ser Glu Asp Phe Phe Phe Ile Leu Pro Val Thr Asp Asp  
 65 70 75 80  
 Leu Thr Pro Val Leu Phe Tyr Asn Arg Leu Thr Asn Glu Pro Cys Phe  
 85 90 95  
 50 Val Ser Asp Gln Gly Ile Thr Glu Tyr Phe Lys Phe Ala Gln Glu Gly  
 100 105 110  
 Asp Tyr Ile Glu Val Glu Gly Ser Val Phe Met Ala Asn Leu Leu  
 115 120 125  
 55 Tyr Tyr Arg Phe Phe Pro Thr Arg Ile Thr Ser Tyr Asn Ala Pro Ile  
 130 135 140  
 Glu Gly Val Val Ser Lys Thr Gly Asn Pro Ala Phe Thr Ile Pro Met  
 145 150 155 160  
 Leu Pro Gly Val Ser Asp Cys Ile Glu Ile Ser Asn Asn Arg Lys Val  
 165 170 175  
 60 Phe Leu Thr Asn Gln Leu Gly Val Val Asn Ile Thr Asp Gly Met Glu  
 180 185 190  
 Pro Pro Ile Ile Ala Gly Val Ser Ala Ser Tyr Gly Ser Ser Val Arg  
 195 200 205  
 65 Val Tyr Gly His Val Ser Gln Arg Trp Asp Ile Ile Gly His Cys Tyr  
 210 215 220  
 Leu Asp Ile Tyr Pro Thr Asn Cys Tyr Pro Leu Ser Thr Lys Pro Val  
 225 230 235 240  
 Ala Gly Asp Asp Glu Val Phe Val Lys Gln Gln Gly Arg Gln Ile Glu  
 245 250 255  
 70 Ile Asp Ser Asn Ser Pro Ile Val Gln Val Val Val Tyr Asp Leu Glu  
 260 265 270  
 Gly Lys Ser Val Phe Arg Lys Arg Met Thr Glu Asn Ala Tyr Thr Leu  
 275 280 285  
 75 Ser Phe Arg Ala Pro Met Leu Gly Phe Met Thr Ile Met Ile Glu Thr  
 290 295 300

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Gln Asn Ser Ile Ile Asn Lys Lys Leu Asn Val Thr Gln Leu  
 305 310 315

## (2) INFORMATION FOR SEQ ID NO:385

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 461 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION: 1...461

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:385

Arg Arg Ala Val Lys Ile Arg Ser Pro Pro His Ile His Ser Leu Phe  
 1 5 10 15  
 Val Arg Lys Cys Leu Phe Ser Asp Phe Lys Tyr Leu Tyr Leu Ser Arg  
 20 25 30  
 Lys Ile Thr Gln Glu Arg Leu Gly Arg Leu Ser Ile Arg Leu Lys Ser  
 35 40 45  
 Tyr Asn Pro Ile Ile Ile Ile Glu Met Lys Lys Thr Thr Ile Ile Ser  
 50 55 60  
 Leu Ile Val Phe Gly Ala Phe Phe Ala Ala Val Gly Gln Thr Lys Asp  
 65 70 75 80  
 Asn Ser Ser Tyr Lys Pro Phe Ser Lys Glu Asp Ile Ala Gly Gly Val  
 85 90 95  
 Tyr Ser Leu Pro Thr Gln Asn Arg Ala Gln Lys Asp Asn Ala Glu Trp  
 100 105 110  
 Leu Leu Thr Ala Thr Val Ser Thr Asn Gln Ser Ala Asp Thr His Phe  
 115 120 125  
 Ile Phe Asp Glu Asn Asn Arg Tyr Ile Ala Arg Asp Ile Lys Ala Asn  
 130 135 140  
 Gly Val Arg Lys Ser Thr Asp Ser Ile Tyr Tyr Asp Ala Asn Gly Arg  
 145 150 155 160  
 Ile Ser His Val Asp Leu Tyr Ile Ser Phe Ser Gly Gly Glu Pro Ala  
 165 170 175  
 Leu Asp Thr Arg Phe Lys Tyr Thr Tyr Asp Asp Glu Gly Lys Met Thr  
 180 185 190  
 Val Arg Glu Val Phe Met Leu Val Met Asp Pro Asn Thr Pro Ile Ser  
 195 200 205  
 Arg Leu Glu Tyr His Tyr Asp Ala Gln Gly Arg Leu Thr His Trp Ile  
 210 215 220  
 Ser Phe Ala Phe Gly Ala Glu Ser Gln Lys Asn Thr Tyr His Tyr Asn  
 225 230 235 240  
 Glu Lys Gly Leu Leu Val Ser Glu Val Leu Ser Asn Ala Met Gly Thr  
 245 250 255  
 Thr Tyr Ser Asp Thr Gly Lys Thr Glu Tyr Ser Tyr Asp Asp Ala Asp  
 260 265 270  
 Asn Met Val Lys Ala Glu Tyr Phe Val Val Gln Gln Gly Lys Ala Trp  
 275 280 285  
 Gln Val Leu Lys Arg Glu Glu Tyr Thr Tyr Glu Asp Asn Ile Cys Ile  
 290 295 300  
 Gln Tyr Leu Ala Ile Asn Gly Thr Asp Thr Lys Val Tyr Lys Arg Asp  
 305 310 315 320  
 Ile Glu Ser Asp Lys Ser Ile Ser Ala Asn Val Ile Asp Ile Pro Ser  
 325 330 335  
 Met Pro Glu Gln Thr Trp Pro Asn Met Tyr Gly Phe Asn Ala Lys Arg  
 340 345 350  
 Leu Lys Glu Thr Tyr Ser Ser Tyr Glu Gly Asp Val Ala Thr Pro Ile  
 355 360 365  
 Phe Asp Tyr Ile Tyr Thr Tyr Lys Ala Leu Thr Ser Met Ala Thr Pro  
 370 375 380  
 Ser Thr Glu Ala Gln Val Ala Val Tyr Leu Asn Pro Ser Thr Asp Arg  
 385 390 395 400  
 Leu Val Ile Leu Ala Asn Gly Ile Thr His Leu Ser Met Tyr Asp Leu  
 405 410 415

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Gln Gly Lys Leu Ile Arg Asp Cys Ala Leu Ser Gly Asp Lys Val Glu  
 420 425 430  
 Met Gly Val Gly Ser Leu Thr Lys Gly Thr Tyr Leu Leu Lys Val Asn  
 435 440 445  
 5 Thr Asp Gln Gly Ala Phe Val Arg Lys Val Val Ile Arg  
 450 455 460

(2) INFORMATION FOR SEQ ID NO:386

- 10 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 451 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear
- 15 (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- 20 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Porphyromonas gingivalis
- (ix) FEATURE:  
 (A) NAME/KEY: misc feature  
 (B) LOCATION 1...451
- 25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:386

Met Ala Lys Val Ile Lys Thr Lys Lys Gly Leu Ala Leu Asn Leu Lys  
 1 5 10 15  
 30 Gly Lys Pro Leu Pro Glu Met Leu Ala Glu Pro Ala Gln Ser Pro Thr  
 20 25 30  
 Tyr Ala Val Val Pro Asp Asp Phe Glu Gly Val Ile Pro Lys Val Thr  
 35 35 40 45  
 Ala Arg Pro Gly Asp Lys Val Arg Ala Gly Ser Ala Leu Met His His  
 50 55 60  
 Lys Ala Tyr Pro Glu Met Lys Phe Thr Ser Pro Val Ser Gly Glu Val  
 65 70 75 80  
 Ile Ala Val Asn Arg Gly Ala Lys Arg Lys Val Leu Ser Ile Glu Val  
 85 90 95  
 40 Lys Pro Asp Gly Leu Asn Glu Tyr Glu Ser Phe Pro Val Gly Asp Pro  
 100 105 110  
 Ser Ala Leu Ser Ala Glu Gln Ile Lys Glu Leu Leu Leu Ser Ser Gly  
 115 120 125  
 45 Met Trp Gly Phe Ile Lys Gln Arg Pro Tyr Asp Ile Val Ala Thr Pro  
 130 135 140  
 Asp Ile Ala Pro Arg Asp Ile Tyr Ile Thr Ala Asn Phe Thr Ala Pro  
 145 150 155 160  
 Leu Ala Pro Asp Phe Asp Phe Ile Val Arg Gly Glu Glu Arg Ala Leu  
 165 170 175  
 50 Gln Thr Ala Ile Asp Ala Leu Ala Lys Leu Thr Thr Gly Lys Val Tyr  
 180 185 190  
 Val Gly Leu Lys Pro Gly Ser Ser Leu Gly Leu His Asn Ala Glu Ile  
 195 200 205  
 55 Val Glu Val His Gly Pro His Pro Ala Gly Asn Val Gly Val Leu Ile  
 210 215 220  
 Asn His Thr Lys Pro Ile Asn Arg Gly Glu Thr Val Trp Thr Leu Lys  
 225 230 235 240  
 Ala Thr Asp Leu Ile Val Ile Gly Arg Phe Leu Leu Thr Gly Lys Ala  
 245 250 255  
 60 Asp Phe Thr Arg Met Ile Ala Met Thr Gly Ser Asp Ala Ala Ala His  
 260 265 270  
 Gly Tyr Val Arg Ile Met Pro Gly Cys Asn Val Phe Ala Ser Phe Pro  
 275 280 285  
 65 Gly Arg Leu Thr Ile Lys Glu Ser His Glu Arg Val Ile Asp Gly Asn  
 290 295 300  
 Val Leu Thr Gly Lys Lys Leu Cys Glu Lys Glu Pro Phe Leu Ser Ala  
 305 310 315 320  
 Arg Cys Asp Gln Ile Thr Val Ile Pro Glu Gly Asp Asp Val Asp Glu  
 325 330 335  
 70 Leu Phe Gly Trp Ala Ala Pro Arg Leu Asp Gln Tyr Ser Met Ser Arg  
 340 345 350  
 Ala Tyr Phe Ser Trp Leu Gln Gly Lys Asn Lys Glu Tyr Val Leu Asp  
 355 360 365  
 75 Ala Arg Ile Lys Gly Gly Glu Arg Ala Met Ile Met Ser Asn Glu Tyr  
 370 375 380

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Asp Arg Val Phe Pro Met Asp Ile Tyr Pro Glu Tyr Leu Leu Lys Ala  
 385 390 395 400  
 Ile Ile Ala Phe Asp Ile Asp Lys Met Glu Asp Leu Gly Ile Tyr Glu  
 405 410 415  
 5 Val Ala Pro Glu Asp Phe Ala Thr Cys Glu Phe Val Asp Thr Ser Lys  
 420 425 430  
 Ile Glu Leu Gln Arg Ile Val Arg Glu Gly Leu Asp Met Leu Tyr Lys  
 435 440 445  
 10 Glu Met Asn  
 450

(2) INFORMATION FOR SEQ ID NO:387

- 15 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 195 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
 20 (ii) MOLECULE TYPE: protein  
 (iii) HYPOTHETICAL: YES  
 (vi) ORIGINAL SOURCE:  
 25 (A) ORGANISM: Porphyromonas gingivalis  
 (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION: 1...195  
 30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:387

Met Asp Lys Val Ser Tyr Ala Leu Gly Leu Ser Ile Gly Asn Asn Phe  
 1 5 10 15  
 35 Lys Ser Ser Gly Ile Asp Ser Val Val Met Asp Asp Phe Met Gln Gly  
 20 25 30  
 Leu Ser Asp Val Leu Glu Glu Lys Ala Pro Gln Leu Ser Tyr Asp Glu  
 35 40 45  
 Ala Lys Arg Glu Ile Glu Ala Tyr Phe Met Asp Leu Gln Gln Lys Ala  
 50 55 60  
 40 Val Lys Leu Asn Lys Glu Ala Gly Glu Glu Phe Leu Lys Ile Asn Ala  
 65 70 75 80  
 His Lys Glu Gly Val Thr Thr Leu Pro Ser Gly Leu Gln Tyr Glu Val  
 85 90 95  
 45 Ile Lys Met Gly Glu Gly Pro Lys Pro Thr Leu Ser Asp Thr Val Thr  
 100 105 110  
 Cys His Tyr His Gly Thr Leu Ile Asn Gly Ile Val Phe Asp Ser Ser  
 115 120 125  
 Met Asp Arg Gly Glu Pro Ala Ser Phe Pro Leu Arg Gly Val Ile Ala  
 130 135 140  
 50 Gly Trp Thr Glu Ile Leu Gln Leu Met Pro Val Gly Ser Lys Trp Lys  
 145 150 155 160  
 Val Thr Ile Pro Ser Asp Leu Ala Tyr Gly Asp Arg Gly Ala Gly Glu  
 165 170 175  
 55 His Ile Lys Pro Gly Ser Thr Leu Ile Phe Ile Ile Glu Leu Leu Ser  
 180 185 190  
 Ile Asn Lys  
 195

(2) INFORMATION FOR SEQ ID NO:388

- 60 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 273 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
 65 (ii) MOLECULE TYPE: protein  
 (iii) HYPOTHETICAL: YES  
 70 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Porphyromonas gingivalis  
 (ix) FEATURE:  
 75 (A) NAME/KEY: misc\_feature  
 (B) LOCATION: 1...273

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## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:388

5 Met Lys Lys Ala Leu Leu Ile Gly Ala Ala Leu Leu Gly Ala Val Ser  
1 5 10 15  
Phe Ala Ser Ala Gln Ser Leu Ser Thr Ile Lys Val Gln Asn Asn Ser  
20 25 30  
Val Gln Gln Pro Arg Glu Glu Ala Thr Ile Gln Val Cys Gly Glu Leu  
35 40 45  
10 Ala Glu Gln Val Asp Cys Ile Gly Thr Gly Asn Ser Ala Ile Ile Ala  
50 55 60  
Ala Ala Ala Lys Phe Glu Ser Asp Asp Leu Glu Ser Tyr Val Gly Trp  
65 70 75 80  
15 Glu Ile Met Ser Val Asp Phe Phe Pro Gly Tyr Lys Ala Cys Lys Tyr  
85 90 95  
Thr Ser Ala Val Trp Ala Asp Asp Met Thr Ile Leu Gly Gln Ser Glu  
100 105 110  
Asp Ser Asp Pro Glu Met Gln Thr Ile Asn Asn Leu Ala Leu Lys Thr  
115 120 125  
20 Ser Val Lys Ile Glu Ala Gly Lys Asn Tyr Ile Val Gly Tyr Ile Ala  
130 135 140  
Asn Thr Ala Gly Gly His Pro Ile Gly Cys Asp Gln Gly Pro Ala Val  
145 150 155 160  
25 Asp Gly Tyr Gly Asp Leu Val Ser Ile Ser Glu Asp Gly Gly Ala Thr  
165 170 175  
Phe Pro Pro Phe Glu Ser Leu His Gln Ala Val Pro Thr Leu Asn Tyr  
180 185 190  
Asn Ile Tyr Val Val Val His Leu Lys Lys Gly Glu Gly Val Glu Ala  
195 200 205  
30 Val Leu Thr Asn Asp Lys Ala Asn Ala Tyr Val Gln Asn Gly Val Ile  
210 215 220  
Tyr Val Ala Gly Ala Asn Gly Arg Gln Val Ser Leu Phe Asp Met Asn  
225 230 235 240  
35 Gly Lys Val Val Tyr Thr Gly Val Ser Glu Thr Ile Ala Ala Pro Gln  
245 250 255  
Lys Gly Met Tyr Ile Leu Arg Val Gly Ala Lys Ser Ile Lys Leu Ala  
260 265 270  
Ile

40

## (2) INFORMATION FOR SEQ ID NO:389

(i) SEQUENCE CHARACTERISTICS:  
45 (A) LENGTH: 554 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear  
  
(ii) MOLECULE TYPE: protein  
  
50 (iii) HYPOTHETICAL: YES  
  
(vi) ORIGINAL SOURCE:  
(A) ORGANISM: Porphyromonas gingivalis  
  
55 (ix) FEATURE:  
(A) NAME/KEY: misc\_feature  
(B) LOCATION 1...554

## 60 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:389

Met Pro Arg Ile Met Lys Leu Lys Ile Ala Leu Arg Leu Leu Leu Ala  
1 5 10 15  
Thr Phe Ala Ile Val Leu Phe Ser Pro Leu Ala Lys Ala Gln Met Asp  
20 25 30  
65 Ile Gly Gly Asp Asp Val Leu Ile Glu Thr Met Ser Thr Leu Ser Gly  
35 40 45  
Tyr Ser Glu Asp Phe Tyr Tyr Lys Met Ala Val Ala Asp Asn Gly Trp  
50 55 60  
70 Ile Tyr Val Met Leu Asp Phe Ser Arg Ile Tyr Phe Asp Asp Val Arg  
65 70 75 80  
Leu Tyr Arg Ser Lys Asp Gly Gly Ala Thr Tyr Gln Lys Leu Gly Ser  
85 90 95  
Leu Gly Ser Leu Val Pro Tyr Asp Phe Asp Val Ser His Cys Asp Phe  
100 105 110  
75 Ile Val Thr Gly Lys Asp Glu Asp Asp Ile Asn Val Trp Thr Val Met



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115 120 125  
 Thr Ala Phe Glu Tyr Val Gly Gly Thr Ile Gly Asn Gly Val Leu Leu  
 130 135 140  
 Met His Arg His Asp Ala Asp Ile Asn Asn Thr Glu Cys Val Tyr Lys  
 145 150 155 160  
 Lys Asp Phe Pro Asn Asn Arg Leu Met Gly Val Ala Ile Ala Ser Asn  
 165 170 175  
 Tyr Arg Ala Pro Ser Pro Tyr Gly Leu Gly Gly Asp Pro Phe Ala Leu  
 180 185 190  
 10 Ala Val Ala Val Ser Gly Ser Gly Ser Asp His Ser Phe Leu Asp Tyr  
 195 200 205  
 Ile Phe Ser Leu Asp Gly Gly Val His Phe Glu Gln Lys Arg Ile Tyr  
 210 215 220  
 15 Thr Arg Pro Gln Lys Leu Thr Ile Asn Arg Val Asp Leu Ser Leu Gly  
 225 230 235 240  
 Ser Thr Ser Pro Ser Leu Gly Phe Asn Thr Trp Pro Leu Met Gly Val  
 245 250 255  
 Val Phe Glu Met Asn Lys Asn Leu Asp Gly Phe Asp Ile Gly Phe Ile  
 260 265 270  
 20 Ser Asn Phe Val Asp Tyr Asp Pro Arg Tyr Ala Trp Ser Glu Pro Ile  
 275 280 285  
 Ile Ile Glu Glu Asp Cys Gly Trp Thr Asp Phe Asn Pro Leu Gly Ala  
 290 295 300  
 25 Leu Ser Ile Glu Ile Gln Met Met Leu Asp Asp Asn Ser Asp Asn Thr  
 305 310 315 320  
 Val Gly Gly Glu Arg Ser His Asn Phe Leu Ile Thr Tyr Pro Gly His  
 325 330 335  
 Tyr Val Tyr Pro Lys Gln Ser Phe Asn Tyr Ser Pro Gly His Thr Pro  
 340 345 350  
 30 Thr Lys Lys Asp Leu Val Phe Lys His Cys Ile Gly Ile Pro Ala Leu  
 355 360 365  
 Ala Tyr Asp Lys Glu Gly Asp Arg Tyr Leu Thr Thr Phe Gln Asp His  
 370 375 380  
 35 Asn Leu Met Arg Tyr Arg Trp Ile Lys Tyr Asp Asp Ile Asn Ser Phe  
 385 390 395 400  
 Tyr Gly Trp Ser Trp Pro Tyr Val Tyr Ala Lys Glu Ala Lys Asp Lys  
 405 410 415  
 Lys Arg Arg Arg Pro Gln Val Ala Leu Asn Pro Thr Asn Gly Lys Ala  
 420 425 430  
 40 Cys Trp Val Trp His Thr Arg Lys Ser Pro Tyr Asp Glu Thr Lys Pro  
 435 440 445  
 His Pro Thr Pro Val Ile Ile Lys His Phe Leu Trp Ser Asp Thr Glu  
 450 455 460  
 45 Trp Val His Ala Leu Asp Val Gly Asp Val Leu Gln Lys Glu Gly Ser  
 465 470 475 480  
 Met Lys Leu Tyr Pro Asn Pro Ala Lys Glu Tyr Val Leu Ile Asn Leu  
 485 490 495  
 Pro Lys Glu Gly Gly His Glu Ala Val Val Tyr Asp Met Gln Gly Arg  
 500 505 510  
 50 Ile Val Glu Lys Val Ser Phe Ser Gly Lys Glu Tyr Lys Leu Asn Val  
 515 520 525  
 Gln Tyr Leu Ser Lys Gly Thr Tyr Met Leu Lys Val Val Ala Asp Thr  
 530 535 540  
 55 Glu Tyr Phe Val Glu Lys Ile Ile Val Glu  
 545 550

(2) INFORMATION FOR SEQ ID NO:390

- 60 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 550 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
  
 65 (ii) MOLECULE TYPE: protein  
 (iii) HYPOTHETICAL: YES  
  
 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Porphyromonas gingivalis  
 70 (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...550  
  
 75 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:390

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5 Met Lys Leu Lys Ile Ala Leu Arg Leu Leu Leu Ala Thr Phe Ala Ile  
 1 5 10 15  
 Val Leu Phe Ser Pro Leu Ala Lys Ala Gln Met Asp Ile Gly Gly Asp  
 20 25 30  
 Asp Val Leu Ile Glu Thr Met Ser Thr Leu Ser Gly Tyr Ser Glu Asp  
 35 40 45  
 Phe Tyr Tyr Lys Met Ala Val Ala Asp Asn Gly Trp Ile Tyr Val Met  
 50 55 60  
 10 Leu Asp Phe Ser Arg Ile Tyr Phe Asp Asp Val Arg Leu Tyr Arg Ser  
 65 70 75 80  
 Lys Asp Gly Gly Ala Thr Tyr Gln Lys Leu Gly Ser Leu Gly Ser Leu  
 85 90 95  
 15 Val Pro Tyr Asp Phe Asp Val Ser His Cys Asp Phe Ile Val Thr Gly  
 100 105 110  
 Lys Asp Glu Asp Asp Ile Asn Val Trp Thr Val Met Thr Ala Phe Glu  
 115 120 125  
 Tyr Val Gly Gly Thr Ile Gly Asn Gly Val Leu Leu Met His Arg His  
 130 135 140  
 20 Asp Ala Asp Ile Asn Asn Thr Glu Cys Val Tyr Lys Lys Asp Phe Pro  
 145 150 155 160  
 Asn Asn Arg Leu Met Gly Val Ala Ile Ala Ser Asn Tyr Arg Ala Pro  
 165 170 175  
 25 Ser Pro Tyr Gly Leu Gly Gly Asp Pro Phe Ala Leu Ala Val Ala Val  
 180 185 190  
 Ser Gly Ser Gly Ser Asp His Ser Phe Leu Asp Tyr Ile Phe Ser Leu  
 195 200 205  
 Asp Gly Gly Val His Phe Glu Gln Lys Arg Ile Tyr Thr Arg Pro Gln  
 210 215 220  
 30 Lys Leu Thr Ile Asn Arg Val Asp Leu Ser Leu Gly Ser Thr Ser Pro  
 225 230 235 240  
 Ser Leu Gly Phe Asn Thr Trp Pro Leu Met Gly Val Val Phe Glu Met  
 245 250 255  
 35 Asn Lys Asn Leu Asp Gly Phe Asp Ile Gly Phe Ile Ser Asn Phe Val  
 260 265 270  
 Asp Tyr Asp Pro Arg Tyr Ala Trp Ser Glu Pro Ile Ile Ile Glu Glu  
 275 280 285  
 Asp Cys Gly Trp Thr Asp Phe Asn Pro Leu Gly Ala Leu Ser Ile Glu  
 290 295 300  
 40 Ile Gln Met Met Leu Asp Asn Ser Asp Asn Thr Val Gly Gly Glu  
 305 310 315 320  
 Arg Ser His Asn Phe Leu Ile Thr Tyr Pro Gly His Tyr Val Tyr Pro  
 325 330 335  
 45 Lys Gln Ser Phe Asn Tyr Ser Pro Gly His Thr Pro Thr Lys Lys Asp  
 340 345 350  
 Leu Val Phe Lys His Cys Ile Gly Ile Pro Ala Leu Ala Tyr Asp Lys  
 355 360 365  
 Glu Gly Asp Arg Tyr Leu Thr Thr Phe Gln Asp His Asn Leu Met Arg  
 370 375 380  
 50 Tyr Arg Trp Ile Lys Tyr Asp Asp Ile Asn Ser Phe Tyr Gly Trp Ser  
 385 390 395 400  
 Trp Pro Tyr Val Tyr Ala Lys Glu Ala Lys Asp Lys Lys Arg Arg Arg  
 405 410 415  
 55 Pro Gln Val Ala Leu Asn Pro Thr Asn Gly Lys Ala Cys Trp Val Trp  
 420 425 430  
 His Thr Arg Lys Ser Pro Tyr Asp Glu Thr Lys Pro His Pro Thr Pro  
 435 440 445  
 Val Ile Ile Lys His Phe Leu Trp Ser Asp Thr Glu Trp Val His Ala  
 450 455 460  
 60 Leu Asp Val Gly Asp Val Leu Gln Lys Glu Gly Ser Met Lys Leu Tyr  
 465 470 475 480  
 Pro Asn Pro Ala Lys Glu Tyr Val Leu Ile Asn Leu Pro Lys Glu Gly  
 485 490 495  
 65 Gly His Glu Ala Val Val Tyr Asp Met Gln Gly Arg Ile Val Glu Lys  
 500 505 510  
 Val Ser Phe Ser Gly Lys Glu Tyr Lys Leu Asn Val Gln Tyr Leu Ser  
 515 520 525  
 Lys Gly Thr Tyr Met Leu Lys Val Val Ala Asp Thr Glu Tyr Phe Val  
 530 535 540  
 70 Glu Lys Ile Ile Val Glu  
 545 550

(2) INFORMATION FOR SEQ ID NO:391

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- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 390 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: *Porphyromonas gingivalis*
- (ix) FEATURE:  
 (A) NAME/KEY: misc feature  
 (B) LOCATION 1...390
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:391
- |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Lys | Arg | Leu | Leu | Pro | Phe | Leu | Leu | Leu | Ala | Gly | Leu | Val | Ala | Val |
| 1   |     |     | 5   |     |     |     | 10  |     |     |     |     | 15  |     |     |     |
| Gly | Asn | Val | Ser | Ala | Gln | Ser | Pro | Arg | Ile | Pro | Gln | Val | Asp | Val | His |
|     | 20  |     |     |     |     |     | 25  |     |     |     |     | 30  |     |     |     |
| Thr | Arg | Ile | Ala | Arg | Asn | Ala | Arg | Tyr | Arg | Leu | Asp | Lys | Ile | Ser | Val |
|     | 35  |     |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Pro | Asp | Ser | Arg | Gln | Ile | Phe | Asp | Tyr | Phe | Tyr | Lys | Glu | Glu | Thr | Ile |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Pro | Thr | Lys | Ile | Gln | Thr | Thr | Thr | Gly | Gly | Ala | Ile | Thr | Ser | Ile | Asp |
|     | 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Ser | Leu | Phe | Tyr | Glu | Asp | Asp | Arg | Leu | Val | Gln | Val | Arg | Tyr | Phe | Asp |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     | 95  |     |     |
| Asn | Asn | Leu | Glu | Leu | Lys | Gln | Ala | Glu | Lys | Tyr | Val | Tyr | Asp | Gly | Ser |
|     |     | 100 |     |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Lys | Leu | Val | Leu | Arg | Glu | Ile | Arg | Lys | Ser | Pro | Thr | Asp | Glu | Thr | Pro |
|     | 115 |     |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Ile | Lys | Lys | Val | Ser | Tyr | His | Tyr | Leu | Cys | Gly | Ser | Asp | Met | Pro | Phe |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Glu | Ile | Thr | Thr | Glu | Met | Ser | Asp | Gly | Tyr | Phe | Glu | Ser | His | Thr | Leu |
|     | 145 |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Asn | Tyr | Leu | Asn | Gly | Lys | Ile | Ala | Arg | Ile | Asp | Ile | Met | Thr | Gln | Gln |
|     |     |     | 165 |     |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Asn | Pro | Ser | Ala | Glu | Leu | Ile | Glu | Thr | Gly | Arg | Met | Val | Tyr | Glu | Phe |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Asp | Ala | Asn | Asn | Asp | Ala | Val | Leu | Leu | Arg | Asp | Ser | Val | Phe | Leu | Pro |
|     | 195 |     |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Leu | Gln | Asn | Lys | Trp | Val | Glu | Met | Phe | Thr | His | Arg | Tyr | Thr | Tyr | Asp |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Asn | Lys | His | Asn | Cys | Ile | Arg | Trp | Glu | Gln | Asp | Glu | Phe | Gly | Thr | Leu |
|     | 225 |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |
| Thr | Leu | Ala | Asn | Asn | Phe | Glu | Tyr | Asp | Thr | Thr | Ile | Pro | Leu | Ser | Ser |
|     |     |     | 245 |     |     |     |     |     | 250 |     |     |     | 255 |     |     |
| Val | Leu | Phe | Pro | Thr | His | Glu | Glu | Phe | Phe | Arg | Pro | Leu | Leu | Pro | Asn |
|     | 260 |     |     |     |     |     |     | 265 |     |     |     |     | 270 |     |     |
| Phe | Met | Lys | His | Met | Arg | Thr | Lys | Gln | Thr | Tyr | Phe | Asn | Asn | Ser | Gly |
|     | 275 |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |     |
| Glu | Gly | Leu | Ser | Glu | Val | Cys | Asp | Tyr | Asn | Tyr | Phe | Tyr | Thr | Asp | Met |
|     | 290 |     |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |
| Gln | Gly | Asn | Ala | Leu | Thr | Asp | Val | Ala | Val | Asn | Glu | Ser | Ile | Lys | Ile |
|     | 305 |     |     |     | 310 |     |     |     |     | 315 |     |     |     |     | 320 |
| Tyr | Pro | Arg | Pro | Ala | Thr | Asp | Phe | Leu | Arg | Ile | Glu | Gly | Ser | Gln | Leu |
|     |     |     | 325 |     |     |     |     | 330 |     |     |     |     | 335 |     |     |
| Leu | Arg | Leu | Ser | Leu | Phe | Asp | Met | Asn | Gly | Lys | Leu | Ile | Arg | Ala | Thr |
|     |     |     | 340 |     |     |     |     | 345 |     |     |     |     | 350 |     |     |
| Glu | Leu | Thr | Gly | Asp | Leu | Ala | Ile | Ile | Gly | Val | Ala | Ser | Leu | Pro | Arg |
|     |     | 355 |     |     |     | 360 |     |     |     |     | 365 |     |     |     |     |
| Gly | Thr | Tyr | Ile | Ala | Glu | Ile | Thr | Ala | Ala | Asn | Ser | Lys | Thr | Ile | Arg |
|     | 370 |     |     |     |     | 375 |     |     |     |     | 380 |     |     |     |     |
| Ala | Lys | Val | Ser | Leu | Arg |     |     |     |     |     |     |     |     |     |     |
|     | 385 |     |     |     | 390 |     |     |     |     |     |     |     |     |     |     |
- (2) INFORMATION FOR SEQ ID NO:392
- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 411 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

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(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

5 (vi) ORIGINAL SOURCE:  
(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:  
(A) NAME/KEY: misc\_feature  
(B) LOCATION 1...411

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:392

15 Met Arg Gln His Leu Ser Leu Phe Pro Phe Ile Leu Phe Leu Leu  
1 5 10 15  
Ala Phe Ser Tyr Val Gly Cys Arg Thr Val Arg Gln Thr Pro Lys Gln  
20 20 25 30  
Ser Glu Arg Tyr Val Val Val Leu Ser Leu Asp Gly Phe Arg Pro Asp  
20 35 40 45  
Tyr Thr Asp Arg Ala Arg Thr Pro Ala Leu Asp Arg Met Ala Gln Glu  
50 55 60  
Gly Leu Ser Gly Ser Leu Gln Pro Cys Phe Pro Ser Leu Thr Phe Pro  
65 70 75 80  
25 Asn His Tyr Ser Met Ala Thr Gly Leu Tyr Pro Asp His His Gly Ile  
85 90 95  
Val Ala Asn Glu Phe Val Asp Ser Leu Leu Gly Ile Phe Arg Ile Ser  
100 105 110  
30 Asp Arg Lys Ala Val Glu Thr Pro Gly Phe Trp Gly Gly Glu Pro Val  
115 120 125  
Trp Asn Thr Ala Ala Arg Gln Gly Ile Arg Thr Gly Val Tyr Phe Trp  
130 135 140  
Val Gly Ser Glu Thr Ala Val Asn Gly Asn Arg Pro Trp Arg Trp Lys  
145 150 155 160  
35 Lys Phe Ser Ser Thr Val Pro Phe Arg Asp Arg Ala Asp Ser Val Ile  
165 170 175  
Ala Trp Leu Gly Leu Pro Glu Lys Glu Arg Pro Arg Leu Leu Met Trp  
180 185 190  
40 Tyr Ile Glu Glu Pro Asp Met Ile Gly His Ser Gln Thr Pro Glu Ser  
195 200 205  
Pro Leu Thr Leu Ala Met Val Glu Arg Leu Asp Ser Val Val Gly Tyr  
210 215 220  
Phe Arg Lys Arg Leu Asp Ser Leu Pro Ile Ala Ala Gln Thr Asp Phe  
225 230 235 240  
45 Ile Ile Val Ser Asp His Gly Met Ala Thr Tyr Glu Asn Glu Lys Cys  
245 250 255  
Val Asn Leu Ser His Tyr Leu Pro Ala Asp Ser Phe Leu Tyr Met Ala  
260 265 270  
50 Thr Gly Ala Phe Thr His Leu Tyr Pro Lys Pro Ser Tyr Thr Glu Arg  
275 280 285  
Ala Tyr Glu Ile Leu Arg Ala Ile Pro His Ile Ser Val Tyr Arg Lys  
290 295 300  
Gly Glu Val Pro Lys Arg Leu Arg Cys Gly Thr Asn Pro Arg Leu Gly  
305 310 315 320  
55 Glu Leu Val Val Ile Pro Asp Ile Gly Ser Thr Val Phe Phe Ala Ile  
325 330 335  
Asn Glu Asp Val Arg Pro Gly Ala Ala His Gly Tyr Asp Asn Gln Ala  
340 345 350  
60 Pro Glu Met Arg Ala Leu Leu Arg Ala Val Gly Pro Asp Phe Arg Pro  
355 360 365  
Gly Ser Arg Val Glu Asn Leu Pro Asn Ile Thr Ile Tyr Pro Leu Ile  
370 375 380  
Cys Arg Leu Leu Gly Ile Glu Pro Ala Pro Asn Asp Ala Asp Glu Thr  
385 390 395 400  
65 Leu Leu Asn Gly Leu Ile Arg Asp Lys Arg Pro  
405 410

(2) INFORMATION FOR SEQ ID NO:393

70 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 246 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

75 (ii) MOLECULE TYPE: protein

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(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:  
(A) ORGANISM: *Porphyromonas gingivalis*

(ix) FEATURE:  
(A) NAME/KEY: misc\_feature  
(B) LOCATION 1...246

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:393

Met	Lys	Val	Gly	Leu	Phe	Ile	Pro	Cys	Tyr	Val	Asn	Ala	Val	Tyr	Pro
1				5					10					15	
Glu	Val	Gly	Ile	Ala	Thr	Tyr	Lys	Leu	Lys	Ser	Leu	Asp	Ile	Asp	
			20				25					30			
Val	Asp	Tyr	Pro	Met	Asp	Gln	Thr	Cys	Cys	Gly	Gln	Pro	Met	Ala	Asn
		35				40					45				
Ala	Gly	Phe	Glu	Gln	Lys	Ala	Gln	Lys	Leu	Ala	Leu	Arg	Phe	Glu	Glu
	50				55					60					
Leu	Phe	Glu	Ser	Tyr	Asp	Val	Val	Val	Gly	Pro	Ser	Ala	Ser	Cys	Val
65				70					75					80	
Ala	Phe	Val	Lys	Glu	Asn	Tyr	Asp	His	Ile	Leu	Arg	Pro	Thr	Gly	His
			85					90					95		
Val	Cys	Lys	Ser	Ala	Ala	Lys	Val	Arg	Asp	Ile	Cys	Glu	Phe	Leu	His
		100				105						110			
Asp	Asp	Leu	Lys	Ile	Thr	Ser	Leu	Pro	Ser	Arg	Phe	Ala	His	Lys	Val
		115				120					125				
Ser	Leu	His	Asn	Ser	Cys	His	Gly	Val	Arg	Glu	Leu	His	Leu	Ser	Thr
	130					135					140				
Pro	Ser	Glu	Val	His	Arg	Pro	Tyr	His	Asn	Lys	Val	Arg	Arg	Leu	Leu
145					150					155				160	
Glu	Met	Val	Gln	Gly	Ile	Glu	Val	Phe	Glu	Pro	Lys	Arg	Ile	Asp	Glu
			165						170				175		
Cys	Cys	Gly	Phe	Gly	Gly	Met	Tyr	Ser	Val	Glu	Glu	Pro	Glu	Val	Ser
		180				185						190			
Thr	Cys	Met	Gly	His	Asp	Lys	Val	Leu	Asp	His	Ile	Ser	Thr	Gly	Ala
		195				200						205			
Glu	Tyr	Ile	Thr	Gly	Pro	Asp	Ser	Ser	Cys	Leu	Met	His	Met	Gln	Gly
	210					215					220				
Val	Ile	Asp	Arg	Glu	Lys	Leu	Pro	Ile	Lys	Thr	Ile	His	Ala	Val	Glu
225					230					235					240
Ile	Leu	Ala	Ala	Asn	Leu										
			245												

(2) INFORMATION FOR SEQ ID NO:394

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 246 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:  
(A) ORGANISM: *Porphyromonas gingivalis*

(ix) FEATURE:  
(A) NAME/KEY: misc\_feature  
(B) LOCATION 1...246

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:394

Met	Asp	Ile	Val	Ser	Met	Ala	Asp	Lys	Ala	Leu	Val	Val	Glu	Met	Arg
1				5					10					15	
Asp	Val	Thr	Leu	Cys	Gln	Glu	Glu	Asn	Val	Ile	Phe	Gln	Asn	Leu	Asn
		20						25				30			
Leu	Thr	Leu	Ser	Ala	Gly	Asp	Phe	Val	Tyr	Leu	Ile	Gly	Ser	Val	Gly
		35				40						45			
Ser	Gly	Lys	Ser	Thr	Leu	Leu	Lys	Ala	Leu	Tyr	Ala	Glu	Val	Pro	Ile
	50				55					60					
Ser	Ala	Gly	Tyr	Ala	Arg	Val	Ile	Asp	Tyr	Asp	Leu	Ala	Lys	Leu	Lys
65					70				75					80	

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Arg Lys Gln Leu Pro Tyr Leu Arg Arg Asn Leu Gly Ile Val Phe Gln  
 85 90 95  
 Asp Phe Gln Leu Leu Asn Gly Arg Thr Val Ala Glu Asn Leu Asp Phe  
 100 105 110  
 5 Val Leu Arg Ala Thr Asp Trp Lys Asn Arg Ala Asp Arg Glu Gln Arg  
 115 120 125  
 Ile Glu Glu Val Leu Thr Arg Val Gly Met Ser Arg Lys Ala Tyr Lys  
 130 135 140  
 10 Arg Pro His Glu Leu Ser Gly Gly Glu Gln Gln Arg Val Gly Ile Ala  
 145 150 155 160  
 Arg Ala Leu Leu Ala Lys Pro Ala Leu Ile Leu Ala Asp Glu Pro Thr  
 165 170 175  
 Gly Asn Leu Asp Ser Val Thr Gly Leu Gln Ile Ala Ser Leu Leu Tyr  
 180 185 190  
 15 Glu Ile Ser Lys Gln Gly Thr Ala Val Leu Met Ser Thr His Asn Ser  
 195 200 205  
 Ser Leu Leu Ser His Leu Pro Ala Arg Thr Leu Ala Val Arg Lys Asn  
 210 215 220  
 20 Gly Asp Ala Ser Ser Leu Val Glu Leu Ser Ala Asp Ala Val Ser Arg  
 225 230 235 240  
 Lys Asn Thr Glu Ile Asp

25 (2) INFORMATION FOR SEQ ID NO:395

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 241 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

30 (ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

35 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Porphyromonas gingivalis

40 (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...241

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:395

45 Met Ala Asp Lys Ala Leu Val Val Glu Met Arg Asp Val Thr Leu Cys  
 1 5 10 15  
 Gln Glu Glu Asn Val Ile Phe Gln Asn Leu Asn Leu Thr Leu Ser Ala  
 20 25 30  
 Gly Asp Phe Val Tyr Leu Ile Gly Ser Val Gly Ser Gly Lys Ser Thr  
 35 40 45  
 50 Leu Leu Lys Ala Leu Tyr Ala Glu Val Pro Ile Ser Ala Gly Tyr Ala  
 50 55 60  
 Arg Val Ile Asp Tyr Asp Leu Ala Lys Leu Lys Arg Lys Gln Leu Pro  
 65 70 75 80  
 Tyr Leu Arg Arg Asn Leu Gly Ile Val Phe Gln Asp Phe Gln Leu Leu  
 85 90 95  
 55 Asn Gly Arg Thr Val Ala Glu Asn Leu Asp Phe Val Leu Arg Ala Thr  
 100 105 110  
 Asp Trp Lys Asn Arg Ala Asp Arg Glu Gln Arg Ile Glu Glu Val Leu  
 115 120 125  
 60 Thr Arg Val Gly Met Ser Arg Lys Ala Tyr Lys Arg Pro His Glu Leu  
 130 135 140  
 Ser Gly Gly Glu Gln Gln Arg Val Gly Ile Ala Arg Ala Leu Leu Ala  
 145 150 155 160  
 Lys Pro Ala Leu Ile Leu Ala Asp Glu Pro Thr Gly Asn Leu Asp Ser  
 165 170 175  
 65 Val Thr Gly Leu Gln Ile Ala Ser Leu Leu Tyr Glu Ile Ser Lys Gln  
 180 185 190  
 Gly Thr Ala Val Leu Met Ser Thr His Asn Ser Ser Leu Leu Ser His  
 195 200 205  
 70 Leu Pro Ala Arg Thr Leu Ala Val Arg Lys Asn Gly Asp Ala Ser Ser  
 210 215 220  
 Leu Val Glu Leu Ser Ala Asp Ala Val Ser Arg Lys Asn Thr Glu Ile  
 225 230 235  
 75 Asp

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## (2) INFORMATION FOR SEQ ID NO:396

- 5 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 232 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- 10 (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Porphyromonas gingivalis
- 15 (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...232
- 20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:396

```

Met Arg Asp Val Thr Leu Cys Gln Glu Glu Asn Val Ile Phe Gln Asn
1      5      10      15
Leu Asn Leu Thr Leu Ser Ala Gly Asp Phe Val Tyr Leu Ile Gly Ser
25      20      25      30
Val Gly Ser Gly Lys Ser Thr Leu Leu Lys Ala Leu Tyr Ala Glu Val
35      40      45
Pro Ile Ser Ala Gly Tyr Ala Arg Val Ile Asp Tyr Asp Leu Ala Lys
50      55      60
Leu Lys Arg Lys Gln Leu Pro Tyr Leu Arg Arg Asn Leu Gly Ile Val
30      65      70      75      80
Phe Gln Asp Phe Gln Leu Leu Asn Gly Arg Thr Val Ala Glu Asn Leu
85      90      95
Asp Phe Val Leu Arg Ala Thr Asp Trp Lys Asn Arg Ala Asp Arg Glu
35      100      105      110
Gln Arg Ile Glu Glu Val Leu Thr Arg Val Gly Met Ser Arg Lys Ala
115      120      125
Tyr Lys Arg Pro His Glu Leu Ser Gly Gly Glu Gln Gln Arg Val Gly
130      135      140
40      145      150      155      160
Ile Ala Arg Ala Leu Leu Ala Lys Pro Ala Leu Ile Leu Ala Asp Glu
165      170      175
Pro Thr Gly Asn Leu Asp Ser Val Thr Gly Leu Gln Ile Ala Ser Leu
180      185      190
45      195      200      205
Leu Tyr Glu Ile Ser Lys Gln Gly Thr Ala Val Leu Met Ser Thr His
210      215      220
50      225      230
Ser Arg Lys Asn Thr Glu Ile Asp

```

## (2) INFORMATION FOR SEQ ID NO:397

- 55 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 219 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear
- 60 (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Porphyromonas gingivalis
- 65 (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...219
- 70 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:397

```

Met Ile Glu Ile Ser Asn Leu Thr Lys Val Phe Arg Thr Glu Glu Ile
1      5      10      15
75      Glu Thr Val Ala Leu Asp Gly Val Ser Leu Lys Val Asp Lys Gly Glu

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20 25 30  
 Phe Ile Ala Ile Met Gly Pro Ser Gly Cys Gly Lys Ser Thr Leu Leu  
 35 40 45  
 5 Asn Ile Leu Gly Leu Leu Asp Asn Pro Thr Ser Gly Ile Tyr Lys Leu  
 50 55 60  
 Asp Gly Ala Glu Val Gly Asn Leu Arg Glu Lys Asp Arg Thr Ala Val  
 65 70 75 80  
 Arg Lys Gly Asn Ile Gly Phe Val Phe Gln Ser Phe Asn Leu Ile Glu  
 85 90 95  
 10 Glu Met Thr Val Ser Glu Asn Val Glu Leu Pro Leu Val Tyr Leu Gly  
 100 105 110  
 Val Lys Ala Ser Glu Arg Lys Glu Arg Val Glu Glu Ala Leu Arg Lys  
 115 120 125  
 15 Met Ser Ile Ser His Arg Ala Gly His Phe Pro Asn Gln Leu Ser Gly  
 130 135 140  
 Gly Gln Gln Gln Arg Val Ala Ile Ala Arg Ala Val Val Ala Asn Pro  
 145 150 155 160  
 Lys Leu Ile Leu Ala Asp Glu Pro Thr Gly Asn Leu Asp Ser Lys Asn  
 165 170 175  
 20 Gly Ala Asp Val Met Glu Leu Leu Arg Gly Leu Asn Arg Glu Gly Ala  
 180 185 190  
 Thr Ile Val Met Val Thr His Ser Glu His Asp Ala Arg Ser Ala Gly  
 195 200 205  
 25 Arg Ile Ile Asn Leu Phe Asp Gly Lys Ile Arg  
 210 215

(2) INFORMATION FOR SEQ ID NO:398

30 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 595 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

35 (ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

40 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...595

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:398

Met Lys Glu Phe Phe Lys Met Phe Phe Ala Ser Ile Leu Gly Val Ile  
 1 5 10 15  
 50 Thr Ala Gly Ile Ile Leu Phe Cys Ile Phe Leu Phe Ile Phe Phe Gly  
 20 25 30  
 Ile Val Ala Gly Ile Ala Ser Lys Ala Thr Gly Gly Thr Ile Pro Lys  
 35 40 45  
 Ile Glu Ala Asn Ser Ile Leu His Ile Unk Asn Ser Ser Phe Pro Glu  
 50 55 60  
 55 Ile Val Ser Ala Asn Pro Trp Ser Met Leu Thr Gly Lys Asp Glu Ser  
 65 70 75 80  
 Val Ser Leu Ser Gln Ala Val Glu Ala Ile Gly Gln Ala Lys Asn Asn  
 85 90 95  
 60 Pro Asn Ile Thr Gly Ile Phe Leu Asp Leu Asp Asn Leu Ser Val Gly  
 100 105 110  
 Met Ala Ser Ala Glu Glu Leu Arg Arg Ala Leu Gln Asp Phe Lys Met  
 115 120 125  
 Ser Gly Lys Phe Val Val Ser Tyr Ala Asp Arg Tyr Thr Gln Lys Gly  
 130 135 140  
 65 Tyr Tyr Leu Ser Ser Ile Ala Asp Lys Leu Tyr Leu Asn Pro Lys Gly  
 145 150 155 160  
 Met Leu Gly Leu Ile Gly Ile Ala Thr Gln Thr Met Phe Tyr Lys Asp  
 165 170 175  
 70 Ala Leu Asp Lys Phe Gly Val Lys Met Glu Ile Phe Lys Val Gly Thr  
 180 185 190  
 Tyr Lys Ala Ala Val Glu Pro Phe Met Leu Asn Arg Met Ser Asp Ala  
 195 200 205  
 Asn Arg Glu Gln Ile Thr Thr Tyr Ile Asn Gly Leu Trp Asp Lys Ile  
 210 215 220  
 75 Thr Ser Asp Ile Ala Glu Ser Arg Lys Thr Ala Met Asp Ser Val Lys



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225 230 235 240  
 Met Phe Ala Asp Lys Gly Glu Met Phe Gly Leu Ala Glu Lys Ala Val  
 245 250 255  
 5 Glu Met Lys Leu Val Asp Glu Leu Ala Tyr Arg Thr Asp Val Glu Lys  
 260 265 270  
 Glu Leu Lys Lys Met Ser Gln Arg Gly Glu Lys Asp Glu Leu Arg Phe  
 275 280 285  
 Val Ser Leu Ser Gln Val Leu Ala Asn Gly Pro Met Asn Lys Thr Lys  
 290 295 300  
 10 Gly Ser Arg Ile Ala Val Leu Phe Ala Glu Gly Glu Ile Thr Glu Glu  
 305 310 315 320  
 Ile Ile Lys Lys Pro Phe Asp Thr Asp Gly Ser Ser Ile Thr Gln Glu  
 325 330 335  
 15 Leu Ala Lys Glu Ile Lys Ala Ala Ala Asp Asp Asp Ile Lys Ala  
 340 345 350  
 Val Val Leu Arg Val Asn Ser Pro Gly Gly Ser Ala Phe Thr Ser Glu  
 355 360 365  
 Gln Ile Trp Lys Gln Val Ala Asp Leu Lys Ala Lys Lys Pro Ile Val  
 370 375 380  
 20 Val Ser Met Gly Asp Val Ala Ala Ser Gly Gly Tyr Tyr Ile Ala Cys  
 385 390 395 400  
 Ala Ala Asn Ser Ile Val Ala Glu His Thr Thr Leu Thr Gly Ser Ile  
 405 410 415  
 25 Gly Ile Phe Gly Met Phe Pro Asn Phe Ala Gly Val Ala Lys Lys Ile  
 420 425 430  
 Gly Val Asn Met Asp Val Val Gln Thr Ser Lys Tyr Ala Asp Leu Gly  
 435 440 445  
 Asn Thr Phe Ala Pro Met Thr Val Glu Asp Arg Ala Leu Ile Gln Arg  
 450 455 460  
 30 Tyr Ile Glu Gln Gly Tyr Asp Leu Phe Leu Thr Arg Val Ser Glu Gly  
 465 470 475 480  
 Arg Asn Arg Thr Lys Ala Gln Ile Asp Ser Ile Ala Gln Gly Arg Val  
 485 490 495  
 35 Trp Leu Gly Asp Lys Ala Leu Ala Leu Gly Leu Val Asp Glu Leu Gly  
 500 505 510  
 Gly Leu Asp Thr Ala Ile Lys Arg Ala Ala Lys Leu Ala Gln Leu Gly  
 515 520 525  
 Gly Asn Tyr Ser Ile Glu Tyr Gly Lys Thr Lys Arg Asn Phe Phe Glu  
 530 535 540  
 40 Glu Leu Leu Ser Ser Ser Ala Ala Asp Met Lys Ser Ala Ile Leu Ser  
 545 550 555 560  
 Thr Ile Leu Ser Asp Pro Glu Ile Glu Val Leu Arg Glu Leu Arg Ser  
 565 570 575  
 45 Met Pro Pro Arg Pro Ser Gly Ile Gln Ala Arg Leu Pro Tyr Tyr Phe  
 580 585 590  
 Met Pro Tyr  
 595  
 (2) INFORMATION FOR SEQ ID NO:399  
 50 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 589 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
 55 (ii) MOLECULE TYPE: protein  
 (iii) HYPOTHETICAL: YES  
 60 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Porphyromonas gingivalis  
 (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 65 (B) LOCATION: 1...589  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:399  
 70 Met Phe Phe Ala Ser Ile Leu Gly Val Ile Thr Ala Gly Ile Ile Leu  
 1 5 10 15  
 Phe Cys Ile Phe Leu Phe Ile Phe Phe Gly Ile Val Ala Gly Ile Ala  
 20 25 30  
 Ser Lys Ala Thr Gly Gly Thr Ile Pro Lys Ile Glu Ala Asn Ser Ile  
 35 40 45  
 75 Leu His Ile Unk Asn Ser Ser Phe Pro Glu Ile Val Ser Ala Asn Pro

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	50		55		60	
	Trp Ser Met Leu Thr Gly Lys Asp Glu Ser Val Ser Leu Ser Gln Ala					
	65		70		75	80
5	Val Glu Ala Ile Gly Gln Ala Lys Asn Asn Pro Asn Ile Thr Gly Ile					
		85		90		95
	Phe Leu Asp Leu Asp Asn Leu Ser Val Gly Met Ala Ser Ala Glu Glu					
		100		105		110
	Leu Arg Arg Ala Leu Gln Asp Phe Lys Met Ser Gly Lys Phe Val Val					
		115		120		125
10	Ser Tyr Ala Asp Arg Tyr Thr Gln Lys Gly Tyr Tyr Leu Ser Ser Ile					
		130		135		140
	Ala Asp Lys Leu Tyr Leu Asn Pro Lys Gly Met Leu Gly Leu Ile Gly					
		145		150		155
15	Ile Ala Thr Gln Thr Met Phe Tyr Lys Asp Ala Leu Asp Lys Phe Gly					
		165		170		175
	Val Lys Met Glu Ile Phe Lys Val Gly Thr Tyr Lys Ala Ala Val Glu					
		180		185		190
	Pro Phe Met Leu Asn Arg Met Ser Asp Ala Asn Arg Glu Gln Ile Thr					
		195		200		205
20	Thr Tyr Ile Asn Gly Leu Trp Asp Lys Ile Thr Ser Asp Ile Ala Glu					
		210		215		220
	Ser Arg Lys Thr Ala Met Asp Ser Val Lys Met Phe Ala Asp Lys Gly					
		225		230		235
25	Glu Met Phe Gly Leu Ala Glu Lys Ala Val Glu Met Lys Leu Val Asp					
		245		250		255
	Glu Leu Ala Tyr Arg Thr Asp Val Glu Lys Glu Leu Lys Lys Met Ser					
		260		265		270
	Gln Arg Gly Glu Lys Asp Glu Leu Arg Phe Val Ser Leu Ser Gln Val					
		275		280		285
30	Leu Ala Asn Gly Pro Met Asn Lys Thr Lys Gly Ser Arg Ile Ala Val					
		290		295		300
	Leu Phe Ala Glu Gly Glu Ile Thr Glu Glu Ile Ile Lys Lys Pro Phe					
		305		310		315
35	Asp Thr Asp Gly Ser Ser Ile Thr Gln Glu Leu Ala Lys Glu Ile Lys					
		325		330		335
	Ala Ala Ala Asp Asp Asp Asp Ile Lys Ala Val Val Leu Arg Val Asn					
		340		345		350
	Ser Pro Gly Gly Ser Ala Phe Thr Ser Glu Gln Ile Trp Lys Gln Val					
		355		360		365
40	Ala Asp Leu Lys Ala Lys Lys Pro Ile Val Val Ser Met Gly Asp Val					
		370		375		380
	Ala Ala Ser Gly Gly Tyr Tyr Ile Ala Cys Ala Ala Asn Ser Ile Val					
		385		390		395
45	Ala Glu His Thr Thr Leu Thr Gly Ser Ile Gly Ile Phe Gly Met Phe					
		405		410		415
	Pro Asn Phe Ala Gly Val Ala Lys Lys Ile Gly Val Asn Met Asp Val					
		420		425		430
	Val Gln Thr Ser Lys Tyr Ala Asp Leu Gly Asn Thr Phe Ala Pro Met					
		435		440		445
50	Thr Val Glu Asp Arg Ala Leu Ile Gln Arg Tyr Ile Glu Gln Gly Tyr					
		450		455		460
	Asp Leu Phe Leu Thr Arg Val Ser Glu Gly Arg Asn Arg Thr Lys Ala					
		465		470		475
55	Gln Ile Asp Ser Ile Ala Gln Gly Arg Val Trp Leu Gly Asp Lys Ala					
		485		490		495
	Leu Ala Leu Gly Leu Val Asp Glu Leu Gly Gly Leu Asp Thr Ala Ile					
		500		505		510
	Lys Arg Ala Ala Lys Leu Ala Gln Leu Gly Gly Asn Tyr Ser Ile Glu					
		515		520		525
60	Tyr Gly Lys Thr Lys Arg Asn Phe Phe Glu Glu Leu Leu Ser Ser Ser					
		530		535		540
	Ala Ala Asp Met Lys Ser Ala Ile Leu Ser Thr Ile Leu Ser Asp Pro					
		545		550		555
65	Glu Ile Glu Val Leu Arg Glu Leu Arg Ser Met Pro Pro Arg Pro Ser					
		565		570		575
	Gly Ile Gln Ala Arg Leu Pro Tyr Tyr Phe Met Pro Tyr					
		580		585		

(2) INFORMATION FOR SEQ ID NO:400

70

- (1) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 313 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

75

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(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

5 (vi) ORIGINAL SOURCE:  
(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:  
10 (A) NAME/KEY: misc\_feature  
(B) LOCATION 1...313

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:400

15 Met Arg Ala Asn Ile Trp Gln Ile Leu Ser Val Ser Val Leu Phe Phe  
1 5 10 15  
Phe Gly Thr Ala Ile Gly Gln Ala Gln Ser Arg Asn Arg Thr Tyr Glu  
20 25 30  
Ala Tyr Val Lys Gln Tyr Ala Asp Glu Ala Ile Arg Gln Met Ser Arg  
35 40 45  
20 Tyr Asn Ile Pro Ala Ser Ile Thr Ile Ala Gln Ala Leu Val Glu Thr  
50 55 60  
Gly Ala Gly Ala Ser Thr Leu Ala Ser Val His Asn Asn His Phe Gly  
65 70 75 80  
25 Ile Lys Cys His Lys Ser Trp Thr Gly Lys Arg Thr Tyr Arg Thr Asp  
85 90 95  
Asp Ala Pro Asn Glu Cys Phe Arg Ser Tyr Ser Ala Ala Arg Glu Ser  
100 105 110  
Tyr Glu Asp His Ser Arg Phe Leu Leu Gln Pro Arg Tyr Arg Pro Leu  
115 120 125  
30 Phe Lys Leu Asp Arg Glu Asp Tyr Arg Gly Trp Ala Thr Gly Leu Gln  
130 135 140  
Arg Cys Gly Tyr Ala Thr Asn Arg Gly Tyr Ala Asn Leu Leu Ile Lys  
145 150 155 160  
35 Met Val Glu Leu Tyr Glu Leu Tyr Ala Leu Asp Arg Glu Lys Tyr Pro  
165 170 175  
Ser Trp Phe His Lys Ser Tyr Pro Gly Ser Asn Lys Lys Ser His Gln  
180 185 190  
Thr Thr Lys Gln Lys Gln Ser Gly Leu Lys His Glu Ala Tyr Phe Ser  
195 200 205  
40 Tyr Gly Leu Leu Tyr Ile Ile Ala Lys Gln Gly Asp Thr Phe Asp Ser  
210 215 220  
Leu Ala Glu Glu Phe Asp Met Arg Ala Ser Lys Leu Ala Lys Tyr Asn  
225 230 235 240  
45 Asp Ala Pro Val Asp Phe Pro Ile Glu Lys Gly Asp Val Ile Tyr Leu  
245 250 255  
Glu Lys Lys His Ala Cys Ser Ile Ser Lys His Thr Gln His Val Val  
260 265 270  
Arg Val Gly Asp Ser Met His Ser Ile Ser Gln Arg Tyr Gly Ile Arg  
275 280 285  
50 Met Lys Asn Leu Tyr Lys Leu Asn Asp Lys Asp Gly Glu Tyr Ile Pro  
290 295 300  
Gln Glu Gly Asp Ile Leu Arg Leu Arg  
305 310

55 (2) INFORMATION FOR SEQ ID NO:401

(i) SEQUENCE CHARACTERISTICS:  
60 (A) LENGTH: 523 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

65 (vi) ORIGINAL SOURCE:  
(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:  
70 (A) NAME/KEY: misc\_feature  
(B) LOCATION 1...523

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:401

75 Met Asp Gly Arg Arg Tyr Ser Asp Gly Leu His Gln Ala Ile Glu Ala

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1 Lys Glu His Val 5 Lys Val Glu Ala Ala Thr Gln Thr Phe Ala Thr Ile  
 20 25 30  
 5 Thr Leu Gln Asn Tyr Phe Arg Met Tyr His Lys Leu Ala Gly Met Thr  
 35 40 45  
 Gly Thr Ala Glu Thr Glu Ala Gly Glu Leu Trp Asp Ile Tyr Lys Leu  
 50 55 60  
 Asp Val Val Val Ile Pro Thr Asn Lys Pro Ile Ala Arg Lys Asp Met  
 65 70 75 80  
 10 Asn Asp Arg Ile Tyr Lys Thr Ala Arg Glu Lys Tyr Ala Ala Val Ile  
 85 90 95  
 Glu Glu Ile Val Arg Leu Val Glu Glu Gly Arg Pro Val Leu Val Gly  
 100 105 110  
 15 Thr Thr Ser Val Glu Ile Ser Glu Leu Leu Ser Arg Met Leu Arg Leu  
 115 120 125  
 Arg Gly Ile Gln His Asn Val Leu Asn Ala Lys Leu His Gln Lys Glu  
 130 135 140  
 Ala Glu Ile Val Ala Gln Ala Gly Gln Lys Gly Thr Val Thr Ile Ala  
 145 150 155 160  
 20 Thr Asn Met Ala Gly Arg Gly Thr Asp Ile Lys Leu Ser Ala Glu Val  
 165 170 175  
 Lys Lys Ala Gly Gly Leu Ala Ile Ile Gly Thr Glu Arg His Glu Ser  
 180 185 190  
 25 Arg Arg Val Asp Arg Gln Leu Arg Gly Arg Ser Gly Arg Gln Gly Asp  
 195 200 205  
 Pro Gly Ser Ser Ile Phe Tyr Val Ser Leu Glu Asp His Leu Met Arg  
 210 215 220  
 Leu Phe Ala Thr Glu Lys Ile Ala Ser Leu Met Asp Arg Leu Gly Phe  
 225 230 235 240  
 30 Lys Glu Gly Glu Val Leu Glu Asn Asn Met Leu Ser Lys Ser Val Glu  
 245 250 255  
 Arg Ala Gln Lys Lys Val Glu Glu Asn Asn Phe Gly Ile Arg Lys His  
 260 265 270  
 35 Leu Leu Glu Tyr Asp Asp Val Met Asn Ser Gln Arg Glu Val Ile Tyr  
 275 280 285  
 Thr Arg Arg Arg His Ala Leu Met Gly Glu Arg Ile Gly Met Asp Val  
 290 295 300  
 Leu Asn Thr Ile Tyr Asp Val Cys Lys Ala Leu Ile Asp Asn Tyr Ala  
 305 310 315 320  
 40 Glu Ala Asn Asp Phe Glu Gly Phe Lys Glu Asp Leu Met Arg Ala Leu  
 325 330 335  
 Ala Ile Glu Ser Pro Ile Thr Gln Glu Ile Phe Arg Gly Lys Lys Ala  
 340 345 350  
 45 Glu Glu Leu Thr Asp Met Leu Phe Asp Glu Ala Tyr Lys Ser Phe Gln  
 355 360 365  
 Arg Lys Met Asp Leu Ile Ala Glu Val Ala His Pro Val Val His Gln  
 370 375 380  
 Val Phe Glu Thr Gln Ala Ala Val Tyr Glu Arg Ile Leu Ile Pro Ile  
 385 390 395 400  
 50 Thr Asp Gly Lys Arg Val Tyr Asn Ile Gly Cys Asn Leu Arg Glu Ala  
 405 410 415  
 Asp Glu Thr Gln Gly Lys Ser Ile Ile Lys Glu Phe Glu Lys Ala Ile  
 420 425 430  
 55 Val Leu His Thr Ile Asp Glu Ser Trp Lys Glu His Leu Arg Glu Met  
 435 440 445  
 Asp Glu Leu Arg Asn Ser Val Gln Asn Ala Ser Tyr Glu Asn Lys Asp  
 450 455 460  
 Pro Leu Leu Ile Tyr Lys Leu Glu Ser Tyr Glu Leu Phe Arg Lys Met  
 465 470 475 480  
 60 Val Glu Ala Met Asn Arg Lys Thr Val Ala Ile Leu Met Arg Ala Arg  
 485 490 495  
 Ile Pro Val Pro Glu Ala Pro Ser Gln Glu Glu Leu Glu His Arg Arg  
 500 505 510  
 65 Gln Ile Glu Ile Arg His Ala Thr Gln Gln Arg  
 515 520

(2) INFORMATION FOR SEQ ID NO:402

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 375 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

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(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

(A) NAME/KEY: misc\_feature

(B) LOCATION 1...375

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:402

```

Met Asn Phe Leu Lys Lys Glu Pro Phe Lys Ile Phe Ser Met Ile Tyr
1      5      10      15
Leu Leu Leu Asp Thr Ile Thr Asn Arg Ala Gly Thr Glu Arg Ala Val
15     20     25     30
Ile Asn Leu Ala Asn Asn Leu His Ala Asn Gly His Arg Val Ser Leu
35     40     45
Val Ser Val Cys Thr Lys Glu Gly Glu Pro Ser Phe Gln Val Glu Lys
50     55     60
Gly Ile Glu Val His Leu Gly Ile Arg Leu Tyr Gly Asn Ala Leu
65     70     75     80
Ala Arg Lys Thr Val Tyr Phe Lys Ala Tyr Arg Arg Ile Lys Ala Leu
85     90     95
Tyr Lys Lys Arg Glu Pro Val Leu Leu Ile Gly Thr Asn Ile Phe Ile
100    105    110
Asn Thr Ile Leu Ser Gln Ile Ser Asn Arg Gly Arg Ile Phe Thr Ile
115    120    125
Gly Cys Glu His Ile Ser Tyr Asp Ile Ala Arg Pro Ile Thr Lys Arg
130    135    140
Ile Arg Gly Phe Leu Tyr Ser Gly Leu Asp Ala Val Val Ala Leu Thr
145    150    155    160
Lys Arg Asp Gln Gln Ser Phe Glu Ala Ile Leu Arg Gly Arg Ser Lys
165    170    175
Ala Tyr Val Ile Pro Asn Gln Val Ser Phe Thr Thr Val Gln Arg Asp
180    185    190
Ala Thr Thr His Lys Gln Met Leu Ala Ile Gly Arg Leu Thr Tyr Gln
195    200    205
Lys Gly Phe Glu Phe Met Ile Glu Asp Ala Ser Arg Val Leu Arg Glu
210    215    220
Arg Pro Asp Trp Lys Leu Ile Ile Val Gly Asp Gly Glu Asn Glu Ser
225    230    235    240
Met Leu Arg Lys Glu Ile Ala Ser Arg Asn Met Glu Ser Gln Ile Glu
245    250    255
Ile His Pro Ser Thr Pro Glu Ile Arg Lys Tyr Tyr Glu Ser Ser Ala
260    265    270
Ile Tyr Leu Met Thr Ser Arg Phe Glu Gly Leu Pro Met Val Leu Leu
275    280    285
Glu Ala Glu Ala Tyr Ala Leu Pro Ile Ile Ser Tyr Asp Cys Pro Thr
290    295    300
Gly Pro Arg Glu Leu Ile Glu Asn Gly Arg Asn Gly Phe Leu Val Pro
305    310    315    320
Met Glu Ala His Glu Asp Phe Ala Asp Lys Leu Arg Leu Leu Met Asp
325    330    335
Asp Glu Thr Leu Arg Lys Lys Met Gly Gln Glu Ser Glu Leu Met Val
340    345    350
Lys Ser Tyr Ser Pro Ala Asn Ile Tyr Glu Cys Trp Lys Lys Leu Phe
355    360    365
Val Glu Ile Gly Tyr Met Asn
370    375

```

(2) INFORMATION FOR SEQ ID NO:403

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 362 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

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(A) NAME/KEY: misc\_feature  
(B) LOCATION: 1...362

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:403

5 Met Ile Tyr Leu Leu Asp Thr Ile Thr Asn Arg Ala Gly Thr Glu  
1 5 10 15  
Arg Ala Val Ile Asn Leu Ala Asn Asn Leu His Ala Asn Gly His Arg  
20 25 30  
10 Val Ser Leu Val Ser Val Cys Thr Lys Glu Gly Glu Pro Ser Phe Gln  
35 40 45  
Val Glu Lys Gly Ile Glu Val His His Leu Gly Ile Arg Leu Tyr Gly  
50 55 60  
15 Asn Ala Leu Ala Arg Lys Thr Val Tyr Phe Lys Ala Tyr Arg Arg Ile  
65 70 75 80  
Lys Ala Leu Tyr Lys Lys Arg Glu Pro Val Leu Leu Ile Gly Thr Asn  
85 90 95  
Ile Phe Ile Asn Thr Ile Leu Ser Gln Ile Ser Asn Arg Gly Arg Ile  
100 105 110  
20 Phe Thr Ile Gly Cys Glu His Ile Ser Tyr Asp Ile Ala Arg Pro Ile  
115 120 125  
Thr Lys Arg Ile Arg Gly Phe Leu Tyr Ser Gly Leu Asp Ala Val Val  
130 135 140  
25 Ala Leu Thr Lys Arg Asp Gln Gln Ser Phe Glu Ala Ile Leu Arg Gly  
145 150 155 160  
Arg Ser Lys Ala Tyr Val Ile Pro Asn Gln Val Ser Phe Thr Thr Val  
165 170 175  
Gln Arg Asp Ala Thr Thr His Lys Gln Met Leu Ala Ile Gly Arg Leu  
180 185 190  
30 Thr Tyr Gln Lys Gly Phe Glu Phe Met Ile Glu Asp Ala Ser Arg Val  
195 200 205  
Leu Arg Glu Arg Pro Asp Trp Lys Leu Ile Ile Val Gly Asp Gly Glu  
210 215 220  
35 Asn Glu Ser Met Leu Arg Lys Glu Ile Ala Ser Arg Asn Met Glu Ser  
225 230 235 240  
Gln Ile Glu Ile His Pro Ser Thr Pro Glu Ile Arg Lys Tyr Tyr Glu  
245 250 255  
Ser Ser Ala Ile Tyr Leu Met Thr Ser Arg Phe Glu Gly Leu Pro Met  
260 265 270  
40 Val Leu Leu Glu Ala Glu Ala Tyr Ala Leu Pro Ile Ile Ser Tyr Asp  
275 280 285  
Cys Pro Thr Gly Pro Arg Glu Leu Ile Glu Asn Gly Arg Asn Gly Phe  
290 295 300  
45 Leu Val Pro Met Glu Ala His Glu Asp Phe Ala Asp Lys Leu Arg Leu  
305 310 315 320  
Leu Met Asp Asp Glu Thr Leu Arg Lys Lys Met Gly Gln Glu Ser Glu  
325 330 335  
Leu Met Val Lys Ser Tyr Ser Pro Ala Asn Ile Tyr Glu Cys Trp Lys  
340 345 350  
50 Lys Leu Phe Val Glu Ile Gly Tyr Met Asn  
355 360

(2) INFORMATION FOR SEQ ID NO:404

55 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 640 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear  
60 (ii) MOLECULE TYPE: protein  
(iii) HYPOTHETICAL: YES  
(vi) ORIGINAL SOURCE:  
65 (A) ORGANISM: Porphyromonas gingivalis  
(ix) FEATURE:  
(A) NAME/KEY: misc\_feature  
70 (B) LOCATION: 1...640

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:404

Met Gly Lys Ile Ile Gly Ile Asp Leu Gly Thr Thr Asn Ser Cys Val  
1 5 10 15  
75 Ser Val Leu Glu Gly Asn Glu Pro Ile Val Ile Thr Asn Ser Glu Gly

[illegible]

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Pro Ser Asp Asp Lys Asn Val Thr Asp Val Asp Phe Glu Glu Val Lys  
625 630 635 640

## (2) INFORMATION FOR SEQ ID NO:405

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 449 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: Porphyromonas gingivalis

## (ix) FEATURE:

- (A) NAME/KEY: misc feature  
(B) LOCATION 1...449

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:405

Met Arg Tyr Asp Leu Ala Ile Ile Gly Gly Gly Pro Ala Gly Tyr Thr  
1 5 10 15  
Ala Ala Glu Arg Ala Ala Lys Gly Gly Leu Lys Thr Leu Leu Ile Glu  
20 25 30  
Lys Asn Ala Leu Gly Gly Val Cys Leu Asn Glu Gly Cys Ile Pro Thr  
35 40 45  
Lys Thr Leu Leu Tyr Ser Ala Lys Val Leu His Gln Ile Ala Thr Ala  
50 55 60  
Ser Lys Tyr Ala Val Ser Gly Thr Ala Asp Gly Leu Asp Leu Gly Lys  
65 70 75 80  
Val Ile Ala Arg Lys Gly Lys Ile Ile Arg Lys Leu Thr Ala Gly Ile  
85 90 95  
Arg Ser Arg Leu Thr Glu Ala Gly Val Glu Met Val Thr Ala Glu Ala  
100 105 110  
Thr Val Thr Gly Cys Asp Ala Asp Gly Ile Ile Gly Ile Thr Ala Gly  
115 120 125  
Glu Ala Gln Tyr Lys Ala Ala Asn Leu Leu Cys Thr Gly Ser Glu  
130 135 140  
Thr Phe Ile Pro Pro Ile Pro Gly Val Glu Gln Thr Glu Tyr Trp Thr  
145 150 155 160  
Asn Arg Glu Ala Leu Gln Asn Lys Glu Ile Pro Thr Ser Leu Val Ile  
165 170 175  
Ile Gly Gly Gly Val Ile Gly Met Glu Phe Ala Ser Phe Phe Asn Gly  
180 185 190  
Ile Gly Thr Gln Val His Val Val Glu Met Leu Pro Glu Ile Leu Asn  
195 200 205  
Gly Ile Asp Pro Glu His Ala Ala Met Leu Arg Ala His Tyr Glu Lys  
210 215 220  
Glu Gly Ile Lys Phe Tyr Leu Gly His Lys Val Thr Ser Val Arg Asn  
225 230 235 240  
Gly Ala Val Thr Val Glu Tyr Glu Gly Glu Ser Lys Glu Ile Glu Gly  
245 250 255  
Glu Arg Ile Leu Met Ser Val Gly Arg Arg Pro Val Leu Gln Gly Phe  
260 265 270  
Glu Ser Leu Gly Leu Val Leu Ala Gly Lys Gly Val Lys Thr Asn Glu  
275 280 285  
Arg Met Gln Thr Ser Leu Pro Asn Val Tyr Ala Ala Gly Asp Ile Thr  
290 295 300  
Gly Phe Ser Leu Leu Ala His Thr Ala Val Arg Glu Ala Glu Val Ala  
305 310 315 320  
Val Asp Gln Ile Leu Gly Lys Thr Asp Glu Thr Met Ser Tyr Arg Ala  
325 330 335  
Val Pro Gly Val Val Tyr Thr Asn Pro Glu Val Ala Gly Val Gly Glu  
340 345 350  
Thr Glu Glu Ser Leu Arg Lys Ala Gly Arg Ala Tyr Thr Val Arg Arg  
355 360 365  
Leu Pro Met Ala Phe Ser Gly Arg Phe Val Ala Glu Asn Glu Gln Gly  
370 375 380  
Asn Gly Glu Cys Lys Leu Leu Leu Asp Glu Glu Asn Arg Leu Ile Gly  
385 390 395 400  
Ala His Leu Ile Gly Asn Pro Ala Gly Glu Leu Ile Val Thr Ala Ala  
405 410 415



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Met Ala Ile Glu Thr Gly Met Thr Asp Arg Gln Ile Glu Arg Ile Ile  
 420 425 430  
 Phe Pro His Pro Thr Val Gly Glu Ile Leu Lys Glu Thr Leu Ala Gly  
 435 440 445  
 5 Gly

## (2) INFORMATION FOR SEQ ID NO:406

10

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 941 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

15

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

20

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

- (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...941

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:406

Met Glu Leu Lys Arg Phe Leu Ser Leu Gly Leu Leu Leu Val Gly Phe  
 1 5 10 15  
 30 Ile Pro Met Lys Leu Ser Ala Gln Gln Ala Gln Pro Leu Pro Thr Asp  
 20 25 30  
 Pro Ala Val Arg Val Gly Lys Leu Asp Asn Gly Leu Thr Tyr Phe Ile  
 35 35 40 45  
 Arg His Asn Glu Asn Pro Lys Asp Arg Ala Asp Phe Phe Ile Ala Gln  
 50 55 60  
 Lys Val Gly Ser Ile Leu Glu Glu Asp Ser Gln Ser Gly Leu Ala His  
 65 70 75 80  
 Phe Leu Glu His Met Ala Phe Asn Gly Thr Lys Asn Phe Pro Gly Lys  
 85 90 95  
 40 Asn Leu Ile Asn Tyr Leu Glu Thr Ile Gly Val Arg Phe Gly Gln Asn  
 100 105 110  
 Leu Asn Ala Ser Thr Gly Phe Asp Lys Thr Glu Tyr Thr Ile Met Asp  
 115 120 125  
 Val Pro Thr Thr Arg Gln Gly Ile Ile Asp Ser Cys Leu Leu Ile Leu  
 130 135 140  
 45 His Asp Trp Ser Asn Asn Ile Thr Leu Asp Gly His Glu Ile Asp Glu  
 145 150 155 160  
 Glu Arg Gly Val Ile Gln Glu Glu Trp Arg Ala Arg Arg Asp Ala Asn  
 165 170 175  
 50 Leu Arg Met Phe Glu Ala Ile Leu Ala Lys Ala Met Pro Gly Asn Lys  
 180 185 190  
 Tyr Ala Glu Arg Met Pro Ile Gly Leu Met Asp Val Val Leu Asn Phe  
 195 200 205  
 Lys His Asp Glu Leu Arg Asn Tyr Tyr Lys Lys Trp Tyr Arg Pro Asp  
 210 215 220  
 55 Leu Gln Gly Leu Val Ile Val Gly Asp Ile Asp Val Asp Tyr Val Glu  
 225 230 235 240  
 Asn Lys Ile Lys Glu Leu Phe Lys Asp Val Pro Ala Pro Val Asn Pro  
 245 250 255  
 60 Ala Glu Arg Ile Tyr Thr Pro Val Glu Asp Asn Asp Glu Pro Ile Val  
 260 265 270  
 Ala Ile Ala Thr Asp Ala Glu Ala Thr Thr Thr Gln Leu Ser Ile Ser  
 275 280 285  
 65 Phe Lys Ser Asp Pro Thr Pro Gln Glu Val Arg Gly Ser Ile Phe Gly  
 290 295 300  
 Leu Val Glu Asp Tyr Met Lys Gln Val Ile Thr Thr Ala Val Asn Glu  
 305 310 315 320  
 Arg Leu Ser Glu Ile Thr His Lys Pro Asn Ala Pro Phe Leu Ser Ala  
 325 330 335  
 70 Gly Ala Phe Phe Ser Asn Phe Met Tyr Ile Thr Gln Thr Lys Asp Ala  
 340 345 350  
 Phe Asn Phe Val Ala Thr Val Arg Glu Gly Glu Ala Glu Lys Ala Met  
 355 360 365  
 75 Asn Ala Leu Val Ala Glu Ile Glu Ser Leu Arg Gln Phe Gly Ile Thr  
 370 375 380

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	Lys	Gly	Glu	Tyr	Asp	Arg	Ala	Arg	Thr	Asn	Val	Leu	Lys	Arg	Tyr	Glu
	385					390					395					400
	Asn	Gln	Tyr	Asn	Glu	Arg	Asp	Lys	Arg	Lys	Asn	Asn	Ala	Tyr	Ala	Asn
					405					410						415
5	Glu	Tyr	Ser	Thr	Tyr	Phe	Thr	Asp	Gly	Gly	Tyr	Ile	Pro	Gly	Ile	Glu
					420				425					430		
	Val	Glu	Tyr	Gln	Thr	Val	Asn	Ala	Phe	Ala	Pro	Gln	Val	Pro	Leu	Glu
					435			440					445			
10	Ala	Phe	Asn	Gln	Ala	Ile	Ala	Gln	Met	Ile	Asp	Pro	Val	Lys	Asn	Ala
		450					455					460				
	Val	Val	Thr	Leu	Thr	Gly	Pro	Ser	Lys	Ala	Glu	Ala	Lys	Ile	Pro	Ser
	465				470						475					480
	Glu	Ala	Asp	Phe	Leu	Ala	Ala	Phe	Lys	Ala	Ala	Arg	Gln	Gln	Lys	Val
					485				490						495	
15	Glu	Ala	Lys	Lys	Asp	Glu	Val	Ser	Asp	Gln	Lys	Leu	Met	Glu	Lys	Ala
					500				505					510		
	Pro	Lys	Ala	Gly	Lys	Ile	Val	Ser	Glu	Lys	Lys	Asp	Gln	Lys	Phe	Gly
			515				520						525			
20	Thr	Thr	Glu	Leu	Thr	Leu	Ser	Asn	Gly	Ile	Lys	Val	Tyr	Leu	Lys	Lys
		530					535						540			
	Thr	Asp	Phe	Lys	Ser	Asn	Glu	Ile	Leu	Met	Ser	Ala	Leu	Ser	Pro	Gly
		545				550					555					560
	Gly	Ile	Leu	Ser	Gly	Lys	His	Ala	Pro	Asn	Gln	Ser	Val	Met	Asn	Ser
					565					570					575	
25	Phe	Met	Asn	Val	Gly	Gly	Leu	Gly	Asn	Phe	Asp	Ala	Ile	Gln	Leu	Asp
					580				585					590		
	Lys	Val	Leu	Thr	Gly	Arg	Ser	Ala	Ser	Val	Ser	Pro	Ser	Leu	Ser	Leu
			595					600					605			
30	Leu	Ser	Glu	Gly	Leu	Ser	Gly	Lys	Thr	Thr	Val	Glu	Asp	Met	Glu	Thr
		610					615					620				
	Phe	Phe	Gln	Leu	Ile	Tyr	Leu	Gln	Met	Thr	Ala	Asn	Arg	Lys	Asp	Pro
		625				630					635					640
	Glu	Ala	Phe	Lys	Ala	Thr	Gln	Glu	Lys	Leu	Tyr	Asn	Asn	Leu	Lys	Asn
					645					650					655	
35	Gln	Glu	Ala	Asn	Pro	Met	Ala	Ala	Leu	Met	Asp	Ser	Ile	Arg	His	Thr
				660					665					670		
	Met	Tyr	Gly	Asp	Asn	Pro	Met	Met	Lys	Pro	Met	Lys	Ala	Ala	Asp	Val
			675					680					685			
40	Glu	Lys	Val	Asn	Tyr	Asp	Gln	Val	Met	Ala	Phe	Tyr	Asn	Glu	Arg	Phe
		690					695					700				
	Ala	Asp	Ala	Gly	Asp	Phe	Met	Phe	Phe	Phe	Ile	Gly	Asn	Leu	Asp	Glu
		705				710					715					720
	Ala	Lys	Met	Lys	Pro	Leu	Ile	Glu	Thr	Tyr	Leu	Ala	Ser	Leu	Pro	Asn
					725					730					735	
45	Leu	Lys	Arg	Gly	Asp	Lys	Met	Asn	Lys	Ala	Gln	Val	Pro	Ala	Ala	Arg
				740					745					750		
	Ser	Gly	Lys	Ile	Asp	Cys	Lys	Phe	Glu	Lys	Glu	Met	Asp	Thr	Pro	Ser
		755					760					765				
50	Thr	Thr	Ile	Phe	Asp	Val	Val	Ser	Gly	Asn	Val	Glu	Tyr	Thr	Leu	Lys
		770					775					780				
	Asn	Ser	Leu	Leu	Leu	Glu	Val	Phe	Ser	Ala	Val	Met	Asp	Gln	Val	Tyr
		785				790					795					800
	Thr	Ala	Thr	Val	Arg	Glu	Lys	Glu	Gly	Gly	Ala	Tyr	Ser	Val	Ala	Ala
					805					810					815	
55	Phe	Gly	Gly	Leu	Glu	Gln	Tyr	Pro	Gln	Pro	Lys	Ala	Leu	Met	Gln	Ile
					820				825					830		
	Tyr	Phe	Pro	Thr	Asp	Pro	Ala	Arg	Ala	Glu	Glu	Met	Asn	Ala	Ile	Val
			835					840					845			
60	Phe	Ala	Glu	Leu	Glu	Lys	Leu	Ala	Lys	Glu	Gly	Pro	Asn	Val	Glu	Tyr
		850					855					860				
	Phe	Lys	Lys	Thr	Ile	Glu	Asn	Leu	Asn	Lys	Gln	His	Lys	Glu	Ser	Leu
		865				870					875					880
	Arg	Glu	Asn	Arg	Phe	Trp	Leu	Glu	Ala	Met	Lys	Ala	Ser	Phe	Phe	Glu
					885					890					895	
65	Gly	Asn	Asp	Phe	Ile	Thr	Asp	Tyr	Glu	Ser	Val	Leu	Asn	Gly	Leu	Thr
					900				905					910		
	Pro	Ala	Glu	Leu	Gln	Lys	Phe	Ala	Ala	Asp	Leu	Leu	Lys	Gln	Gln	Asn
					915				920				925			
70	Arg	Val	Val	Val	Met	Met	Ala	Pro	Val	Ala	Lys	Ala	Gln			
		930					935					940				

(2) INFORMATION FOR SEQ ID NO:407

(1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 684 amino acids

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(E) TYPE: amino acid  
(D) TOPOLOGY: linear

5 (ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

10 (A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

(A) NAME/KEY: misc\_feature

(B) LOCATION 1...684

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:407

	Met	Ser	Lys	Lys	Gly	Thr	Ile	Gly	Val	Thr	Ser	Asp	Asn	Ile	Phe	Pro
	1			5						10					15	
20	Val	Ile	Lys	Lys	Phe	Leu	Tyr	Ser	Asp	His	Glu	Ile	Phe	Leu	Arg	Glu
			20						25					30		
	Ile	Val	Ser	Asn	Ala	Val	Asp	Ala	Thr	Gln	Lys	Leu	Lys	Thr	Leu	Thr
			35					40					45			
	Ser	Val	Gly	Glu	Phe	Lys	Gly	Glu	Thr	Gly	Asp	Leu	Arg	Val	Thr	Val
		50				55					60					
25	Ser	Val	Asp	Glu	Val	Ala	Arg	Thr	Ile	Thr	Val	Ser	Asp	Arg	Gly	Val
	65				70					75					80	
	Gly	Met	Thr	Glu	Glu	Glu	Val	Glu	Lys	Tyr	Ile	Asn	Gln	Ile	Ala	Phe
				85					90					95		
	Ser	Ser	Ala	Glu	Glu	Phe	Leu	Glu	Lys	Tyr	Lys	Asp	Asp	Lys	Ala	Ala
			100					105						110		
30	Ile	Ile	Gly	His	Phe	Gly	Leu	Gly	Phe	Tyr	Ser	Ala	Phe	Met	Val	Ser
			115				120						125			
	Glu	Arg	Val	Asp	Val	Ile	Thr	Arg	Ser	Phe	Arg	Glu	Asp	Ala	Thr	Ala
		130				135						140				
35	Val	Lys	Trp	Ser	Cys	Asp	Gly	Ser	Pro	Glu	Tyr	Thr	Leu	Glu	Pro	Ala
	145				150					155					160	
	Asp	Lys	Ala	Asp	Arg	Gly	Thr	Asp	Ile	Val	Met	His	Ile	Asp	Glu	Glu
				165						170				175		
40	Asn	Ser	Glu	Phe	Leu	Lys	Lys	Glu	Lys	Ile	Glu	Gly	Leu	Leu	Gly	Lys
			180					185					190			
	Tyr	Cys	Lys	Phe	Leu	Thr	Val	Pro	Ile	Ile	Phe	Gly	Lys	Lys	Gln	Glu
		195				200						205				
	Trp	Lys	Asp	Gly	Lys	Met	Gln	Asp	Thr	Asp	Glu	Asp	Asn	Gln	Ile	Asn
		210			215							220				
45	Asp	Thr	His	Pro	Ala	Trp	Thr	Lys	Lys	Pro	Ala	Asp	Leu	Lys	Asp	Glu
	225				230					235					240	
	Asp	Tyr	Lys	Glu	Phe	Tyr	Arg	Ser	Leu	Tyr	Pro	Met	Ser	Glu	Glu	Pro
			245							250				255		
50	Leu	Phe	Trp	Ile	His	Leu	Asn	Val	Asp	Tyr	Pro	Phe	Asn	Leu	Thr	Gly
		260						265						270		
	Ile	Leu	Tyr	Phe	Pro	Lys	Ile	Lys	Asn	Asn	Leu	Asp	Leu	Gln	Arg	Asn
		275					280						285			
	Lys	Ile	Gln	Leu	Tyr	Cys	Asn	Gln	Val	Tyr	Val	Thr	Asp	Glu	Val	Gln
		290				295						300				
55	Gly	Ile	Val	Pro	Asp	Phe	Leu	Thr	Leu	Leu	His	Gly	Val	Ile	Asp	Ser
	305					310				315					320	
	Pro	Asp	Ile	Pro	Leu	Asn	Val	Ser	Arg	Ser	Tyr	Leu	Gln	Ser	Asp	Ala
			325						330					335		
60	Asn	Val	Lys	Lys	Ile	Ser	Ser	His	Ile	Thr	Lys	Lys	Val	Ala	Asp	Arg
		340							345					350		
	Leu	Glu	Glu	Ile	Phe	Lys	Asn	Asp	Arg	Pro	Thr	Phe	Glu	Glu	Lys	Trp
		355					360					365				
	Asp	Ser	Leu	Lys	Leu	Phe	Val	Glu	Tyr	Gly	Met	Leu	Thr	Asp	Glu	Lys
		370				375					380					
65	Phe	Tyr	Glu	Arg	Ala	Ala	Lys	Phe	Phe	Leu	Phe	Thr	Asp	Met	Asp	Gly
	385				390					395					400	
	His	Lys	Tyr	Thr	Phe	Asp	Glu	Tyr	Arg	Thr	Leu	Val	Glu	Gly	Val	Gln
				405						410				415		
70	Thr	Asp	Lys	Asp	Gly	Gln	Val	Val	Tyr	Leu	Tyr	Ala	Thr	Asp	Lys	His
		420							425				430			
	Gly	Gln	Tyr	Ser	His	Val	Lys	Arg	Ala	Ser	Asp	Lys	Gly	Tyr	Ser	Val
		435					440					445				
	Met	Leu	Leu	Asp	Gly	Gln	Leu	Asp	Pro	His	Ile	Val	Ser	Leu	Leu	Glu
		450				455						460				
75	Gln	Lys	Leu	Glu	Lys	Thr	His	Phe	Val	Arg	Val	Asp	Ser	Asp	Thr	Ile

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465  
 Asn Asn Leu Ile Arg Lys Glu Glu Arg Ala Glu Val Lys Leu Ser Asp  
 485 490 495  
 Thr Glu Arg Ala Thr Leu Val Lys Leu Phe Glu Ala Arg Leu Pro Arg  
 500 505 510  
 Asp Glu Lys Lys His Phe Asn Val Ala Phe Glu Ser Leu Gly Ala Glu  
 515 520 525  
 Gly Glu Ala Ile Leu Ile Thr Gln Ala Glu Phe Met Arg Arg Met Arg  
 530 535 540  
 Asp Met Ala Gln Leu Gln Pro Gly Met Ser Phe Tyr Gly Glu Leu Pro  
 545 550 555 560  
 Asp Ser Tyr Asn Leu Val Leu Asn Thr Asp His Pro Leu Ile Asp Arg  
 565 570 575  
 Val Leu Ser Gly Glu Lys Glu Ser Val Glu Pro Ser Leu Thr Glu Leu  
 580 585 590  
 Arg Ala Lys Ile Ala Glu Leu Lys Ala Glu Glu Ala Lys Leu Leu Asp  
 595 600 605  
 Glu Glu Lys Gly Lys Lys Pro Glu Glu Ile Pro Val Ala Thr Lys Glu  
 610 615 620  
 Ala Lys Glu Asn Asn Ala Val Glu Gln Ala Lys Thr Glu Gly Ser Ile  
 625 630 635 640  
 Asn Asp Gln Leu Thr Lys Tyr Ala Gln Asp Asn Glu Leu Ile Gly Gln  
 645 650 655  
 Leu Ile Asp Leu Ala Leu Leu Gly Ser Gly Leu Leu Thr Gly Glu Ala  
 660 665 670  
 Leu Ala Glu Phe Ile Arg Arg Ser Gln Arg Leu Leu  
 675 680

- (2) INFORMATION FOR SEQ ID NO:408
- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 464 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Porphyromonas gingivalis
- (ix) FEATURE:  
 (A) NAME/KEY: misc feature  
 (E) LOCATION 1...464
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:408

Met Glu Lys Leu Ile Asp Ile Leu Val Val Asp Asp Asp Val Ala Val  
 1 5 10 15  
 Cys Ala Ala Leu Arg Leu Val Leu Lys Arg Ala Gly Tyr Asn Pro Val  
 20 25 30  
 Ile Ala Asn Ser Pro Asp Glu Ala Leu Ser Ile Met Arg Asn Pro Asp  
 35 40 45  
 Gly Gly Cys Lys Pro Ala Val Ile Leu Met Asp Met Asn Phe Ser Leu  
 50 55 60  
 Ser Thr Ser Gly Arg Glu Gly Leu Glu Leu Leu Glu Lys Met Gln Ile  
 65 70 75 80  
 Phe Thr Ser Cys Pro Val Ile Leu Met Thr Ala Trp Ala Ser Ile Pro  
 85 90 95  
 Leu Ala Val Glu Gly Met Arg Leu Gly Ala Phe Asp Phe Ile Gly Lys  
 100 105 110  
 Pro Trp Asp Asn Asp Arg Leu Leu Arg Thr Ile Asp Thr Ala Leu His  
 115 120 125  
 Leu Ala Ala Pro Ser Ala Val Ala Asn Pro Ser Glu Gln Ser Asp Arg  
 130 135 140  
 Asp Thr Ala Arg Gln Pro Lys Ala Thr Val Gln Glu Asn Asp Pro Cys  
 145 150 155 160  
 Ala His Ile Ile Gly Arg Ser Asp Ala Ile Cys Lys Ile Lys Glu Arg  
 165 170 175  
 Ile Arg Arg Ile Ala Pro Thr His Ala Ser Val Leu Ile Thr Gly Glu  
 180 185 190  
 Ser Gly Thr Gly Lys Glu Leu Ile Ala Glu Ala Leu His Arg Gly Ser  
 195 200 205  
 Lys Arg Ala Ser Ala Pro Phe Val Lys Val Asn Leu Gly Gly Ile Pro

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210 215 220  
 Glu Ser Leu Phe Glu Ser Glu Leu Phe Gly His Lys Lys Gly Ala Phe  
 225 230 235 240  
 Thr Asn Ala Phe Ser Asp Arg Lys Gly Arg Phe Glu Leu Ala Asp Gly  
 245 250 255  
 Gly Thr Ile Phe Leu Asp Glu Ile Gly Glu Leu Pro Val Gly Asn Gln  
 260 265 270  
 Val Lys Leu Leu Arg Val Leu Gln Glu Thr Phe Glu Pro Leu Gly  
 275 280 285  
 Glu Ser Val Ser His Arg Val Asp Ile Arg Val Val Ser Ala Thr Asn  
 290 295 300  
 Ala Ser Leu Glu Arg Met Val Ala Glu Gly Arg Phe Arg Glu Asp Leu  
 305 310 315 320  
 Tyr Tyr Arg Ile Asn Leu Ile His Leu His Leu Pro Pro Leu Arg Glu  
 325 330 335  
 Arg Gln Glu Asp Ile Gln Leu Leu Val Glu Ala Phe Ser Glu Ala Phe  
 340 345 350  
 Ala Gln Ser Asn Gly Leu Pro His Ala Val Trp Ser Ala Glu Ala Met  
 355 360 365  
 Arg Arg Ile Cys Ala Met Pro Leu Pro Gly Asn Val Arg Glu Leu Lys  
 370 375 380  
 Asn Val Val Glu Arg Thr Leu Leu Leu Ser Gly Ser Arg Glu Ile Ser  
 385 390 395 400  
 Ala Arg Asp Val Ala Asp Phe Gly Ser Gln Val Thr Ala Ala Asp His  
 405 410 415  
 Ser Asp Glu Arg Ala Leu Thr Asp Met Glu Glu Ala Ala Ile Arg Glu  
 420 425 430  
 Thr Leu Thr Lys Tyr Asn Gly Asn Val Ser Arg Ala Ala Arg Ala Leu  
 435 440 445  
 Gly Leu Ser Arg Ala Ala Leu Tyr Arg Arg Met Glu Lys Tyr Gly Leu  
 450 455 460

(2) INFORMATION FOR SEQ ID NO:409

- 35 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 250 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
 40 (ii) MOLECULE TYPE: protein  
 (iii) HYPOTHETICAL: YES  
 45 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Porphyromonas gingivalis  
 (ix) FEATURE:  
 (A) NAME/KEY: misc feature  
 (B) LOCATION 1...250  
 50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:409

Met Leu Lys Ile Lys Asn Leu His Ala Thr Val Gln Gly Lys Glu Ile  
 1 5 10 15  
 55 Leu Lys Gly Ile Asn Leu Glu Ile Asn Ala Gly Glu Ile His Ala Ile  
 20 25 30  
 Met Gly Pro Asn Gly Ser Gly Lys Ser Thr Leu Ser Ser Val Leu Val  
 35 40 45  
 60 Gly His Pro Ser Phe Glu Val Thr Glu Gly Glu Val Thr Phe Asn Gly  
 50 55 60  
 Ile Asp Leu Leu Glu Leu Glu Pro Glu Glu Arg Ala His Leu Gly Leu  
 65 70 75 80  
 Phe Leu Ser Phe Gln Tyr Pro Val Glu Ile Pro Gly Val Ser Met Val  
 85 90 95  
 65 Asn Phe Met Arg Ala Ala Val Asn Glu His Arg Lys Ala Ile Gly Ala  
 100 105 110  
 Glu Pro Val Ser Ala Ser Asp Phe Leu Lys Met Met Arg Glu Lys Arg  
 115 120 125  
 70 Ala Ile Val Glu Leu Asp Asn Lys Leu Ala Ser Arg Ser Val Asn Glu  
 130 135 140  
 Gly Phe Ser Gly Gly Glu Lys Lys Arg Asn Glu Ile Phe Gln Met Ala  
 145 150 155 160  
 Met Leu Glu Pro Lys Leu Ala Ile Leu Asp Glu Thr Asp Ser Gly Leu  
 165 170 175  
 75 Asp Ile Asp Ala Leu Arg Ile Val Ala Gly Gly Val Asn Arg Leu Arg

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180 185 190  
 Ser Pro Glu Asn Ala Ala Ile Val Ile Thr His Tyr Gln Arg Leu Leu  
 195 200 205  
 Glu Tyr Ile Lys Pro Asp Phe Val His Val Leu Tyr Lys Gly Arg Ile  
 210 215 220  
 Val Lys Ser Gly Gly Ala Glu Leu Ala Leu Thr Leu Glu Glu Lys Gly  
 225 230 235 240  
 Tyr Asp Trp Ile Lys Glu Glu Ile Gly Glu  
 245 250

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 10  
 (2) INFORMATION FOR SEQ ID NO:410  
 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 461 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
 (ii) MOLECULE TYPE: protein  
 (iii) HYPOTHETICAL: YES  
 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Porphyromonas gingivalis  
 (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...461  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:410

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Met Ala Lys Glu Lys Thr Ile Tyr Val Cys Arg Ser Cys Gly Thr Lys  
 1 5 10 15  
 Tyr Ala Lys Trp Gln Gly Asn Cys Asn Ala Cys Gly Glu Trp Asn Cys  
 20 25 30  
 Ile Asp Glu Glu Lys Val Pro Ala Pro Ala Ser Gly Lys His Ala Ala  
 35 40 45  
 Lys Ser Phe Met Pro Arg Glu Gln Asp Asn Arg Pro Arg Leu Leu Gln  
 50 55 60  
 Asp Val Glu Ser Gly Asp Glu Glu Arg Ile Arg Leu Gly Asp Glu Glu  
 65 70 75 80  
 Phe Asp Arg Val Leu Gly Gly Gly Ile Val Lys Gly Ala Phe Val Leu  
 85 90 95  
 Leu Gly Gly Glu Pro Gly Ile Gly Lys Ser Thr Leu Ile Leu Gln Thr  
 100 105 110  
 Val Leu Arg Leu Pro Gln Leu Arg Thr Leu Tyr Val Ser Gly Glu Glu  
 115 120 125  
 Ser Ala Arg Gln Leu Lys Met Arg Ala Glu Arg Leu Gly Gln Ala Met  
 130 135 140  
 Asn Gly Cys Tyr Val Tyr Cys Glu Thr Asn Ile Glu Arg Ile Leu Ser  
 145 150 155 160  
 Arg Ala Glu Glu Leu Thr Pro Asp Leu Leu Val Ile Asp Ser Ile Gln  
 165 170 175  
 Thr Val Tyr Thr Glu Glu Met Glu Ser Ser Ala Gly Ser Val Gly Gln  
 180 185 190  
 Ile Arg Glu Cys Ala Ala Leu Leu Lys Tyr Cys Lys Thr Thr Gly  
 195 200 205  
 Ile Pro Val Ile Val Ile Gly His Ile Thr Lys Glu Gly Ser Ile Ala  
 210 215 220  
 Gly Pro Lys Val Leu Glu His Ile Val Asp Thr Val Leu Leu Phe Asp  
 225 230 235 240  
 Gly Asp Lys His His Leu Tyr Arg Ile Leu Arg Gly Gln Lys Asn Arg  
 245 250 255  
 Tyr Gly Ser Thr Ser Glu Leu Gly Ile Tyr Glu Met Arg Gln Asp Gly  
 260 265 270  
 Leu Arg Gly Val Glu Asn Pro Ser Glu His Leu Ile Thr Arg Asn Arg  
 275 280 285  
 Glu Asp Leu Ser Gly Ile Ala Ile Ala Val Ala Met Glu Gly Ile Arg  
 290 295 300  
 Pro Ile Leu Ile Glu Ala Gln Ala Leu Val Ser Ser Ala Ile Tyr Ala  
 305 310 315 320  
 Asn Pro Gln Arg Ser Ala Thr Gly Phe Asp Ile Arg Arg Met Asn Met  
 325 330 335  
 Leu Leu Ala Val Leu Glu Lys Arg Ala Gly Phe Lys Leu Ile Gln Lys  
 340 345 350  
 Asp Val Phe Leu Asn Ile Ala Gly Gly Ile Lys Ile Ala Asp Pro Ala

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5                   355                   360                   365  
 Thr Asp Leu Ala Val Ile Ser Ala Val Leu Ala Ser Ser Leu Asp Ile  
 370                   375                   380  
 Val Ile Pro Pro Ala Val Cys Met Thr Gly Glu Val Gly Leu Ser Gly  
 385                   390                   395                   400  
 Glu Ile Arg Pro Val Ser Arg Ile Glu Gln Arg Ile Thr Glu Ala Arg  
 405                   410                   415  
 Arg Ile Gly Phe Lys Glu Ile Leu Val Pro Ala Asp Asn Phe Arg Gln  
 420                   425                   430  
 10 Glu Asp Ala Gly Arg Phe Gly Ile Arg Leu Val Pro Val Arg Lys Val  
 435                   440                   445  
 Glu Glu Ala Phe Arg His Leu Phe Ser Lys Gly Arg Glu  
 450                   455                   460

15 (2) INFORMATION FOR SEQ ID NO:411

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 271 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...271

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:411

35 Met Asn Ser Arg His Leu Thr Ile Thr Ile Ile Ala Gly Leu Ser Leu  
 1                   5                   10                   15  
 Phe Val Leu Thr Leu Gly Gly Cys Ser Val Ala Gln Gln Asp Thr Gln  
 20                   25                   30  
 40 Trp Thr Leu Gly Gly Lys Leu Phe Thr Ser Ala Trp Ile Gln Arg Ser  
 35                   40                   45  
 Ala Glu Tyr Gln Ala Leu Cys Ile Gln Ala Tyr Asn Ile Ala Thr Glu  
 50                   55                   60  
 Arg Val Asp Ala Leu Pro Ala Glu Arg Lys Gln Gly Asp Arg Pro Tyr  
 65                   70                   75                   80  
 45 Ala Ile Val Thr Asp Ile Asp Glu Thr Ile Leu Asp Asn Thr Pro Asn  
 85                   90                   95  
 Ser Val Tyr Gln Ala Leu Arg Gly Lys Asp Tyr Asp Glu Glu Thr Trp  
 100                   105                   110  
 50 Gly Lys Trp Cys Ala Gln Ala Asp Ala Asp Thr Leu Ala Gly Ala Leu  
 115                   120                   125  
 Ser Phe Phe Leu His Ala Ala Asn Lys Gly Ile Glu Val Phe Tyr Val  
 130                   135                   140  
 Thr Asn Arg Arg Asp Asn Leu Arg Glu Ala Thr Leu Gln Asn Leu Gln  
 145                   150                   155                   160  
 55 Arg Tyr Gly Phe Pro Phe Ala Asp Glu Glu His Leu Leu Thr Thr His  
 165                   170                   175  
 Gly Pro Ser Asp Lys Glu Pro Arg Arg Leu Lys Ile Gln Glu Gln Tyr  
 180                   185                   190  
 60 Glu Ile Val Leu Leu Ile Gly Asp Asn Leu Gly Asp Phe His His Phe  
 195                   200                   205  
 Phe Asn Thr Lys Glu Glu Ser Gly Arg Lys Gln Ala Leu Gly Leu Thr  
 210                   215                   220  
 Ala Gly Glu Phe Gly Arg His Phe Ile Met Leu Pro Asn Pro Asn Tyr  
 225                   230                   235                   240  
 65 Gly Ser Trp Glu Pro Ala Trp Tyr Gly Gly Lys Tyr Pro Pro Leu Pro  
 245                   250                   255  
 Glu Arg Asp Lys Ala Leu Lys Gln Leu His Ser Gln Asn Ser Arg  
 260                   265                   270

70 (2) INFORMATION FOR SEQ ID NO:412

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 417 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

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(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

5 (vi) ORIGINAL SOURCE:  
(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:  
10 (A) NAME/KEY: misc\_feature  
(B) LOCATION 1...417

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:412

15 Met Ser Thr Asn Ile Asp Val Gln Gln Ile Lys Gln Arg Phe Gly Ile  
1 5 10 15  
Ile Gly Ser Ser Pro Leu Met Glu His Ala Ile Arg Val Ala Ala Gln  
20 25 30  
Val Ala Pro Thr Asp Met Ser Val Leu Val Thr Gly Glu Ser Gly Ser  
20 35 40 45  
Gly Lys Glu Phe Phe Pro Gln Ile Ile His Tyr Tyr Ser Ala Arg Lys  
50 55 60  
His His Ser Tyr Ile Ala Val Asn Cys Gly Ala Ile Pro Glu Gly Thr  
65 70 75 80  
25 Ile Asp Ser Glu Leu Phe Gly His Arg Lys Gly Ser Phe Thr Gly Ala  
85 90 95  
Val Ser Asp Arg Lys Gly Tyr Phe Glu Glu Ala Ser Gly Gly Thr Ile  
100 105 110  
30 Phe Leu Asp Glu Val Gly Glu Leu Pro Leu Pro Thr Gln Ala Arg Leu  
115 120 125  
Leu Arg Val Leu Glu Thr Gly Glu Phe Ile Pro Val Gly Ala Ser Gln  
130 135 140  
Ser Gln Lys Thr Asp Val Arg Ile Val Ala Ala Thr Asn Val Asn Leu  
145 150 155 160  
35 Lys Glu Ala Val Ala Asn Gly Lys Phe Arg Glu Asp Leu Phe Phe Arg  
165 170 175  
Leu Asn Thr Val Pro Ile Glu Val Pro Ala Leu Arg Met Arg Pro Asp  
180 185 190  
40 Asp Val Pro Leu Leu Phe Arg Arg Phe Ala Ala Asp Ser Ala Glu Lys  
195 200 205  
Tyr Arg Met Pro Pro Leu Arg Leu Ser Asp Glu Ala Arg Thr Ile Leu  
210 215 220  
Met Arg Tyr Arg Trp Pro Gly Asn Val Arg Glu Leu Arg Asn Ile Thr  
225 230 235 240  
45 Asp Arg Leu Ser Ile Leu Glu Glu Glu Arg Thr Val Ser Ala Glu Thr  
245 250 255  
Ile Thr Arg Tyr Leu Asp Ala Glu Gly Met Gln Asp Leu His Pro Val  
260 265 270  
50 Val Ile Arg Arg Asn Glu Thr Thr Glu Ala Asp Lys Gln Ile Pro His  
275 280 285  
Tyr Glu Arg Glu Ile Ile Tyr Gln Val Leu Tyr Asp Met Lys Lys Glu  
290 295 300  
Ile Ala Asp Leu Lys Gly Met Met Asn Arg Leu Ala His His Glu Gln  
305 310 315 320  
55 Pro Ser Trp Pro Val Gly Ser Asp Val Trp Gly Asn Asp Asp Lys Arg  
325 330 335  
Thr Ala Asp Pro Lys Trp Gly Val Ser Thr His Lys Ala Pro Ile Ala  
340 345 350  
Asn Ala Ala Glu Pro Val Glu Pro Ile Gln Glu Ala Ser Glu Tyr Thr  
355 360 365  
60 Glu Asp Pro Val Ser Leu Glu Glu Val Glu Lys Lys Met Ile Ser Leu  
370 375 380  
Ala Leu Glu Arg His Gly Gly Arg Arg Lys Gln Thr Ala Glu Glu Leu  
385 390 395 400  
65 Lys Ile Ser Glu Arg Thr Leu Tyr Arg Lys Ile Lys Glu Tyr Gly Leu  
405 410 415  
Glu

70 (2) INFORMATION FOR SEQ ID NO:413

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 602 amino acids  
(B) TYPE: amino acid  
75 (D) TOPOLOGY: linear



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(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:  
(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:  
(A) NAME/KEY: misc\_feature  
(B) LOCATION 1...602

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:413

15	Met	Ile	Leu	Leu	Phe	Gly	Gly	Thr	Thr	Glu	Gly	Arg	Ala	Ala	Ala	Arg
	1				5					10				15		
	Val	Leu	Asp	Glu	Ala	Gly	Ser	Pro	Phe	Phe	Tyr	Ser	Thr	Lys	Gly	Asn
			20					25						30		
20	Leu	Gln	Glu	Ile	Gln	Ser	Ser	His	Gly	His	Arg	Leu	Thr	Gly	Ala	Met
		35						40					45			
	Thr	Val	Ala	Asp	Met	Val	Ser	Phe	Cys	Arg	Lys	Glu	Glu	Ile	Arg	Leu
		50					55					60				
	Ile	Val	Asp	Ala	Ala	His	Pro	Phe	Ala	Glu	Glu	Leu	His	Ala	Ser	Val
		65				70				75				80		
25	Ala	Glu	Ala	Ser	Glu	Gln	Thr	Gly	Ile	Pro	Val	Val	Arg	Tyr	Glu	Arg
				85					90					95		
	Gln	Tyr	Pro	Pro	Arg	Glu	Glu	Gly	Ile	Val	Trp	Cys	Ala	Asn	Tyr	Asp
			100					105						110		
30	Thr	Ala	Ala	Glu	Arg	Met	Leu	Gly	Asp	Gly	Val	Gln	Arg	Leu	Leu	Met
		115					120					125				
	Leu	Thr	Gly	Val	Asn	Thr	Ile	Pro	Lys	Leu	Ala	Ala	Phe	Trp	Lys	Glu
		130				135						140				
	Arg	Thr	Thr	Phe	Cys	Arg	Ile	Leu	Lys	Arg	Asp	Glu	Ser	Val	Ala	Leu
		145				150				155					160	
35	Ala	Glu	Lys	Asn	Gly	Phe	Pro	Ala	Glu	Arg	Ile	Val	Phe	Phe	Glu	Pro
				165					170						175	
	His	Ala	Asp	Glu	Glu	Leu	Met	Gln	Ala	Val	Arg	Pro	Asp	Ala	Ile	Ile
		180						185						190		
40	Thr	Lys	Glu	Ser	Gly	Glu	Ser	Gly	Tyr	Phe	Arg	Glu	Lys	Ile	Glu	Ala
		195						200					205			
	Ala	Arg	Arg	Met	Gly	Ile	Arg	Ile	Tyr	Ala	Val	Val	Arg	Pro	Pro	Leu
		210				215						220				
	Pro	Pro	Ser	Phe	Ile	Pro	Val	Gly	Gly	Pro	Val	Gly	Leu	Arg	Arg	Ala
		225				230						235			240	
45	Val	Glu	Arg	Leu	Val	Pro	Gly	Phe	Phe	Ser	Leu	Arg	Ser	Gly	Phe	Thr
				245						250				255		
	Thr	Gly	Thr	Thr	Ala	Thr	Ala	Ala	Val	Val	Ala	Ala	Met	Tyr	Arg	Leu
		260						265					270			
50	Met	Gly	Leu	Gly	Ser	Leu	Ala	Glu	Ala	Pro	Val	Glu	Leu	Pro	Ser	Gly
		275						280					285			
	Glu	Ile	Val	Ser	Leu	Pro	Ile	Ala	Glu	Ile	Arg	Glu	Glu	Glu	Asp	Ala
		290					295					300				
	Val	Val	Ser	Ala	Val	Leu	Lys	Asp	Ala	Gly	Asp	Asp	Pro	Asp	Val	Thr
		305				310					315				320	
55	Asn	Gly	Met	Ala	Val	Cys	Ala	Thr	Ile	Arg	Leu	Asn	Pro	Glu	His	Glu
				325					330					335		
	Glu	Val	Arg	Phe	Leu	Gln	Gly	Glu	Gly	Val	Gly	Val	Val	Thr	Leu	Pro
		340							345					350		
60	Gly	Leu	Gly	Leu	Glu	Val	Gly	Gly	Pro	Ala	Ile	Asn	Leu	Val	Pro	Arg
		355					360						365			
	Arg	Met	Met	Thr	Ala	Glu	Val	Arg	Arg	Leu	Tyr	Ala	Gln	Gly	Gly	Val
		370					375						380			
	Asp	Ile	Thr	Ile	Ser	Val	Pro	Glu	Gly	Arg	Glu	Ala	Ala	Thr	Gln	Thr
		385				390					395				400	
65	Phe	Asn	Pro	Arg	Leu	Gly	Ile	Arg	Asp	Gly	Ile	Ser	Ile	Ile	Gly	Thr
				405						410					415	
	Ser	Gly	Val	Val	Lys	Pro	Phe	Ser	Ala	Glu	Ala	Phe	Val	Gly	Ala	Ile
				420					425					430		
70	Arg	Lys	Gln	Val	Gly	Ile	Ala	Thr	Ala	Leu	Gly	Ala	Asn	His	Ile	Val
		435						440					445			
	Leu	Asn	Ser	Gly	Ala	Lys	Ser	Glu	Arg	Tyr	Val	Lys	Gly	Ala	Tyr	Pro
		450				455						460				
	Ala	Leu	Ile	Pro	Gln	Ala	Phe	Val	Gln	Tyr	Gly	Asn	Phe	Val	Gly	Glu
		465				470						475			480	
75	Ser	Leu	Ser	Cys	Val	Ala	Ser	Phe	Pro	Ser	Val	Arg	Ser	Val	Thr	Val

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485 490 495  
 Gly Ile Met Leu Gly Lys Ala Val Lys Leu Ala Glu Gly Tyr Leu Asp  
 500 505 510  
 5 Thr His Ser Lys Lys Val Val Met Asn Arg Asp Phe Leu His Glu Leu  
 515 520 525  
 5 Ala Arg Gln Ala Gly Cys Ser Glu Asp Ile His Ala Ile Ile Asp Ser  
 530 535 540  
 Leu Asn Leu Ala Arg Glu Leu Trp Thr Met Pro Ser Ala Glu Asp Ser  
 545 550 555 560  
 10 Asp Arg Leu Leu Arg Lys Ile Ala Glu Arg Ser Trp Glu Thr Cys Arg  
 565 570 575  
 Pro Ser Val Pro Ser Ala Glu Leu Glu Leu Leu Leu Ile Asp Glu Ser  
 580 585 590  
 15 Gly Ala Ile Arg Phe Arg Ile Gly Gly Glu  
 595 600

(2) INFORMATION FOR SEQ ID NO:414

20 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 443 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
 25 (ii) MOLECULE TYPE: protein  
 (iii) HYPOTHETICAL: YES  
 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Porphyromonas gingivalis  
 30 (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...443

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:414

Met Leu Arg Thr Phe Arg Ile Gly Gly Ile His Pro Pro Glu Asn Lys  
 1 5 10 15  
 40 Leu Ser Ala Gly Lys Pro Val Glu Val Leu Pro Ile Pro Ser Gln Val  
 20 25 30  
 Val Ile Pro Leu Gly Gln His Ile Gly Ala Pro Ala Thr Ala Thr Val  
 35 40 45  
 Lys Lys Gly Asp Glu Val Lys Val Gly Thr Ile Ile Ala Gln Ala Gly  
 50 55 60  
 45 Gly Phe Val Ser Ala Asn Ile His Ser Ser Val Ser Gly Lys Val Leu  
 65 70 75 80  
 Lys Ile Asp Asn Val Tyr Asp Ser Ser Gly Tyr Pro Lys Pro Ala Val  
 85 90 95  
 Phe Ile Ser Val Glu Gly Asp Glu Trp Glu Glu Gly Ile Asp Arg Ser  
 100 105 110  
 50 Pro Ala Ile Val Lys Glu Cys Asn Leu Asp Ala Lys Glu Ile Val Ala  
 115 120 125  
 Lys Ile Ser Ala Ala Gly Ile Val Gly Leu Gly Gly Ala Thr Phe Pro  
 130 135 140  
 55 Thr His Val Lys Leu Ser Pro Pro Pro Gly Asn Lys Ala Glu Ile Leu  
 145 150 155 160  
 Ile Ile Asn Ala Val Glu Cys Glu Pro Tyr Leu Thr Ser Asp His Val  
 165 170 175  
 Leu Met Leu Glu His Gly Glu Glu Ile Met Ile Gly Val Ser Ile Leu  
 180 185 190  
 60 Met Lys Ala Ile Gln Val Asn Lys Ala Val Ile Gly Val Glu Asn Asn  
 195 200 205  
 Lys Lys Asp Ala Ile Ala His Leu Thr Lys Leu Ala Thr Ala Tyr Pro  
 210 215 220  
 65 Gly Ile Glu Val Met Pro Leu Lys Val Gln Tyr Pro Gln Gly Gly Glu  
 225 230 235 240  
 Lys Gln Leu Ile Asp Ala Val Ile Arg Lys Gln Val Lys Ser Gly Ala  
 245 250 255  
 70 Leu Pro Ile Ser Thr Gly Ala Val Val Gln Asn Val Gly Thr Val Phe  
 260 265 270  
 Ala Val Tyr Glu Ala Val Gln Lys Asn Lys Pro Leu Val Glu Arg Ile  
 275 280 285  
 Val Thr Val Thr Gly Lys Lys Leu Ser Arg Pro Ser Asn Leu Leu Val  
 290 295 300  
 75 Arg Ile Gly Thr Pro Ile Ala Ala Leu Ile Glu Ala Ala Gly Gly Leu

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	305				310					315					320	
	Pro	Glu	Asn	Thr	Gly	Lys	Ile	Ile	Gly	Gly	Gly	Pro	Met	Met	Gly	Arg
					325					330					335	
5	Ala	Leu	Leu	Ser	Pro	Asp	Val	Pro	Val	Thr	Lys	Gly	Ser	Ser	Gly	Val
				340					345					350		
	Leu	Ile	Leu	Asp	Arg	Glu	Glu	Ala	Val	Arg	Lys	Pro	Met	Arg	Asp	Cys
			355					360					365			
	Ile	Arg	Cys	Ala	Lys	Cys	Val	Gly	Val	Cys	Pro	Met	Gly	Leu	Asn	Pro
10			370				375					380				
	Ala	Phe	Leu	Met	Arg	Asp	Thr	Leu	Tyr	Lys	Ser	Trp	Glu	Thr	Ala	Glu
	385					390					395					400
	Lys	Gly	Asn	Val	Val	Asp	Cys	Ile	Glu	Cys	Gly	Ser	Cys	Ser	Phe	Thr
				405						410					415	
15	Cys	Pro	Ala	Asn	Arg	Pro	Leu	Leu	Asp	Tyr	Ile	Arg	Gln	Ala	Lys	Lys
				420					425					430		
	Thr	Val	Met	Gly	Ile	Gln	Arg	Ala	Arg	Lys	Gln					
			435					440								

20 (2) INFORMATION FOR SEQ ID NO:415

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 479 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

25

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

30

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

(A) NAME/KEY: misc feature

35 (B) LOCATION 1...479

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:415

40	Met 1	Lys	Arg	Ile 5	Gln	Leu	Thr	Leu	Ile 10	Ala	Leu	Phe	Ala	Ala	Val 15	Ala
	Gly	Leu	Val	Ala 20	Gln	Asn	Ala	Tyr	Glu 25	Gly	Val	Ile	Ser	Tyr 30	Lys	Ile
	Ser	Leu	Asp 35	Lys	Thr	Gly	Asn	Lys 40	Val	Val	Leu	Asn	Gly 45	Ala	Ala	Asp
45	Met 50	Ser	Asn	Leu	Lys	Leu	Lys 55	Ser	Thr	Gln	Met	Ile 60	Ile	Val	Thr	Pro
	Ile 65	Leu	Arg	Ser	Glu	Asp 70	Gly	Thr	Ser	Arg	Val 75	Glu	Phe	Pro	Ser	Val 80
	Val	Ile	Thr	Gly 85	Arg	Asn	Arg	Thr	Lys 90	Ala	Leu	Lys	Arg	Glu 95	Ile	Ala
50	Phe	Ser	Ser	Ala 100	Leu	Pro	Gln	Ala	Lys 105	His	Ala	Ala	Gln	Tyr 110	Ile	Arg
	Arg	His	Asn 115	Gly	Lys	Ser	Glu	Gln 120	Phe	Ala	Phe	Thr	Gly 125	Glu	His	Ala
	Tyr 130	Ala	Ser	Trp	Met	Met	Asp 135	Ala	Lys	Phe	Val	Val 140	Arg	Glu	Glu	Val
55	Arg 145	Gly	Cys	Ala	Lys	Cys 150	Pro	Val	Gly	Leu	Ser 155	Asn	Ile	Val	Pro	
	Phe	Asp	Pro	Leu 165	Phe	Asn	Pro	Ala	Glu 170	Ala	Pro	Tyr	Leu	Leu 175	Ala	His
	Ile	Thr	Pro	Ala 180	Glu	Glu	Val	Glu	Lys 185	Gln	Arg	Glu	Ser	Ser 190	Phe	Asp
60	Ala	Tyr	Ile 195	Asn	Phe	Lys	Val	Asn 200	Lys	Ala	Asp	Val	Leu 205	Pro	Glu	Tyr
	Arg	Asn 210	Asn	Lys	Ala	Glu	Leu 215	Glu	Lys	Ile	Lys	Glu 220	Phe	Val	Ser	Thr
	Val 225	Lys	Ala	Asn	Pro	Asn 230	Tyr	Ser	Val	Asn	Lys 235	Met	Ile	Ile	Glu	Gly 240
70	Phe	Ala	Ser	Pro 245	Glu	Ala	Ser	Ile	Ala	His 250	Asn	Lys	Ala	Leu 255	Ser	Glu
	Arg	Arg	Ala 260	Lys	Arg	Leu	Ala	Glu 265	Glu	Leu	Val	Arg	Lys	Tyr 270	Gly	Lys
	Thr	Leu	Pro 275	Asn	Ile	Thr	Thr	Glu 280	Phe	Gly	Gly	Glu	Asp 285	Trp	Lys	Gly
75	Leu	Lys	Leu	Ala	Ile	Glu	Lys	Ser	Asp	Ile	Ala	Asp	Arg	Asp	Arg	Val

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290 295 300  
 Leu Glu Ile Ile Asn Ser Asp Lys Tyr Ala Asp Asp Asp Ala Arg Glu  
 305 310 315 320  
 5 Gln Ala Leu Lys Gln Leu Ser Ser Tyr Arg Tyr Ile Leu Asp Gln Ile  
 325 330 335  
 Tyr Pro Asn Leu Arg Arg Asn Thr Ile Thr Met Gly Tyr Ile Val Arg  
 340 345 350  
 Asp Tyr Thr Leu Glu Glu Ala Arg Glu Ile Ile Lys Thr Ala Pro Lys  
 355 360 365  
 10 Glu Leu Ser Glu Ala Glu Met Tyr Arg Val Ala Met Ser Tyr Pro Glu  
 370 375 380  
 Gly His Gln Glu Arg Leu Phe Ala Leu Asn Thr Thr Leu Lys Tyr Phe  
 385 390 395 400  
 15 Pro Glu Ser Val Thr Gly Arg Ile Asn Leu Ala Val Ala Ala Phe Asn  
 405 410 415  
 Gly Gly Asp Val Gln Gln Ala Ile Ala Leu Leu Ser Pro Ile Gln Thr  
 420 425 430  
 Glu Lys Gly Val Ser Asn Ile Leu Gly Ala Ala Tyr Ala Arg Thr Gly  
 435 440 445  
 20 Asp Phe Ala Arg Ala Glu Thr Phe Phe Arg Lys Ala Val Ala Glu Gly  
 450 455 460  
 Asp Ala Asn Ala Gln Arg Asn Leu Asp Met Leu Leu Gly Lys Lys  
 465 470 475  
 25 (2) INFORMATION FOR SEQ ID NO:416  
 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 383 amino acids  
 (B) TYPE: amino acid  
 30 (D) TOPOLOGY: linear  
 (ii) MOLECULE TYPE: protein  
 (iii) HYPOTHETICAL: YES  
 35 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Porphyromonas gingivalis  
 (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 40 (B) LOCATION 1...383  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:416  
 45 Met Ala Glu Lys Arg Asp Tyr Tyr Glu Val Leu Gly Val Ser Lys Asn  
 1 5 10 15  
 Ala Thr Asp Asp Glu Leu Lys Lys Ala Tyr Arg Lys Lys Ala Ile Gln  
 20 25 30  
 50 Tyr His Pro Asp Lys Asn Pro Gly Asp Lys Glu Ala Glu Glu His Phe  
 35 40 45  
 Lys Glu Val Ala Glu Ala Tyr Asp Val Leu Ser Asp Pro Gln Lys Arg  
 50 55 60  
 Ser Gln Tyr Asp Gln Phe Gly His Ala Gly Leu Gly Gly Ala Ala Gly  
 65 70 75 80  
 55 Gly Gly Phe Ser Gly Gly Gly Met Ser Met Glu Asp Ile Phe Ser Arg  
 85 90 95  
 Phe Gly Asp Leu Phe Gly Gly Phe Gly Gly Phe Gly Gly Phe Ser Asp  
 100 105 110  
 60 Met Gly Gly Gly Ser Arg Arg Arg Val Arg Arg Gly Ser Asp Leu Arg  
 115 120 125  
 Val Arg Val Lys Leu Ser Leu Ala Asp Ile Ser Lys Gly Val Glu Lys  
 130 135 140  
 Lys Val Lys Val Lys Lys Gln Val Val Cys Ser Lys Cys Arg Gly Asp  
 145 150 155 160  
 65 Gly Thr Glu Glu Ala Asn Gly Lys Thr Thr Cys Gln Thr Cys His Gly  
 165 170 175  
 Thr Gly Val Val Thr Arg Val Ser Asn Thr Phe Leu Gly Ala Met Gln  
 180 185 190  
 70 Thr Gln Ser Thr Cys Pro Thr Cys His Gly Glu Gly Glu Ile Ile Thr  
 195 200 205  
 Lys Pro Cys Ser Lys Cys Lys Gly Glu Gly Val Glu Ile Gly Glu Glu  
 210 215 220  
 Val Ile Ser Phe His Ile Pro Ala Gly Val Ala Glu Gly Met Gln Met  
 225 230 235 240  
 75 Ser Val Asn Gly Lys Gly Asn Ala Ala Pro Arg Gly Gly Val Asn Gly

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245 250 255  
 Asp Leu Ile Val Val Ile Ala Glu Glu Pro Asp Pro Asn Leu Ile Arg  
 260 265 270  
 5 Asn Gly Asn Asp Leu Ile Tyr Asn Leu Leu Ile Ser Val Pro Leu Ala  
 275 280 285  
 Ile Lys Gly Gly Ser Val Glu Val Pro Thr Ile Asp Gly Arg Ala Lys  
 290 295 300  
 Ile Arg Ile Glu Ala Gly Thr Gln Pro Gly Lys Met Leu Arg Leu Arg  
 305 310 315  
 10 Asn Lys Gly Leu Pro Ser Val Asn Gly Tyr Gly Met Gly Asp Gln Leu  
 325 330 335  
 Val Asn Val Asn Val Tyr Ile Pro Glu Ser Ile Asp Ala Lys Asp Glu  
 340 345 350  
 15 Gln Ala Ile Ala Ala Met Glu Asn Ser Asp Ser Phe Lys Pro Thr Asp  
 355 360 365  
 Ala Ala Arg Lys Asp Ile Asp Lys Lys Tyr Arg Glu Met Leu Asp  
 370 375 380

(2) INFORMATION FOR SEQ ID NO:417

20

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 293 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

25

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

30

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:  
 (A) NAME/KEY: misc feature  
 (B) LOCATION 1...293

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:417

40 Met Lys Lys Leu Ile Leu Ala Thr Leu Gly Leu Met Ala Ile Ala Met  
 1 5 10 15  
 Leu Ser Cys Ser Ser Asn Asn Lys Asp Leu Glu Asn Lys Gly Glu Ala  
 20 25 30  
 Thr Leu Leu Val Thr Phe Gly Ser Ser Tyr Lys Ala Pro Arg Glu Thr  
 35 40 45  
 45 Tyr Ala Lys Ile Glu Lys Thr Phe Ala Ala Ala Tyr Pro Asp Gln Arg  
 50 55 60  
 Ile Ser Trp Thr Tyr Thr Ser Ser Ile Ile Arg Lys Lys Leu Ala Gln  
 65 70 75 80  
 50 Gln Gly Ile Tyr Ile Asp Ala Pro Asp Glu Ala Leu Glu Lys Leu Ala  
 85 90 95  
 Arg Leu Gly Tyr Lys Lys Ile Asn Val Gln Ser Leu His Val Ile Pro  
 100 105 110  
 Gly Arg Glu Tyr Asp Glu Met Ile Asp Phe Val Asn Lys Phe Lys Ala  
 115 120 125  
 55 Ala His Ser Asp Ile Thr Val Lys Val Gly Ala Pro Leu Phe Asp Thr  
 130 135 140  
 Asp Glu Asp Met Arg Glu Val Ala Glu Ile Leu His Lys Arg Phe Gln  
 145 150 155 160  
 60 Gln Thr Ile Glu Lys Gly Glu Ala Ile Val Phe Met Gly His Gly Thr  
 165 170 175  
 Glu His Ala Ala Asn Asp Arg Tyr Ala Arg Ile Asn Lys Ile Met Lys  
 180 185 190  
 Asn Tyr Ser Lys Phe Met Ile Val Gly Thr Val Glu Ser Asp Pro Ser  
 195 200 205  
 65 Ile Asn Asp Val Ile Ala Glu Leu Lys Glu Thr Gly Ala Thr Ala Val  
 210 215 220  
 Thr Met Met Pro Leu Met Ser Val Ala Gly Asp His Ala Thr Asn Asp  
 225 230 235 240  
 70 Met Ala Gly Asp Glu Asp Asp Ser Trp Lys Thr Leu Leu Thr Asn Ala  
 245 250 255  
 Gly Tyr Thr Val Ser Ile Asp Lys Leu Asp Asn Gly Asn Phe Ser Ala  
 260 265 270  
 Leu Gly Asp Ile Glu Glu Ile Arg Asn Ile Trp Leu Lys His Met Lys  
 275 280 285  
 75 Ala Thr Ser Ala Arg

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(2) INFORMATION FOR SEQ ID NO:418

5

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 356 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

10

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

15

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Porphyromonas gingivalis

20

(ix) FEATURE:  
 (A) NAME/KEY: misc feature  
 (B) LOCATION 1...356

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:418

Met Thr Ser Val Ser His Leu Arg Thr Ile Ser Val Ala Gly Ile Leu  
 1 5 10 15  
 25 Ala Ala Leu Gly Gly Ala Val Leu Ile Leu Phe Gly Val Asn Leu Phe  
 20 25 30  
 Leu Gly Ser Val Ala Ile Pro Met Ser Glu Ile Phe Arg His Leu Phe  
 35 40 45  
 30 Ser Asp Arg Pro Glu Gly Gly Glu Ala Leu Val His Tyr Asn Ile Leu  
 50 55 60  
 Trp Lys Ser Arg Leu Pro Glu Ala Leu Thr Ala Ala Phe Ala Gly Ala  
 65 70 75 80  
 Gly Leu Ser Val Ser Gly Leu Gln Met Gln Thr Val Phe Arg Asn Pro  
 85 90 95  
 35 Leu Ala Gly Pro Ser Val Leu Gly Ile Ser Ser Gly Ala Ser Leu Gly  
 100 105 110  
 Val Ala Leu Val Val Leu Leu Ser Gly Ser Leu Gly Gly Val Ala Leu  
 115 120 125  
 40 Ser Ser Leu Gly Tyr Met Gly Glu Val Ala Met Asn Ile Ala Ala Ala  
 130 135 140  
 Val Gly Ser Leu Ala Val Met Gly Leu Ile Val Phe Val Ser Thr Lys  
 145 150 155 160  
 Val Arg Ser His Val Thr Leu Leu Ile Ile Gly Val Met Ile Gly Tyr  
 165 170 175  
 45 Val Ala Thr Ala Val Ile Gly Val Phe Lys Phe Phe Ser Ile Glu Glu  
 180 185 190  
 Asp Ile Arg Ala Tyr Val Ile Trp Gly Leu Gly Ser Phe Ser Arg Ala  
 195 200 205  
 50 Thr Asp Ser Gln Leu Ser Phe Phe Ala Ile Leu Met Leu Ile Phe Ile  
 210 215 220  
 Pro Ala Gly Met Leu Leu Val Lys Gln Leu Asn Leu Leu Leu Gly  
 225 230 235 240  
 Glu Ser Tyr Ala Arg Asn Leu Gly Leu Asn Thr Arg Arg Ala Arg Leu  
 245 250 255  
 55 Leu Val Ile Ser Ser Ala Gly Leu Leu Ile Ala Thr Val Thr Ala Tyr  
 260 265 270  
 Cys Gly Pro Ile Gly Phe Leu Gly Met Ala Val Pro His Leu Ala Arg  
 275 280 285  
 60 Val Ile Phe His Thr Ser Asp His Arg Ile Leu Met Pro Ala Thr Cys  
 290 295 300  
 Leu Ile Gly Ser Ala Leu Ala Leu Phe Cys Asn Ile Ile Ala Arg Met  
 305 310 315 320  
 Pro Gly Phe Glu Gly Ala Leu Pro Val Asn Ser Val Thr Ala Leu Val  
 325 330 335  
 65 Gly Ala Pro Ile Ile Val Thr Val Leu Phe Arg Arg Arg Arg Phe Lys  
 340 345 350  
 Glu Glu Thr Asp  
 355

70

(2) INFORMATION FOR SEQ ID NO:419

75

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 757 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

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(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:  
(A) ORGANISM: *Porphyromonas gingivalis*

(ix) FEATURE:  
(A) NAME/KEY: misc\_feature  
(B) LOCATION 1...757

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:419

15	Met	Arg	Thr	Lys	Thr	Ile	Phe	Phe	Ala	Ile	Ile	Ser	Phe	Ile	Ala	Leu
	1				5					10				15		
	Leu	Ser	Ser	Ser	Leu	Ser	Ala	Gln	Ser	Lys	Ala	Val	Leu	Thr	Gly	Ser
				20					25				30			
20	Val	Ser	Asp	Ala	Glu	Thr	Gly	Glu	Pro	Leu	Ala	Gly	Ala	Arg	Ile	Glu
		35					40					45				
	Val	Lys	His	Thr	Asn	Ile	Val	Ala	Gly	Ala	Asp	Ala	Gly	Gly	His	Phe
		50					55					60				
	Glu	Ile	Lys	Asn	Leu	Pro	Ala	Gly	Gln	His	Thr	Ile	Ile	Cys	Ser	Leu
		65				70					75			80		
25	Gly	Gly	Tyr	Gly	Gln	Lys	Glu	Glu	Val	Val	Ala	Ile	Glu	Ala	Gly	Gln
				85					90				95			
	Thr	Lys	Thr	Ile	Ser	Phe	Ala	Leu	Arg	Leu	Arg	Thr	Asn	Asn	Leu	Glu
				100					105				110			
30	Glu	Val	Val	Val	Thr	Gly	Thr	Gly	Thr	Arg	Tyr	Arg	Leu	Val	Asp	Ala
				115				120					125			
	Pro	Val	Ala	Thr	Glu	Val	Leu	Thr	Ala	Lys	Asp	Ile	Ala	Ser	Phe	Ser
		130					135					140				
	Ala	Pro	Thr	Ser	Glu	Ala	Leu	Leu	Gln	Gly	Leu	Ser	Pro	Ser	Phe	Asp
		145				150				155			160			
35	Phe	Gly	Pro	Asn	Leu	Met	Gly	Ser	Phe	Met	Gln	Leu	Asn	Gly	Leu	Ser
				165					170				175			
	Ser	Lys	Tyr	Ile	Leu	Ile	Leu	Ile	Asp	Gly	Lys	Arg	Val	Tyr	Gly	Asp
				180					185				190			
40	Val	Gly	Gly	Gln	Ala	Asp	Leu	Ser	Arg	Ile	Ser	Pro	Asp	Gln	Ile	Glu
			195					200					205			
	Arg	Ile	Glu	Leu	Val	Lys	Gly	Ala	Ser	Ser	Ser	Leu	Tyr	Gly	Ser	Asp
		210					215					220				
	Ala	Ile	Ala	Gly	Val	Ile	Asn	Val	Ile	Thr	Lys	Lys	Asn	Thr	Asn	Arg
		225				230					235					240
45	Leu	Ser	Ala	Tyr	Thr	Ser	His	Arg	Ile	Ser	Lys	Tyr	Asn	Asp	Arg	Gln
				245						250				255		
	Thr	Asn	Thr	Ser	Leu	Asp	Ile	Asn	Ile	Gly	Lys	Phe	Ser	Ser	Asn	Thr
				260					265				270			
	Asn	Tyr	Phe	Phe	Tyr	His	Thr	Asp	Gly	Trp	Gln	Asn	Ser	Pro	Phe	Glu
		275						280					285			
50	Ile	Lys	Lys	Lys	Lys	Gly	Ser	Gly	Glu	Pro	Val	Leu	Glu	Glu	Thr	Tyr
		290					295					300				
	Lys	Lys	Thr	Phe	Arg	Ala	Gln	Glu	Asn	Gln	Gly	Val	Ser	Gln	Ser	Leu
		305				310					315			320		
55	Ser	Tyr	Tyr	Ala	Thr	Asn	Asn	Leu	Ser	Phe	Ser	Gly	Asn	Val	Gln	Tyr
				325						330				335		
	Asn	Lys	Arg	Gln	Ile	Phe	Thr	Pro	Thr	Phe	Ser	Glu	Lys	Lys	Ala	Tyr
				340					345				350			
60	Asp	Met	Asp	Tyr	Arg	Ala	Leu	Thr	Ala	Ser	Leu	Gly	Thr	Asn	Tyr	Leu
			355					360					365			
	Phe	Pro	Asn	Gly	Leu	His	Thr	Leu	Ser	Phe	Asp	Ala	Val	Tyr	Asp	Arg
			370				375					380				
	Phe	Arg	Phe	Gly	Tyr	Leu	Tyr	His	Asp	Lys	Asp	Ser	Ser	Glu	Ser	Leu
		385				390					395			400		
65	Ile	Asn	Asn	Gln	Gly	Gln	Thr	Glu	Gln	Pro	Thr	Phe	Phe	Pro	Gly	Gln
				405						410				415		
	Leu	Arg	Asn	Lys	Asn	Asp	Gln	Ile	Arg	Tyr	Thr	Ala	Glu	Ala	Arg	Gly
			420					425					430			
70	Val	Phe	Thr	Leu	Pro	Tyr	Ala	Gln	Lys	Leu	Thr	Gly	Gly	Leu	Glu	Tyr
			435					440					445			
	Phe	Arg	Glu	Glu	Leu	Ile	Ser	Pro	Tyr	Asn	Leu	Ile	Thr	Asp	Lys	Ala
		450					455					460				
	Asp	Ala	Ser	Thr	Leu	Ser	Ala	Tyr	Val	Gln	Asp	Glu	Trp	Lys	Pro	Leu
		465				470				475				480		
75	Asp	Trp	Phe	Asn	Met	Thr	Ala	Gly	Phe	Arg	Leu	Val	His	His	Gln	Glu

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485 490 495  
 Phe Gly Thr Arg Met Thr Pro Lys Val Ser Ile Leu Ala Lys Tyr Gly  
 500 505 510  
 5 10 15 20 25 30 35  
 Pro Leu Asn Phe Arg Ala Thr Tyr Ala Asn Gly Tyr Lys Thr Pro Thr  
 515 520 525  
 Leu Lys Glu Leu Phe Ala Arg Asn Glu Leu Thr Thr Met Gly Ser His  
 530 535 540  
 Asn Leu Tyr Leu Gly Asn Ala Asp Leu Lys Pro Gln Met Ser Asp Tyr  
 545 550 555  
 10 Tyr Ala Leu Gly Leu Glu Tyr Asn Gln Gly Pro Ile Ser Phe Ser Ala  
 565 570 575  
 Thr Val Tyr Asp Asn Glu Leu Arg Asn Leu Ile Ser Phe Met Asp Ile  
 580 585 590  
 15 Pro Thr Ser Pro Glu His Glu Ala Gln Gly Ile Lys Lys Thr Lys Gln  
 595 600 605  
 Tyr Ala Asn Ile Gly Lys Ala Arg Ser Arg Gly Leu Asp Val Leu Cys  
 610 615 620  
 Asp Ala Ser Ile Gly Trp Gly Ile Lys Leu Gly Ala Gly Tyr Ser Leu  
 625 630 635  
 20 Val Glu Ala Lys Asn Leu Gln Thr Asp Glu Trp Leu Glu Gly Ala Ala  
 645 650 655  
 Arg His Arg Ala Asn Val His Ala Asp Trp Val His Tyr Trp Gly Gln  
 660 665 670  
 25 Tyr Arg Leu Gly Val Ser Leu Phe Gly Arg Ile Gln Ser Glu Arg Tyr  
 675 680 685  
 Tyr Lys Asp Gly Asn Ala Pro Asp Tyr Thr Leu Trp Arg Leu Ala Thr  
 690 695 700  
 Ser His Arg Phe Ala His Phe Arg His Ile Ile Leu Asp Gly Thr Leu  
 705 710 715  
 30 Gly Ile Asp Asn Leu Phe Asp Tyr Val Asp Asp Arg Pro Met Gly Val  
 725 730 735  
 Asn Tyr Ala Thr Val Thr Pro Gly Arg Thr Phe Phe Ala Gln Ile Ala  
 740 745 750  
 35 Ile Arg Phe Asn Asn  
 755

(2) INFORMATION FOR SEQ ID NO:420

- 40 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 331 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
 45 (ii) MOLECULE TYPE: protein  
 (iii) HYPOTHETICAL: YES  
 (vi) ORIGINAL SOURCE:  
 50 (A) ORGANISM: Porphyromonas gingivalis  
 (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...331  
 55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:420

Met Thr Asp Asn Lys Gln Arg Asn Ile Val Phe Pro Ala Phe Leu Leu  
 1 5 10 15  
 60 Leu Leu Gly Val Ile Ala Val Val Thr Ile Val Gly Phe Phe Met Leu  
 20 25 30  
 Arg Pro Ala Glu Glu Ile Ile Gln Gly Gln Ile Glu Val Thr Glu Tyr  
 35 40 45  
 Arg Val Ser Ser Lys Val Pro Gly Arg Ile Lys Glu Leu Arg Val Ser  
 50 55 60  
 65 Glu Gly Gln Gln Val Gln Ala Gly Asp Thr Leu Ala Val Ile Glu Ala  
 65 70 75 80  
 Pro Asp Val Ala Ala Lys Met Glu Gln Ala Lys Ala Ala Glu Ala Ala  
 85 90 95  
 70 Ala Gln Ala Gln Asn Ala Lys Ala Leu Lys Gly Ala Arg Ser Glu Gln  
 100 105 110  
 Ile Gln Ala Ala Tyr Glu Met Trp Gln Lys Ala Gln Ala Gly Val Ala  
 115 120 125  
 Ile Ala Thr Lys Thr His Gln Arg Val Gln Asn Leu Tyr Asp Gln Gly  
 130 135 140  
 75 Val Val Pro Ala Gln Lys Leu Asp Glu Ala Thr Ala Gln Arg Asp Ala



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5	145	150	155	160													
	Ala	Ile	Ala	Thr	Gln	Lys	Ala	Ala	Glu	Ala	Gln	Tyr	Asn	Met	Ala	Arg	
					165					170					175		
	Asn	Gly	Ala	Glu	Arg	Glu	Asp	Lys	Leu	Ala	Ala	Ser	Ala	Leu	Val	Asp	
10				180					185					190			
	Arg	Ala	Arg	Gly	Ala	Val	Ala	Glu	Val	Glu	Ser	Tyr	Ile	Asn	Glu	Thr	
				195				200					205				
	Tyr	Leu	Ile	Ala	Pro	Arg	Ala	Gly	Glu	Val	Ser	Glu	Ile	Phe	Pro	Lys	
15				210			215				220						
	Ala	Gly	Glu	Leu	Val	Gly	Thr	Gly	Ala	Pro	Ile	Met	Asn	Ile	Ala	Glu	
				225		230					235					240	
	Met	Gly	Asp	Met	Trp	Ala	Ser	Phe	Ala	Val	Arg	Glu	Asp	Phe	Leu	Ser	
20				245					250					255			
	Ser	Met	Thr	Met	Gly	Ala	Val	Leu	Glu	Thr	Val	Val	Pro	Ala	Leu	Asn	
				260					265				270				
	Glu	Glu	Lys	Val	Arg	Phe	Lys	Ile	Thr	Phe	Ile	Lys	Asn	Met	Gly	Thr	
25				275			280					285					
	Tyr	Ala	Ala	Trp	Lys	Ala	Thr	Lys	Thr	Thr	Gly	Gln	Tyr	Asp	Leu	Lys	
				290			295					300					
	Thr	Phe	Glu	Val	Lys	Ala	Thr	Leu	Ala	Asp	Lys	Asp	Lys	Ala	Gln	Lys	
30				305		310				315						320	
	Leu	Arg	Pro	Gly	Met	Ser	Val	Ile	Ile	Arg	Lys						
				325					330								

## 25 (2) INFORMATION FOR SEQ ID NO:421

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 267 amino acids

(P) TYPE: amino acid

(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

(A) NAME/KEY: misc feature

(B) LOCATION 1...267

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:421

[illegible]

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245 250 255  
 Thr Leu Thr Ile Thr Ile Ile Asp Lys Thr Lys  
 260 265

## 5 (2) INFORMATION FOR SEQ ID NO:422

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 569 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

10

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

15

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

(A) NAME/KEY: misc feature

(B) LOCATION 1...569

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:422

25 Met Lys Lys Thr Asn Leu Phe Leu Ser Leu Leu Val Ile Phe Ile Thr  
 1 5 10 15  
 Gly Ser Phe Met Thr Ala Cys Ala Gln Lys Ser Lys Thr Asn Lys Leu  
 20 25 30  
 30 Thr Glu Glu Asp Arg Ser Arg Asn Glu Tyr Val Gln Ser Met Asp Val  
 35 40 45  
 Leu Ser Asn Ile Ile Gly Asn Val Arg Leu Tyr Phe Val Asp Thr Ile  
 50 55 60  
 Ser Ile Lys His Met Thr Arg Arg Gly Ile Asp Ala Met Leu Gly Gly  
 65 70 75 80  
 35 Leu Asp Pro Tyr Thr Glu Tyr Ile Pro Tyr Glu Glu Met Asp Glu Leu  
 85 90 95  
 Lys Leu Met Thr Thr Gly Glu Tyr Ala Gly Val Gly Ala Ile Ile Ser  
 100 105 110  
 40 Gln Arg Pro Asp Ser Ala Val Ile Ile Gln Arg Pro Met Glu Gly Met  
 115 120 125  
 Pro Ala Asp Glu Ala Gly Leu Ile Ala Gly Asp Arg Ile Leu Thr Ile  
 130 135 140  
 Asp Gly Lys Asp Phe Arg Lys Ser Thr Thr Pro Lys Val Ser Gln Ala  
 145 150 155 160  
 45 Leu Lys Gly Ile Ala Gly Thr Val Ala Lys Val Thr Val Met Arg Tyr  
 165 170 175  
 Gly Glu Thr Lys Pro Arg Thr Phe Ser Val Lys Arg Gln Lys Val Ile  
 180 185 190  
 50 Met Asn Ser Val Thr Tyr Ser Gly Met Leu Asp Gly Ser Ile Gly Tyr  
 195 200 205  
 Ile Arg Leu Asn Asn Phe Thr Asp Lys Ser Ala Glu Glu Val Arg Thr  
 210 215 220  
 Ala Leu Leu Asp Leu Arg Asp Lys Gln Gly Ala Lys Gly Leu Ile Leu  
 225 230 235 240  
 55 Asp Leu Arg Gly Asn Gly Gly Gly Leu Met Gln Ala Ala Ile Glu Ile  
 245 250 255  
 Val Asn Leu Phe Val Pro Lys Gly Lys Glu Val Val Thr Thr Lys Gly  
 260 265 270  
 Arg Ile Ala Glu Ser Ala Ser Val Phe Arg Thr Leu Thr Glu Pro Ile  
 275 280 285  
 60 Asp Thr Lys Leu Pro Ile Val Val Leu Ile Asp Gly Gln Ser Ala Ser  
 290 295 300  
 Ser Ser Glu Ile Val Ala Gly Ala Leu Gln Asp Met Asp Arg Ala Val  
 305 310 315 320  
 65 Leu Met Gly Gln Lys Ser Tyr Gly Lys Gly Leu Val Gln Thr Thr Arg  
 325 330 335  
 Gln Leu Pro Tyr Asn Gly Val Ile Lys Leu Thr Thr Ala Lys Tyr Tyr  
 340 345 350  
 70 Ile Pro Ser Gly Arg Cys Ile Gln Arg Leu Asp Tyr Ser Arg Thr Asn  
 355 360 365  
 Arg Thr Gly Met Ala Thr Ala Ile Pro Asp Ser Leu His Lys Ile Phe  
 370 375 380  
 Tyr Thr Ala Ala Gly Arg Val Glu Asp Ala Gly Gly Ile Leu Pro  
 385 390 395 400  
 75 Asp Ile Glu Val Lys Gln Asp Thr Ala Ala Thr Leu Leu Tyr Tyr Met

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5                                   405                                   410                                   415  
 Ala Ile Asn Asn Asp Val Phe Asp Phe Val Thr Gly Tyr Val Leu Lys  
                                   420                                   425                                   430  
 His Lys Thr Ile Ala Lys Pro Glu Asp Phe Ser Ile Thr Asn Glu Asp  
                                   435                                   440                                   445  
 Tyr Ala Ala Phe Cys Lys Met Met Glu Glu Lys Lys Phe Asp Tyr Asp  
                                   450                                   455                                   460  
 Arg Glu Ser Gly Lys Met Leu Asp Lys Leu Glu Glu Leu Ala Lys Ile  
                                   465                                   470                                   475                                   480  
 10 Glu Gly Tyr Leu Pro Glu Ala Asn Ser Glu Leu Lys Ala Leu Arg Glu  
                                   485                                   490                                   495  
 Lys Leu Lys Pro Asn Leu Ser Arg Asp Leu Leu Arg Phe Lys Lys Glu  
                                   500                                   505                                   510  
 15 Ile Thr Asn Tyr Leu Asn Asn Glu Ile Val Thr Arg Tyr Tyr Tyr Glu  
                                   515                                   520                                   525  
 Arg Gly Ser Ile Arg Gln Ser Leu Pro Glu Asp Lys Val Val Lys Glu  
                                   530                                   535                                   540  
 Ala Ile Lys Leu Leu Lys Asp His Pro Glu Gln Ile Arg Gln Ile Leu  
                                   545                                   550                                   555                                   560  
 20 Ala Ala Pro Lys Ala Glu Asn Lys Gly  
                                   565

(2) INFORMATION FOR SEQ ID NO:423

25           (i) SEQUENCE CHARACTERISTICS:  
             (A) LENGTH: 981 amino acids  
             (B) TYPE: amino acid  
             (D) TOPOLOGY: linear  
 30           (ii) MOLECULE TYPE: protein  
             (iii) HYPOTHETICAL: YES  
             (vi) ORIGINAL SOURCE:  
 35                 (A) ORGANISM: Porphyromonas gingivalis  
             (ix) FEATURE:  
                 (A) NAME/KEY: misc\_feature  
                 (B) LOCATION 1...981  
 40           (xii) SEQUENCE DESCRIPTION: SEQ ID NO:423

Met Gln Asn Lys Gly Phe Val Ile Val Ile Thr Ser Ala Leu Ala Ile  
 1                                   5                                   10                                   15  
 45 Ile Cys Ala Phe Tyr Leu Ser Phe Ser Phe Val Thr Asn Arg Tyr Glu  
                                   20                                   25                                   30  
 Lys Lys Ala Lys Ala Met Gly Asp Val Ala Gly Met Ala Tyr Leu Asp  
                                   35                                   40                                   45  
 50 Ser Met Ser Asn Glu Lys Val Trp Phe Gly Tyr Thr Leu Lys Glu Ala  
                                   50                                   55                                   60  
 Gln Ala Gln Gln Ile Gly Leu Gly Leu Asp Leu Lys Gly Gly Met Asn  
                                   65                                   70                                   75                                   80  
 Val Ile Leu Lys Leu Asn Ala Ser Asp Leu Leu Arg Asn Leu Ser Asn  
                                   85                                   90                                   95  
 55 Lys Ser Leu Asp Pro Asn Phe Asn Lys Ala Leu Glu Asn Ala Ala Lys  
                                   100                                   105                                   110  
 Ser Thr Glu Gln Ser Asp Phe Ile Asp Ile Phe Val Lys Glu Tyr Arg  
                                   115                                   120                                   125  
 60 Lys Leu Asp Pro Asn Gly Arg Leu Ala Val Ile Phe Gly Ser Gly Asp  
                                   130                                   135                                   140  
 Leu Arg Asp Gln Ile Thr Ala Lys Ser Thr Asp Ala Asp Val Val Arg  
                                   145                                   150                                   155                                   160  
 Leu Leu Lys Glu Lys Tyr Asn Ser Ala Val Glu Ala Ser Phe Asn Val  
                                   165                                   170                                   175  
 65 Leu Arg Ala Arg Ile Asp Ala Phe Gly Val Val Ala Pro Asn Leu Gln  
                                   180                                   185                                   190  
 Arg Leu Glu Gly Gln Gly Arg Ile Leu Val Glu Leu Pro Gly Val Lys  
                                   195                                   200                                   205  
 70 Asp Pro Glu Arg Val Arg Thr Leu Leu Gln Arg Ser Ala Asn Leu Gln  
                                   210                                   215                                   220  
 Phe Trp Arg Thr Tyr Lys Phe Glu Glu Val Ser Gly Asp Leu Ile Ala  
                                   225                                   230                                   235                                   240  
 Ala Asn Asp Arg Leu Ser Glu Leu Ala Met Asn Asn Thr Asp Ala Thr  
                                   245                                   250                                   255  
 75 Pro Glu Thr Glu Pro Ala Thr Thr Asp Ser Val Ala Ala Thr Ala Asp

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				260						265					270		
	Ser	Ala	Ala	Val	Gln	Ala	Val	Ala	Asp	Ser	Ala	Thr	Val	Ala	Gln	Lys	
			275					280					285				
5	Glu	Ala	Lys	Asp	Ala	Thr	Arg	Lys	Asp	Ala	Leu	Phe	Ser	Leu	Leu	Thr	
		290					295					300					
	Pro	Val	Asn	Arg	Gly	Gly	Ala	Val	Val	Gly	Val	Ala	Arg	Arg	Ala	Asn	
		305				310					315					320	
	Met	Ala	Gln	Ile	Ser	Glu	Met	Leu	Gln	Gln	Ala	His	Asp	Leu	Lys	Val	
10					325						330				335		
	Thr	Arg	Glu	Asp	Val	Leu	Phe	Leu	Trp	Gly	Ala	Lys	Ala	Ile	Glu	Asp	
				340					345					350			
	Pro	Glu	Thr	Lys	Lys	Glu	Thr	Asp	Leu	Tyr	Glu	Leu	Tyr	Ala	Ile	Arg	
			355					360					365				
15	Thr	Asn	Arg	Thr	Gly	Asp	Pro	Asp	Leu	Gly	Gly	Asp	Val	Val	Thr	Ser	
		370					375					380					
	Ala	Lys	Ser	Asp	Ile	Gln	Asn	Asp	Phe	Gly	Arg	Ser	Glu	Pro	Ile	Val	
		385				390					395					400	
	Ser	Met	Thr	Met	Asn	Glu	Glu	Gly	Ala	Arg	Lys	Trp	Ala	Arg	Ile	Thr	
20					405					410					415		
	Lys	Asp	Asn	Val	Gly	Arg	Ala	Ile	Ala	Ile	Val	Leu	Asp	Gly	Val	Val	
				420					425					430			
	Tyr	Ser	Ala	Pro	Asn	Val	Asn	Asp	Glu	Ile	Thr	Gly	Gly	Arg	Ser	Gln	
		435						440					445				
25	Ile	Ser	Gly	His	Phe	Thr	Val	Glu	Glu	Ala	Gly	Asp	Leu	Ala	Asn	Val	
		450					455					460					
	Leu	Asn	Ser	Gly	Lys	Met	Asp	Ala	Thr	Val	Ser	Ile	Glu	Gln	Glu	Asn	
		465				470					475					480	
	Val	Ile	Gly	Pro	Thr	Leu	Gly	Ala	Glu	Ser	Ile	Lys	Ala	Gly	Phe	Leu	
30					485					490					495		
	Ser	Phe	Leu	Leu	Ala	Leu	Val	Ile	Leu	Met	Cys	Tyr	Met	Cys	Leu	Ala	
				500					505					510			
	Tyr	Gly	Phe	Leu	Pro	Gly	Leu	Ile	Ala	Asn	Gly	Ala	Leu	Ile	Val	Asn	
		515						520					525				
35	Ser	Phe	Phe	Thr	Leu	Gly	Val	Leu	Ala	Ser	Phe	His	Ala	Val	Leu	Thr	
		530					535					540					
	Leu	Ser	Gly	Ile	Ala	Gly	Leu	Val	Leu	Thr	Leu	Gly	Met	Ala	Val	Asp	
		545				550					555					560	
	Ala	Asn	Val	Leu	Ile	Phe	Glu	Arg	Ile	Lys	Glu	Glu	Leu	Arg	Ala	Gly	
40					565					570					575		
	Lys	Thr	Pro	Ile	Arg	Ala	Val	Thr	Asp	Gly	Tyr	Gly	Asn	Ala	Phe	Ser	
				580					585					590			
	Ala	Ile	Phe	Asp	Ser	Asn	Val	Thr	Thr	Ile	Ile	Thr	Gly	Ile	Ile	Leu	
		595						600					605				
45	Phe	Leu	Tyr	Gly	Thr	Gly	Pro	Ile	Arg	Gly	Phe	Ala	Thr	Thr	Leu	Ile	
		610					615					620					
	Ile	Gly	Leu	Ile	Ala	Ser	Phe	Ile	Thr	Ala	Val	Phe	Leu	Thr	Arg	Ile	
		625				630					635					640	
	Val	Phe	Glu	Lys	Leu	Ala	Lys	Lys	Gly	Arg	Leu	Asp	Lys	Ile	Thr	Phe	
50					645					650					655		
	Thr	Thr	Ser	Ile	Thr	Arg	Asn	Leu	Leu	Val	Asn	Pro	Ser	Tyr	Asn	Ile	
				660					665					670			
	Leu	Gly	Lys	Arg	Lys	Thr	Gly	Phe	Ile	Ile	Pro	Val	Ile	Ile	Ile	Val	
		675						680					685				
55	Leu	Gly	Leu	Ile	Ala	Ser	Phe	Thr	Ile	Gly	Leu	Asn	Arg	Gly	Ile	Glu	
		690					695					700					
	Phe	Ser	Gly	Gly	Arg	Asn	Tyr	Val	Val	Lys	Phe	Asp	Gln	Pro	Val	Ser	
		705				710					715					720	
	Ser	Glu	Ala	Val	Arg	Ser	Ala	Leu	Ser	Ser	Pro	Leu	Gln	Glu	Lys	Val	
60					725						730				735		
	Leu	Val	Thr	Ser	Ile	Gly	Thr	Glu	Gly	Thr	Glu	Val	Arg	Ile	Ser	Thr	
				740					745					750			
	Asn	Tyr	Lys	Ile	Gln	Glu	Glu	Ser	Glu	Glu	Thr	Glu	Ala	Glu	Ile	Thr	
		755						760					765				
65	Asp	Lys	Leu	Tyr	Gln	Ser	Leu	Lys	Gly	Phe	Tyr	Thr	Gln	Gln	Pro	Thr	
		770					775					780					
	Ala	Asp	Gln	Phe	Leu	Asp	Asn	Ile	Ile	Ser	Ser	Gln	Lys	Val	Ser	Pro	
		785				790					795					800	
	Ser	Met	Ser	Ser	Asp	Ile	Thr	Arg	Gly	Ala	Ile	Trp	Ala	Val	Leu	Leu	
70					805					810					815		
	Ser	Met	Ile	Phe	Met	Ala	Ile	Tyr	Ile	Leu	Ile	Arg	Phe	Arg	Asp	Ile	
				820					825					830			
	Ser	Phe	Ser	Ala	Gly	Val	Phe	Val	Ser	Val	Ala	Ala	Thr	Thr	Phe	Cys	
		835						840					845				
75	Ile	Ile	Ala	Leu	Tyr	Ala	Leu	Leu	Trp	Lys	Ile	Leu	Pro	Phe	Thr	Met	
		850					855					860					

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Glu Ile Asp Gln Asn Phe Ile Ala Ala Ile Leu Ala Ile Ile Gly Tyr  
 865 870 875 880  
 Ser Leu Asn Asp Thr Val Val Val Phe Asp Arg Ile Arg Glu Thr Met  
 885 890 895  
 5 Lys Leu Tyr Pro Asn Arg Asp Arg Tyr Gln Val Ile Asn Asp Ala Leu  
 900 905 910  
 Asn Ser Thr Leu Gly Arg Thr Leu Asn Thr Ser Leu Thr Thr Phe Ile  
 915 920 925  
 10 Val Met Leu Val Ile Phe Ile Phe Gly Gly Ala Thr Met Arg Ser Phe  
 930 935 940  
 Thr Phe Ser Ile Leu Leu Gly Ile Val Ile Gly Thr Tyr Ser Thr Leu  
 945 950 955 960  
 Phe Val Ala Thr Pro Leu Ala Tyr Glu Ile Gln Lys Arg Lys Leu Asn  
 965 970 975  
 15 Lys Ala Ala Lys Lys  
 980

(2) INFORMATION FOR SEQ ID NO:424

- 20 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1017 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
 25 (ii) MOLECULE TYPE: protein  
 (iii) HYPOTHETICAL: YES  
 30 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Porphyromonas gingivalis  
 (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...1017  
 35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:424

Met Lys Arg Met Thr Leu Phe Phe Leu Cys Leu Leu Thr Ser Ile Gly  
 1 5 10 15  
 40 Trp Ala Met Ala Gln Asn Arg Thr Val Lys Gly Thr Val Ile Ser Ser  
 20 25 30  
 Glu Asp Asn Glu Pro Leu Ile Gly Ala Asn Val Val Val Gly Asn  
 35 40 45  
 45 Thr Thr Ile Gly Ala Ala Thr Asp Leu Asp Gly Asn Phe Thr Leu Ser  
 50 55 60  
 Val Pro Ala Asn Ala Lys Met Leu Arg Val Ser Tyr Ser Gly Met Thr  
 65 70 75 80  
 Thr Lys Glu Val Ala Ile Ala Asn Val Met Lys Ile Val Leu Asp Pro  
 85 90 95  
 50 Asp Ser Lys Val Leu Glu Gln Val Val Val Leu Gly Tyr Gly Thr Gly  
 100 105 110  
 Gln Lys Leu Ser Thr Val Ser Gly Ser Val Ala Lys Val Ser Ser Glu  
 115 120 125  
 55 Lys Leu Ala Glu Lys Pro Val Ala Asn Ile Met Asp Ala Leu Gln Gly  
 130 135 140  
 Gln Val Ala Gly Met Gln Val Met Thr Thr Ser Gly Asp Pro Thr Ala  
 145 150 155 160  
 Val Ala Ser Val Glu Ile His Gly Thr Gly Ser Leu Gly Ala Ser Ser  
 165 170 175  
 60 Ala Pro Leu Tyr Ile Val Asp Gly Met Gln Thr Ser Leu Asp Val Val  
 180 185 190  
 Ala Thr Met Asn Pro Asn Asp Phe Glu Ser Met Ser Val Leu Lys Asp  
 195 200 205  
 65 Ala Ser Ala Thr Ser Ile Tyr Gly Ala Arg Ala Ala Asn Gly Val Val  
 210 215 220  
 Phe Ile Gln Thr Lys Lys Gly Lys Met Ser Glu Arg Gly Arg Ile Thr  
 225 230 235 240  
 Phe Asn Ala Ser Tyr Gly Ile Ser Gln Ile Leu Asn Thr Lys Pro Leu  
 245 250 255  
 70 Asp Asn Met Met Thr Gly Asp Glu Leu Leu Asp Phe Gln Val Lys Ala  
 260 265 270  
 Gly Phe Trp Gly Asn Asn Gln Thr Val Gln Lys Val Lys Asp Met Ile  
 275 280 285  
 75 Leu Ala Gly Ala Glu Asp Leu Tyr Gly Asn Tyr Asp Ser Leu Lys Asp  
 290 295 300

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	Glu	Tyr	Gly	Lys	Thr	Leu	Phe	Pro	Val	Asp	Phe	Asn	His	Asp	Ala	Asp
	305					310					315					320
	Trp	Leu	Lys	Ala	Leu	Phe	Lys	Thr	Ala	Pro	Thr	Ser	Gln	Gly	Asp	Ile
					325					330						335
5	Ser	Phe	Ser	Gly	Gly	Ser	Gln	Gly	Thr	Ser	Tyr	Tyr	Ala	Ser	Ile	Gly
				340					345					350		
	Tyr	Phe	Asp	Gln	Glu	Gly	Met	Ala	Arg	Glu	Pro	Ala	Asn	Phe	Lys	Arg
			355					360					365			
10	Tyr	Ser	Gly	Arg	Leu	Asn	Phe	Glu	Ser	Arg	Ile	Asn	Glu	Trp	Leu	Lys
		370					375					380				
	Val	Gly	Ala	Asn	Leu	Ser	Gly	Ala	Ile	Ala	Asn	Arg	Arg	Ser	Ala	Asp
		385					390				395					400
	Tyr	Phe	Gly	Lys	Tyr	Met	Gly	Ser	Gly	Thr	Phe	Gly	Val	Leu	Thr	
				405					410					415		
15	Met	Pro	Arg	Tyr	Tyr	Asn	Pro	Phe	Asp	Val	Asn	Gly	Asp	Leu	Ala	Asp
				420					425					430		
	Val	Tyr	Tyr	Met	Tyr	Gly	Ala	Thr	Arg	Pro	Ser	Met	Thr	Glu	Pro	Tyr
				435				440					445			
20	Phe	Ala	Lys	Met	Arg	Pro	Phe	Ser	Ser	Glu	Ser	His	Gln	Ala	Asn	Val
		450					455					460				
	Asn	Gly	Phe	Ala	Gln	Ile	Thr	Pro	Ile	Lys	Gly	Leu	Thr	Leu	Lys	Ala
		465					470				475					480
	Gln	Ala	Gly	Val	Asp	Ile	Thr	Asn	Thr	Arg	Thr	Ser	Ser	Lys	Arg	Met
					485					490					495	
25	Pro	Asn	Asn	Pro	Tyr	Asp	Ser	Thr	Pro	Leu	Gly	Glu	Arg	Arg	Glu	Arg
				500					505					510		
	Ala	Tyr	Arg	Asp	Val	Ser	Lys	Ser	Phe	Thr	Asn	Thr	Ala	Glu	Tyr	Lys
			515					520					525			
30	Phe	Ser	Ile	Asp	Glu	Lys	His	Asp	Leu	Thr	Ala	Leu	Met	Gly	His	Glu
		530					535					540				
	Tyr	Ile	Glu	Tyr	Glu	Gly	Asp	Val	Ile	Gly	Ala	Ser	Ser	Lys	Gly	Phe
		545				550				555						560
	Glu	Ser	Asp	Lys	Leu	Met	Leu	Leu	Ser	Gln	Gly	Lys	Thr	Gly	Asn	Ser
					565					570					575	
35	Leu	Ser	Leu	Pro	Glu	His	Arg	Val	Ala	Glu	Tyr	Ala	Tyr	Leu	Ser	Phe
				580					585					590		
	Phe	Ser	Arg	Phe	Asn	Tyr	Gly	Phe	Asp	Lys	Trp	Met	Tyr	Ile	Asp	Phe
			595					600					605			
40	Ser	Val	Arg	Asn	Asp	Gln	Ser	Ser	Arg	Phe	Gly	Ser	Asn	Asn	Arg	Ser
						615							620			
	Ala	Trp	Phe	Tyr	Ser	Val	Gly	Gly	Met	Phe	Asp	Ile	Tyr	Asn	Lys	Phe
		625				630				635						640
	Ile	Gln	Glu	Ser	Asn	Trp	Leu	Ser	Asp	Leu	Arg	Leu	Lys	Met	Ser	Tyr
					645					650					655	
45	Gly	Thr	Thr	Gly	Asn	Ser	Glu	Ile	Gly	Asn	Tyr	Asn	His	Gln	Ala	Leu
				660					665					670		
	Val	Thr	Val	Asn	Asn	Tyr	Thr	Glu	Asp	Ala	Met	Gly	Leu	Ser	Ile	Ser
			675					680					685			
50	Thr	Ala	Gly	Asn	Pro	Asp	Leu	Ser	Trp	Glu	Lys	Gln	Ser	Gln	Phe	Asn
		690					695					700				
	Phe	Gly	Leu	Ala	Ala	Gly	Ala	Phe	Asn	Asn	Arg	Leu	Ser	Ala	Glu	Val
		705				710					715					720
	Asp	Phe	Tyr	Val	Arg	Thr	Thr	Asn	Asp	Met	Leu	Ile	Asp	Val	Pro	Met
					725					730					735	
55	Pro	Tyr	Ile	Ser	Gly	Phe	Phe	Ser	Gln	Tyr	Gln	Asn	Val	Gly	Ser	Met
			740						745					750		
	Lys	Asn	Thr	Gly	Val	Asp	Leu	Ser	Leu	Lys	Gly	Thr	Ile	Tyr	Gln	Asn
			755				760						765			
60	Lys	Asp	Trp	Asn	Val	Tyr	Ala	Ser	Ala	Asn	Phe	Asn	Tyr	Asn	Arg	Gln
		770					775					780				
	Glu	Ile	Thr	Lys	Leu	Phe	Phe	Gly	Leu	Asn	Lys	Tyr	Met	Leu	Pro	Asn
		785				790				795						800
	Thr	Gly	Thr	Ile	Trp	Glu	Ile	Gly	Tyr	Pro	Asn	Ser	Phe	Tyr	Met	Ala
					805					810					815	
65	Glu	Tyr	Ala	Gly	Ile	Asp	Lys	Lys	Thr	Gly	Lys	Gln	Leu	Trp	Tyr	Val
				820					825					830		
	Pro	Gly	Gln	Val	Asp	Ala	Asp	Gly	Asn	Lys	Val	Thr	Thr	Ser	Gln	Tyr
			835					840					845			
70	Ser	Ala	Asp	Leu	Glu	Thr	Arg	Ile	Asp	Lys	Ser	Val	Thr	Pro	Pro	Ile
		850					855					860				
	Thr	Gly	Gly	Phe	Ser	Leu	Gly	Ala	Ser	Trp	Lys	Gly	Leu	Ser	Leu	Asp
		865				870				875						880
	Ala	Asp	Phe	Ala	Tyr	Ile	Val	Gly	Lys	Trp	Met	Ile	Asn	Asn	Asp	Arg
					885					890					895	
75	Tyr	Phe	Thr	Glu	Asn	Ala	Gly	Gly	Leu	Met	Gln	Leu	Asn	Lys	Asp	Lys

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5 Met Leu Leu Asn Ala Trp Thr Glu Asp Asn Lys Glu Thr Asp Val Pro  
 900 905 910  
 Lys Leu Gly Gln Ser Pro Gln Phe Asp Thr His Leu Glu Asn Ala  
 915 920 925  
 Ser Phe Leu Arg Leu Lys Asn Leu Lys Leu Thr Tyr Val Leu Pro Asn  
 930 935 940  
 Ser Leu Phe Ala Gly Gln Asn Val Ile Gly Gly Ala Arg Val Tyr Leu  
 945 950 955 960  
 10 Met Ala Arg Asn Leu Leu Thr Val Thr Lys Tyr Lys Gly Phe Asp Pro  
 965 970 975  
 Glu Ala Gly Asn Val Gly Lys Asn Gln Tyr Pro Asn Ser Lys Gln  
 980 985 990  
 Tyr Val Ala Gly Ile Gln Leu Ser Phe  
 995 1000 1005  
 15 1010 1015

(2) INFORMATION FOR SEQ ID NO:425

20 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1014 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
 25 (ii) MOLECULE TYPE: protein  
 (iii) HYPOTHETICAL: YES  
 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Porphyromonas gingivalis  
 30 (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...1014  
 35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:425

Met Thr Leu Phe Phe Leu Cys Leu Leu Thr Ser Ile Gly Trp Ala Met  
 1 5 10 15  
 40 Ala Gln Asn Arg Thr Val Lys Gly Thr Val Ile Ser Ser Glu Asp Asn  
 20 25 30  
 Glu Pro Leu Ile Gly Ala Asn Val Val Val Val Gly Asn Thr Thr Ile  
 35 40 45  
 Gly Ala Ala Thr Asp Leu Asp Gly Asn Phe Thr Leu Ser Val Pro Ala  
 50 55  
 Asn Ala Lys Met Leu Arg Val Ser Tyr Ser Gly Met Thr Thr Lys Glu  
 60 65 70 75 80  
 Val Ala Ile Ala Asn Val Met Lys Ile Val Leu Asp Pro Asp Ser Lys  
 85 90 95  
 50 Val Leu Glu Gln Val Val Val Leu Gly Tyr Gly Thr Gly Gln Lys Leu  
 100 105 110  
 Ser Thr Val Ser Gly Ser Val Ala Lys Val Ser Ser Glu Lys Leu Ala  
 115 120 125  
 Glu Lys Pro Val Ala Asn Ile Met Asp Ala Leu Gln Gly Gln Val Ala  
 130 135 140  
 55 Gly Met Gln Val Met Thr Thr Ser Gly Asp Pro Thr Ala Val Ala Ser  
 145 150 155 160  
 Val Glu Ile His Gly Thr Gly Ser Leu Gly Ala Ser Ser Ala Pro Leu  
 165 170 175  
 60 Tyr Ile Val Asp Gly Met Gln Thr Ser Leu Asp Val Val Ala Thr Met  
 180 185 190  
 Asn Pro Asn Asp Phe Glu Ser Met Ser Val Leu Lys Asp Ala Ser Ala  
 195 200 205  
 Thr Ser Ile Tyr Gly Ala Arg Ala Ala Asn Gly Val Val Phe Ile Gln  
 210 215 220  
 65 Thr Lys Lys Gly Lys Met Ser Glu Arg Gly Arg Ile Thr Phe Asn Ala  
 225 230 235 240  
 Ser Tyr Gly Ile Ser Gln Ile Leu Asn Thr Lys Pro Leu Asp Asn Met  
 245 250 255  
 70 Met Thr Gly Asp Glu Leu Leu Asp Phe Gln Val Lys Ala Gly Phe Trp  
 260 265 270  
 Gly Asn Asn Gln Thr Val Gln Lys Val Lys Asp Met Ile Leu Ala Gly  
 275 280 285  
 Ala Glu Asp Leu Tyr Gly Asn Tyr Asp Ser Leu Lys Asp Glu Tyr Gly  
 290 295 300  
 75 Lys Thr Leu Phe Pro Val Asp Phe Asn His Asp Ala Asp Trp Leu Lys

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5	305					310					315					320
	Ala	Leu	Phe	Lys	Thr	Ala	Pro	Thr	Ser	Gln	Gly	Asp	Ile	Ser	Phe	Ser
					325					330					335	
	Gly	Gly	Ser	Gln	Gly	Thr	Ser	Tyr	Tyr	Ala	Ser	Ile	Gly	Tyr	Phe	Asp
10				340					345					350		
	Gln	Glu	Gly	Met	Ala	Arg	Glu	Pro	Ala	Asn	Phe	Lys	Arg	Tyr	Ser	Gly
			355					360					365			
	Arg	Leu	Asn	Phe	Glu	Ser	Arg	Ile	Asn	Glu	Trp	Leu	Lys	Val	Gly	Ala
15			370				375					380				
	Asn	Leu	Ser	Gly	Ala	Ile	Ala	Asn	Arg	Arg	Ser	Ala	Asp	Tyr	Phe	Gly
			385				390				395					400
	Lys	Tyr	Tyr	Met	Gly	Ser	Gly	Thr	Phe	Gly	Val	Leu	Thr	Met	Pro	Arg
20				405						410					415	
	Tyr	Tyr	Asn	Pro	Phe	Asp	Val	Asn	Gly	Asp	Leu	Ala	Asp	Val	Tyr	Tyr
			420						425					430		
	Met	Tyr	Gly	Ala	Thr	Arg	Pro	Ser	Met	Thr	Glu	Pro	Tyr	Phe	Ala	Lys
25				435					440					445		
	Met	Arg	Pro	Phe	Ser	Ser	Glu	Ser	His	Gln	Ala	Asn	Val	Asn	Gly	Phe
			450				455					460				
	Ala	Gln	Ile	Thr	Pro	Ile	Lys	Gly	Leu	Thr	Leu	Lys	Ala	Gln	Ala	Gly
30				465			470				475					480
	Val	Asp	Ile	Thr	Asn	Thr	Arg	Thr	Ser	Ser	Lys	Arg	Met	Pro	Asn	Asn
				485					490						495	
	Pro	Tyr	Asp	Ser	Thr	Pro	Leu	Gly	Glu	Arg	Arg	Glu	Arg	Ala	Tyr	Arg
35				500					505					510		
	Asp	Val	Ser	Lys	Ser	Phe	Thr	Asn	Thr	Ala	Glu	Tyr	Lys	Phe	Ser	Ile
			515					520					525			
	Asp	Glu	Lys	His	Asp	Leu	Thr	Ala	Leu	Met	Gly	His	Glu	Tyr	Ile	Glu
40				530			535					540				
	Tyr	Glu	Gly	Asp	Val	Ile	Gly	Ala	Ser	Ser	Lys	Gly	Phe	Glu	Ser	Asp
				545			550				555					560
	Lys	Leu	Met	Leu	Leu	Ser	Gln	Gly	Lys	Thr	Gly	Asn	Ser	Leu	Ser	Leu
45				565						570					575	
	Pro	Glu	His	Arg	Val	Ala	Glu	Tyr	Ala	Tyr	Leu	Ser	Phe	Phe	Ser	Arg
				580					585					590		
	Phe	Asn	Tyr	Gly	Phe	Asp	Lys	Trp	Met	Tyr	Ile	Asp	Phe	Ser	Val	Arg
50				595					600					605		
	Asn	Asp	Gln	Ser	Ser	Arg	Phe	Gly	Ser	Asn	Asn	Arg	Ser	Ala	Trp	Phe
			610				615					620				
	Tyr	Ser	Val	Gly	Gly	Met	Phe	Asp	Ile	Tyr	Asn	Lys	Phe	Ile	Gln	Glu
55				625			630				635					640
	Ser	Asn	Trp	Leu	Ser	Asp	Leu	Arg	Leu	Lys	Met	Ser	Tyr	Gly	Thr	Thr
				645						650					655	
	Gly	Asn	Ser	Glu	Ile	Gly	Asn	Tyr	Asn	His	Gln	Ala	Leu	Val	Thr	Val
60				660						665					670	
	Asn	Asn	Tyr	Thr	Glu	Asp	Ala	Met	Gly	Leu	Ser	Ile	Ser	Thr	Ala	Gly
				675					680				685			
	Asn	Pro	Asp	Leu	Ser	Trp	Glu	Lys	Gln	Ser	Gln	Phe	Asn	Phe	Gly	Leu
65				690			695					700				
	Ala	Ala	Gly	Ala	Phe	Asn	Asn	Arg	Leu	Ser	Ala	Glu	Val	Asp	Phe	Tyr
				705			710				715					720
	Val	Arg	Thr	Thr	Asn	Asp	Met	Leu	Ile	Asp	Val	Pro	Met	Pro	Tyr	Ile
70				725						730					735	
	Ser	Gly	Phe	Phe	Ser	Gln	Tyr	Gln	Asn	Val	Gly	Ser	Met	Lys	Asn	Thr
				740					745					750		
	Gly	Val	Asp	Leu	Ser	Leu	Lys	Gly	Thr	Ile	Tyr	Gln	Asn	Lys	Asp	Trp
75				755					760					765		
	Asn	Val	Tyr	Ala	Ser	Ala	Asn	Phe	Asn	Tyr	Asn	Arg	Gln	Glu	Ile	Thr
				770			775					780				
	Lys	Leu	Phe	Phe	Gly	Leu	Asn	Lys	Tyr	Met	Leu	Pro	Asn	Thr	Gly	Thr
80				785			790				795					800
	Ile	Trp	Glu	Ile	Gly	Tyr	Pro	Asn	Ser	Phe	Tyr	Met	Ala	Glu	Tyr	Ala
				805						810					815	
	Gly	Ile	Asp	Lys	Lys	Thr	Gly	Lys	Gln	Leu	Trp	Tyr	Val	Pro	Gly	Gln
85				820					825					830		
	Val	Asp	Ala	Asp	Gly	Asn	Lys	Val	Thr	Thr	Ser	Gln	Tyr	Ser	Ala	Asp
				835					840					845		
	Leu	Glu	Thr	Arg	Ile	Asp	Lys	Ser	Val	Thr	Pro	Pro	Ile	Thr	Gly	Gly
90				850			855					860				
	Phe	Ser	Leu	Gly	Ala	Ser	Trp	Lys	Gly	Leu	Ser	Leu	Asp	Ala	Asp	Phe
				865			870				875					880
	Ala	Tyr	Ile	Val	Gly	Lys	Trp	Met	Ile	Asn	Asn	Asp	Arg	Tyr	Phe	Thr
95				885						890					895	
	Glu	Asn	Ala	Gly	Gly	Leu	Met	Gln	Leu	Asn	Lys	Asp	Lys	Met	Leu	Leu
				900						905				910		

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Asn Ala Trp Thr Glu Asp Asn Lys Glu Thr Asp Val Pro Lys Leu Gly  
                   915                  920                  925  
 Gln Ser Pro Gln Phe Asp Thr His Leu Leu Glu Asn Ala Ser Phe Leu  
                   930                  935                  940  
 5 Arg Leu Lys Asn Leu Lys Leu Thr Tyr Val Leu Pro Asn Ser Leu Phe  
    945                  950                  955                  960  
 Ala Gly Gln Asn Val Ile Gly Gly Ala Arg Val Tyr Leu Met Ala Arg  
                   965                  970                  975  
 10 Asn Leu Leu Thr Val Thr Lys Tyr Lys Gly Phe Asp Pro Glu Ala Gly  
                   980                  985                  990  
 Gly Asn Val Gly Lys Asn Gln Tyr Pro Asn Ser Lys Gln Tyr Val Ala  
                   995                  1000                  1005  
 Gly Ile Gln Leu Ser Phe  
                   1010  
 15  
 (2) INFORMATION FOR SEQ ID NO:426  
     (i) SEQUENCE CHARACTERISTICS:  
         (A) LENGTH: 821 amino acids  
         (B) TYPE: amino acid  
         (D) TOPOLOGY: linear  
 20  
     (ii) MOLECULE TYPE: protein  
 25  
     (iii) HYPOTHETICAL: YES  
     (vi) ORIGINAL SOURCE:  
         (A) ORGANISM: Porphyromonas gingivalis  
 30  
     (ix) FEATURE:  
         (A) NAME/KEY: misc\_feature  
         (B) LOCATION 1...821  
 35  
     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:426  
 Met Lys Lys Lys Asn Phe Leu Leu Leu Gly Ile Phe Val Ala Leu Leu  
   1                  5                  10                  15  
 Thr Phe Ile Gly Ser Met Gln Ala Gln Gln Ala Lys Asp Tyr Phe Asn  
                   20                  25                  30  
 40 Phe Asp Glu Arg Gly Glu Ala Tyr Phe Ser Phe Lys Val Pro Asp Arg  
    35                  40                  45  
 Ala Val Leu Gln Glu Leu Ala Leu Ile Met Ser Ile Asp Glu Phe Asp  
    50                  55                  60  
 45 Pro Val Thr Asn Glu Ala Ile Ala Tyr Ala Ser Glu Glu Glu Phe Glu  
    65                  70                  75                  80  
 Ala Phe Leu Arg Tyr Gly Leu Lys Pro Thr Phe Leu Thr Pro Pro Ser  
                   85                  90                  95  
 Met Gln Arg Ala Val Glu Met Phe Asp Tyr Arg Ser Gly Glu Lys Tyr  
                   100                  105                  110  
 50 Glu Trp Asn Ala Tyr Pro Thr Tyr Glu Ala Tyr Ile Ser Met Met Glu  
                   115                  120                  125  
 Glu Phe Gln Thr Lys Tyr Pro Ser Leu Cys Thr Thr Ser Val Ile Gly  
                   130                  135                  140  
 55 Lys Ser Val Lys Asp Arg Lys Leu Met Ile Cys Lys Leu Thr Ser Ser  
    145                  150                  155                  160  
 Ala Asn Thr Gly Lys Lys Pro Arg Val Leu Tyr Thr Ser Thr Met His  
                   165                  170                  175  
 Gly Asp Glu Thr Thr Gly Tyr Val Val Leu Leu Arg Leu Ile Asp His  
                   180                  185                  190  
 60 Leu Leu Ser Asn Tyr Glu Ser Asp Pro Arg Ile Lys Asn Ile Leu Asp  
                   195                  200                  205  
 Lys Thr Glu Val Trp Ile Cys Pro Leu Thr Asn Pro Asp Gly Ala Tyr  
                   210                  215                  220  
 65 Arg Ala Gly Asn His Thr Val Gln Gly Ala Thr Arg Tyr Asn Ala Asn  
    225                  230                  235                  240  
 Asn Val Asp Leu Asn Arg Asn Phe Lys Asp Asp Val Ala Gly Asp His  
                   245                  250                  255  
 Pro Asp Gly Lys Pro Trp Gln Pro Glu Ala Thr Ala Phe Met Asp Leu  
                   260                  265                  270  
 70 Glu Gly Asn Thr Ser Phe Val Leu Gly Ala Asn Ile His Gly Gly Thr  
                   275                  280                  285  
 Glu Val Val Asn Tyr Pro Trp Asp Asn Lys Lys Glu Arg His Ala Asp  
                   290                  295                  300  
 75 Asp Glu Trp Tyr Lys Leu Ile Ser Arg Asn Tyr Ala Ala Ala Cys Gln  
    305                  310                  315                  320

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Ser Ile Ser Ala Ser Tyr Met Thr Ser Glu Thr Asn Ser Gly Ile Ile  
 325 330 335  
 Asn Gly Ser Asp Trp Tyr Val Ile Arg Gly Ser Arg Gln Asp Asn Ala  
 340 345 350  
 5 Asn Tyr Phe His Arg Leu Arg Glu Ile Thr Leu Glu Ile Ser Asn Thr  
 355 360 365  
 Lys Leu Val Pro Ala Ser Gln Leu Pro Lys Tyr Trp Asn Leu Asn Lys  
 370 375 380  
 10 Glu Ser Leu Leu Ala Leu Ile Glu Glu Ser Leu Tyr Gly Ile His Gly  
 385 390 395 400  
 Thr Val Thr Ser Ala Ala Asn Gly Gln Pro Leu Lys Cys Gln Ile Leu  
 405 410 415  
 Ile Glu Asn His Asp Lys Arg Asn Ser Asp Val Tyr Ser Asp Ala Thr  
 420 425 430  
 15 Thr Gly Tyr Tyr Val Arg Pro Ile Lys Ala Gly Thr Tyr Thr Val Lys  
 435 440 445  
 Tyr Lys Ala Glu Gly Tyr Pro Glu Ala Thr Arg Thr Ile Thr Lys  
 450 455 460  
 20 Asp Lys Glu Thr Val Ile Met Asp Ile Ala Leu Gly Asn Ser Val Pro  
 465 470 475 480  
 Leu Pro Val Pro Asp Phe Thr Ala Ser Pro Met Thr Ile Ser Val Gly  
 485 490 495  
 Glu Ser Val Gln Phe Gln Asp Gln Thr Thr Asn Asn Pro Thr Asn Trp  
 500 505 510  
 25 Glu Trp Thr Phe Glu Gly Gly Gln Pro Ala Met Ser Thr Glu Gln Asn  
 515 520 525  
 Pro Leu Val Ser Tyr Ser His Pro Gly Gln Tyr Asp Val Thr Leu Lys  
 530 535 540  
 30 Val Trp Asn Ala Ser Gly Ser Asn Thr Ile Thr Lys Glu Lys Phe Ile  
 545 550 555 560  
 Thr Val Asn Ala Val Met Pro Val Ala Glu Phe Val Gly Thr Pro Thr  
 565 570 575  
 Glu Ile Glu Glu Gly Gln Thr Val Ser Phe Gln Asn Gln Ser Thr Asn  
 580 585 590  
 35 Ala Thr Asn Tyr Val Trp Ile Phe Asp Gly Gly Thr Pro Ala Thr Ser  
 595 600 605  
 Glu Asp Glu Asn Pro Thr Val Leu Tyr Ser Lys Ala Gly Gln Tyr Asp  
 610 615 620  
 40 Val Thr Leu Lys Ala Ile Ser Ala Ser Gly Glu Thr Val Lys Thr Lys  
 625 630 635 640  
 Glu Lys Tyr Ile Thr Val Lys Lys Ala Pro Val Pro Ala Pro Val Ala  
 645 650 655  
 Asp Phe Glu Gly Thr Pro Arg Lys Val Lys Lys Gly Glu Thr Val Thr  
 660 665 670  
 45 Phe Lys Asp Leu Ser Thr Asn Asn Pro Thr Ser Trp Leu Trp Val Phe  
 675 680 685  
 Glu Gly Gly Ser Pro Ala Thr Ser Thr Glu Gln Asn Pro Val Val Thr  
 690 695 700  
 50 Tyr Asn Glu Thr Gly Lys Tyr Asp Val Gln Leu Thr Ala Thr Asn Glu  
 705 710 715 720  
 Gly Gly Ser Asn Val Lys Lys Ala Glu Asp Tyr Ile Glu Val Ile Leu  
 725 730 735  
 Asp Asp Ser Val Glu Asp Ile Val Ala Gln Thr Gly Ile Val Ile Arg  
 740 745 750  
 55 Pro Gln Asn Gly Thr Lys Gln Ile Leu Ile Glu Ala Asn Ala Ala Ile  
 755 760 765  
 Lys Ala Ile Val Leu Tyr Asp Ile Asn Gly Arg Val Val Leu Lys Thr  
 770 775 780  
 60 Thr Pro Asn Gln Leu Arg Ser Thr Val Asp Leu Ser Ile Leu Pro Glu  
 785 790 795 800  
 Gly Ile Tyr Thr Ile Asn Ile Lys Thr Glu Lys Ser Ala Arg Thr Glu  
 805 810 815  
 Lys Ile His Ile Gly  
 820

(2) INFORMATION FOR SEQ ID NO:427

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 76 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

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(vi) ORIGINAL SOURCE:  
(A) ORGANISM: Porphyromonas gingivalis

5 (ix) FEATURE:  
(A) NAME/KEY: misc\_feature  
(B) LOCATION 1...76

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:427

10 Met Arg Leu Ile Lys Ala Phe Leu Val Gln Leu Leu Leu Leu Pro Ile  
1 5 10 15  
Phe Phe Tyr Lys Arg Phe Ile Ser Pro Leu Thr Pro Pro Ser Cys Arg  
20 25 30  
15 Phe Thr Pro Ser Cys Ser Ser Tyr Ala Ile Glu Ala Leu Arg Lys Tyr  
35 40 45  
Gly Pro Gly Lys Gly Leu Leu Leu Ser Ile Lys Arg Ile Leu Arg Cys  
50 55 60  
20 His Pro Trp Gly Gly Ser Gly Tyr Asp Pro Val Pro  
65 70 75

(2) INFORMATION FOR SEQ ID NO:428

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 859 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

30 (iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:  
(A) ORGANISM: Porphyromonas gingivalis

35 (ix) FEATURE:  
(A) NAME/KEY: misc\_feature  
(B) LOCATION 1...859

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:428

Met Ala Tyr Asp Phe Thr Gln Thr Phe Arg Asn Ser Leu Glu Tyr Ser  
1 5 10 15  
Tyr Gln Glu Ala Thr Arg Leu Gly Val Val Ala Val Thr Gln Asp Met  
20 25 30  
45 Leu Val Leu Gly Ile Ile Arg Asp Gly Asp Asn Gly Ala Ile Asp Ile  
35 40 45  
Met Arg His Tyr Gly Ile Asn Leu Tyr Glu Leu Lys Arg Leu Ile Glu  
50 55 60  
50 Leu Glu Ala Ile Ala Glu Ser Leu Pro Ala Ser Pro Glu Gly Ser Pro  
65 70 75 80  
Ile Phe Thr Pro Ser Ala Arg Glu Ala Ile Asp Asp Ala Thr Asp Ile  
85 90 95  
55 Cys Ala Asp Met Glu Asp Glu Ala Val Ser Pro Val His Leu Leu Leu  
100 105 110  
Ser Ile Leu Asn Ser Thr Gln Glu Ser Leu Val Gln Lys Ile Phe Met  
115 120 125  
Lys Gln Gly Ile Lys Tyr Asp Thr Ile Leu Ser Asp Tyr Phe Gly Gln  
130 135 140  
60 Arg Asn Pro Ser Glu Gly Lys Ser Pro Ser Glu Met Glu Ile Leu Asp  
145 150 155 160  
Gly Tyr Gln Asp Asn Asp Phe Asp Asp Glu Glu Asp Glu Ser Ser Pro  
165 170 175  
65 Pro Ser Gly Asn Ser Gly Thr Gly Gly Ser Gly Asp Ala Pro Glu  
180 185 190  
Gln Asn Thr Gly Gly Gly Asp Thr Thr Thr Thr Thr Arg Ser Gly Gly  
195 200 205  
Asp Thr Pro Ala Leu Asp Thr Phe Gly Thr Asp Ile Thr Ala Met Ala  
210 215 220  
70 Ala Ala Gly Lys Leu Asp Pro Val Val Gly Arg Glu Gln Glu Ile Glu  
225 230 235 240  
Arg Val Ile Gln Ile Leu Ser Arg Arg Lys Lys Asn Asn Pro Val Leu  
245 250 255  
Ile Gly Glu Pro Gly Val Gly Lys Ser Ala Ile Val Glu Gly Leu Ala  
260 265 270

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	Glu	Arg	Ile	Val	Asn	Arg	Lys	Val	Ser	Arg	Ile	Leu	Phe	Asp	Lys	Arg
			275					280					285			
	Ile	Ile	Ser	Leu	Asp	Leu	Ala	Gln	Met	Val	Ala	Gly	Thr	Lys	Tyr	Arg
			290					295				300				
5	Gly	Gln	Phe	Glu	Glu	Arg	Leu	Lys	Ala	Val	Leu	Asp	Glu	Leu	Lys	Lys
			305			310					315				320	
	Asn	Pro	Gln	Ile	Ile	Leu	Phe	Ile	Asp	Glu	Ile	His	Thr	Ile	Val	Gly
				325					330					335		
10	Ala	Gly	Ser	Ala	Ala	Gly	Ser	Met	Asp	Thr	Ala	Asn	Met	Leu	Lys	Pro
				340					345					350		
	Ala	Leu	Ala	Arg	Gly	Gln	Val	Gln	Cys	Ile	Gly	Ala	Thr	Thr	Leu	Asp
			355					360					365			
	Glu	Tyr	Arg	Lys	Asn	Ile	Glu	Lys	Asp	Gly	Ala	Leu	Glu	Arg	Arg	Phe
			370			375						380				
15	Gln	Lys	Val	Pro	Ile	Ala	Pro	Ser	Thr	Ala	Glu	Glu	Thr	Leu	Thr	Ile
			385			390					395					400
	Leu	Gln	Asn	Ile	Lys	Glu	Lys	Tyr	Glu	Asp	Tyr	His	Gly	Val	Arg	Tyr
				405					410					415		
20	Thr	Asp	Glu	Ala	Ile	Lys	Ala	Ala	Val	Glu	Leu	Thr	Asp	Arg	Tyr	Val
				420					425					430		
	Ser	Asp	Arg	Phe	Phe	Pro	Asp	Lys	Ala	Ile	Asp	Ala	Met	Asp	Glu	Ala
			435					440					445			
	Gly	Ala	Ser	Val	His	Ile	Thr	Asn	Val	Val	Ala	Pro	Lys	Glu	Ile	Glu
			450				455					460				
25	Ile	Leu	Glu	Ala	Glu	Leu	Ala	Ser	Val	Arg	Glu	Asn	Lys	Leu	Ser	Ala
			465			470					475					480
	Val	Lys	Ala	Gln	Asn	Tyr	Glu	Leu	Ala	Ala	Ser	Phe	Arg	Asp	Gln	Glu
				485					490					495		
30	Arg	Arg	Thr	Gln	Gln	Gln	Ile	Ala	Glu	Glu	Lys	Lys	Lys	Trp	Glu	Glu
				500					505					510		
	Gln	Met	Ser	Lys	His	Arg	Glu	Thr	Val	Asp	Glu	Asn	Val	Val	Ala	His
			515					520					525			
	Val	Val	Ala	Leu	Met	Thr	Gly	Val	Pro	Ala	Glu	Arg	Leu	Ser	Thr	Gly
			530				535					540				
35	Glu	Gly	Glu	Arg	Leu	Arg	Thr	Met	Ala	Asp	Asp	Leu	Lys	Thr	Lys	Val
			545			550				555						560
	Val	Gly	Gln	Asp	Thr	Ala	Ile	Glu	Lys	Met	Val	His	Ala	Ile	Gln	Arg
				565					570					575		
40	Asn	Arg	Leu	Gly	Leu	Arg	Asn	Glu	Lys	Lys	Pro	Ile	Gly	Ser	Phe	Leu
				580					585					590		
	Phe	Leu	Gly	Pro	Thr	Gly	Val	Gly	Lys	Thr	Tyr	Leu	Ala	Lys	Lys	Leu
			595					600					605			
	Ala	Glu	Tyr	Leu	Phe	Glu	Asp	Glu	Asn	Ala	Met	Ile	Arg	Val	Asp	Met
			610			615						620				
45	Ser	Glu	Tyr	Met	Glu	Lys	Phe	Ser	Val	Ser	Arg	Leu	Val	Gly	Ala	Pro
			625			630					635					640
	Pro	Gly	Tyr	Val	Gly	Tyr	Glu	Glu	Gly	Gly	Gln	Leu	Thr	Glu	Arg	Val
				645					650					655		
50	Arg	Arg	Lys	Pro	Tyr	Ser	Val	Val	Leu	Leu	Asp	Glu	Ile	Glu	Lys	Ala
				660					665					670		
	His	Ala	Asp	Val	Phe	Asn	Leu	Leu	Leu	Gln	Val	Met	Asp	Glu	Gly	Gln
			675				680					685				
	Leu	Thr	Asp	Ser	Leu	Gly	Arg	Arg	Val	Asn	Phe	Lys	Asn	Thr	Val	Ile
			690				695					700				
55	Ile	Ile	Thr	Ser	Asn	Val	Gly	Thr	Arg	Gln	Leu	Lys	Asp	Phe	Gly	Gln
			705			710					715					720
	Gly	Ile	Gly	Phe	Arg	Ser	Glu	Lys	Asp	Glu	Glu	Ala	Asn	Lys	Glu	His
				725						730				735		
60	Ser	Arg	Ser	Val	Ile	Gln	Lys	Ala	Leu	Asn	Lys	Thr	Phe	Ser	Pro	Glu
				740					745					750		
	Phe	Leu	Asn	Arg	Leu	Asp	Asp	Ile	Ile	Leu	Phe	Asp	Gln	Leu	Gly	Lys
			755					760					765			
	Thr	Glu	Ile	Arg	Arg	Met	Val	Asp	Ile	Glu	Leu	Lys	Ala	Val	Leu	Ala
			770				775					780				
65	Arg	Ile	His	Arg	Ala	Gly	Tyr	Asp	Leu	Val	Leu	Thr	Asp	Glu	Ala	Lys
			785			790					795					800
	Asp	Val	Ile	Ala	Thr	Lys	Gly	Tyr	Asp	Leu	Gln	Tyr	Gly	Ala	Arg	Pro
				805					810					815		
70	Leu	Lys	Arg	Thr	Leu	Gln	Asn	Glu	Val	Glu	Asp	Arg	Leu	Thr	Asp	Leu
				820					825					830		
	Ile	Leu	Ser	Gly	Gln	Ile	Glu	Lys	Gly	Gln	Thr	Leu	Thr	Leu	Ser	Ala
			835					840					845			
75	Arg	Asp	Gly	Glu	Ile	Ile	Val	Gln	Glu	Gln	Ala					
			850				855									

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## (2) INFORMATION FOR SEQ ID NO:429

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 417 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

(A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...417

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:429

Met Asn Tyr Leu Tyr Ile Leu Ile Thr Leu Leu Leu Ser Gly Phe Phe  
 1 5 10 15  
 Ser Gly Ala Glu Ile Ala Phe Leu Ser Ser Asp Lys Leu Arg Leu Glu  
 20 25 30  
 Leu Asp Arg Asn Arg Gly Asp Leu Thr Gly Arg Ala Leu Asn Leu Leu  
 35 40 45  
 Tyr Arg His Pro Asp Gln Leu Val Thr Thr Leu Leu Val Gly Asn Asn  
 50 55 60  
 Ile Val Leu Val Val Tyr Gly Leu Leu Met Ala Gly Leu Leu Ala Ala  
 65 70 75 80  
 Pro Leu Ala Gln Trp Ile Asp Asn Asp Ala Met Ile Val Val Leu Gln  
 85 90 95  
 Ser Val Leu Ser Thr Ile Ile Ile Leu Phe Thr Gly Glu Phe Leu Pro  
 100 105 110  
 Lys Ala Ile Phe Lys Thr Asn Ala Asn Met Met Met Arg Val Phe Ala  
 115 120 125  
 Leu Pro Ile Val Ala Ile Tyr Tyr Leu Leu Tyr Pro Leu Ser Lys Leu  
 130 135 140  
 Phe Thr Gly Leu Ser Arg Ser Phe Ile Arg Leu Val Asp Lys Asn Tyr  
 145 150 155 160  
 Val Pro Thr Thr Val Gly Leu Gly Arg Val Asp Leu Asp His Tyr Leu  
 165 170 175  
 Ala Glu Asn Met Ser Gly Glu Asn Glu Gln Asn Asp Leu Thr Thr Glu  
 180 185 190  
 Val Lys Ile Ile Gln Asn Ala Leu Asp Phe Ser Gly Ile Gln Val Arg  
 195 200 205  
 Asp Cys Met Ile Pro Arg Asn Glu Met Ile Ala Cys Glu Leu Gln Thr  
 210 215 220  
 Asp Ile Glu Val Leu Lys Thr Thr Phe Ile Asp Thr Gly Leu Ser Lys  
 225 230 235 240  
 Ile Ile Ile Tyr Arg Gln Asn Ile Asp Asp Val Val Gly Tyr Ile His  
 245 250 255  
 Ser Ser Glu Met Phe Arg Gly Gln Asp Trp Gln Lys Arg Ile Asn Thr  
 260 265 270  
 Thr Val Phe Val Pro Glu Ser Met Tyr Ala Asn Lys Leu Met Arg Leu  
 275 280 285  
 Leu Met Gln Arg Lys Lys Ser Ile Ala Ile Val Ile Asp Glu Leu Gly  
 290 295 300  
 Gly Thr Ala Gly Met Val Thr Leu Glu Asp Leu Val Glu Glu Ile Phe  
 305 310 315 320  
 Gly Asp Ile Glu Asp Glu His Asp Thr Arg Lys Ile Ile Ala Lys Gln  
 325 330 335  
 Leu Gly Pro His Thr Tyr Leu Val Ser Gly Arg Met Glu Ile Asp Asp  
 340 345 350  
 Val Asn Glu Arg Phe Gly Leu Ser Leu Pro Glu Ser Asp Asp Tyr Leu  
 355 360 365  
 Thr Val Ala Gly Phe Ile Leu Asn Ser His Gln Asn Ile Pro Gln Ala  
 370 375 380  
 Asn Glu Val Val Glu Ile Ala Pro Tyr Thr Phe Thr Ile Leu Arg Ser  
 385 390 395 400  
 Ser Ser Thr Lys Ile Glu Leu Val Lys Met Ser Ile Asp Asp Gln Ser  
 405 410 415  
 Asn

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## (2) INFORMATION FOR SEQ ID NO:430

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 293 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Porphyromonas gingivalis
- (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION: 1...293
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:430

Met Lys Gln Asn Tyr Phe Lys Arg Val Cys Ser Leu Leu Trp Leu Val  
 1 5 10 15  
 Leu Pro Met Leu Ile Met Pro Leu Glu Val Ala Ala Gln Glu Ile Ile  
 20 25 30  
 Pro Asn Glu Glu Val Leu Glu Ser Leu Thr Phe Val Ala Pro Val Glu  
 35 40 45  
 Glu Thr Asp Ala Ile Glu Ala Glu Val Glu Ala Leu Gln Glu Ile Val  
 50 55 60  
 Ala Thr Glu Glu Ile Ala Glu Gln Ala Val Arg Ser Tyr Thr Tyr Thr  
 65 70 75 80  
 Val Tyr Arg Asp Gly Val Lys Ile Ala Ser Gly Leu Thr Glu Pro Thr  
 85 90 95  
 Phe Leu Asp Glu Asp Val Pro Ala Gly Glu His Thr Tyr Cys Val Glu  
 100 105 110  
 Val Gln Tyr Gln Gly Gly Val Ser Asp Lys Val Cys Val Asp Val Glu  
 115 120 125  
 Val Lys Asp Phe Lys Pro Val Thr Asn Leu Thr Gly Thr Ala Ser Asn  
 130 135 140  
 Asp Glu Val Ser Leu Asp Trp Asp Gly Val Glu Glu Lys Ala Glu Glu  
 145 150 155 160  
 Pro Ala Ser Asp Lys Ala Val Ser Tyr Asn Val Tyr Lys Asn Gly Thr  
 165 170 175  
 Leu Ile Gly Asn Thr Ala Glu Thr His Tyr Val Glu Thr Gly Val Ala  
 180 185 190  
 Asn Gly Thr Tyr Ile Tyr Glu Val Glu Val Lys Tyr Pro Asp Gly Val  
 195 200 205  
 Ser Pro Lys Val Ala Val Thr Val Thr Val Thr Asn Ser Ser Leu Ser  
 210 215 220  
 Asn Val Asp Gly Gln Ala Pro Tyr Thr Leu Arg Val Glu Gly Lys Lys  
 225 230 235 240  
 Ile Ile Ala Glu Ala His Gly Met Ile Thr Leu Tyr Asp Ile Asn Gly  
 245 250 255  
 Arg Thr Val Ala Val Ala Pro Asn Arg Leu Glu Tyr Met Ala Gln Thr  
 260 265 270  
 Gly Phe Tyr Ala Val Arg Phe Asp Val Gly Asn Lys His His Val Ser  
 275 280 285  
 Lys Ile Gln Val Arg  
 290

## 60 (2) INFORMATION FOR SEQ ID NO:431

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 312 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Porphyromonas gingivalis
- (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature

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(B) LOCATION 1...312

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:431

5 Met Ile Pro Leu Ser Glu Ser Phe Glu Ser Gly Ile Pro Ala Ile Trp  
 1 5 10 15  
 Lys Thr Ile Asp Ala Asp Gly Asp Gly Tyr Asn Trp Met His Leu Thr  
 20 25 30  
 10 Asn Phe Thr Gly Gln Ser Gly Leu Cys Val Ser Ser Ala Ser Tyr Ile  
 35 40 45  
 Gly Gly Val Gly Ala Leu Thr Pro Asp Asn Tyr Leu Ile Thr Pro Glu  
 50 55 60  
 Leu Lys Leu Pro Thr Asp Ala Leu Val Glu Ile Ile Tyr Trp Val Cys  
 65 70 75 80  
 15 Thr Gln Asp Leu Thr Ala Pro Ser Glu His Tyr Ala Val Tyr Ser Ser  
 85 90 95  
 Ser Thr Gly Asn Asn Ala Ala Asp Phe Val Asn Leu Leu Tyr Glu Glu  
 100 105 110  
 20 Thr Leu Thr Ala Lys Arg Ile Gln Ser Pro Glu Leu Ile Arg Gly Asn  
 115 120 125  
 Arg Thr Gln Gly Val Trp Tyr Gln Arg Lys Val Val Leu Pro Asn Asp  
 130 135 140  
 Thr Lys Tyr Val Ala Phe Arg His Phe Asn Ser Thr Asp Asn Phe Trp  
 145 150 155 160  
 25 Leu Asn Leu Asp Glu Val Ser Ile Leu Tyr Thr Pro Leu Pro Arg Arg  
 165 170 175  
 Ala Pro Cys Pro His Pro Gly Gly Tyr Thr Tyr Ser Val Phe Arg Asp  
 180 185 190  
 30 Gly Gln Lys Ile Ala Ser Gly Leu Ser Ala Leu Ala Tyr Ile Asp Thr  
 195 200 205  
 Asp Val Pro Tyr Gly Thr Gln Asp Tyr Cys Val Gln Val Asn Tyr Leu  
 210 215 220  
 Gln Gly Asp Ser Tyr Lys Val Cys Lys Asn Ile Val Val Ala Asn Ser  
 225 230 235 240  
 35 Ala Asn Ile Tyr Gly Ala Asp Lys Pro Phe Ala Leu Thr Val Val Gly  
 245 250 255  
 Lys Thr Ile Val Ala Ser Ala Phe Lys Gly Glu Ile Thr Leu Tyr Asp  
 260 265 270  
 40 Ile Arg Gly Arg Leu Ile Ala Ser Gly Cys Asp Thr Leu Arg Tyr Lys  
 275 280 285  
 Ala Glu Asn Gly Phe Tyr Leu Ile Lys Ile Gln Val Asn Gly Thr Val  
 290 295 300  
 Tyr Thr Glu Lys Ile Gln Ile Gln  
 305 310

(2) INFORMATION FOR SEQ ID NO:432

(i) SEQUENCE CHARACTERISTICS:  
 50 (A) LENGTH: 843 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
 (ii) MOLECULE TYPE: protein  
 55 (iii) HYPOTHETICAL: YES  
 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Porphyromonas gingivalis  
 60 (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION: 1...843

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:432

65 Met Lys Lys Ser Phe Leu Leu Ala Ile Val Met Leu Phe Gly Ile Ala  
 1 5 10 15  
 Met Gln Gly His Ser Ala Pro Val Thr Lys Glu Arg Ala Leu Ser Leu  
 20 25 30  
 70 Ala Arg Leu Ala Leu Arg Gln Val Ser Leu Arg Met Gly Gln Thr Ala  
 35 40 45  
 Val Ser Asp Lys Ile Ser Ile Asp Tyr Val Tyr Arg Gln Gly Asp Ala  
 50 55 60  
 75 Glu Arg Gly Ile Thr Ser Gln Glu Glu Gly Ser Pro Ala Tyr Phe Tyr  
 65 70 75 80

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	Val	Ala	Asn	Arg	Gly	Asn	Asn	Glu	Gly	Tyr	Ala	Leu	Val	Ala	Ala	Asp
				85						90					95	
	Asp	Arg	Ile	Pro	Thr	Ile	Leu	Ala	Tyr	Ser	Pro	Ile	Gly	Arg	Phe	Asp
				100					105					110		
5	Met	Asp	Ser	Met	Pro	Asp	Asn	Leu	Arg	Met	Trp	Leu	Gln	Ile	Tyr	Asp
			115					120					125			
	Gln	Glu	Ile	Gly	Leu	Ile	Leu	Ser	Gly	Lys	Ala	Gln	Leu	Asn	Glu	Glu
			130				135					140				
10	Ile	Leu	Arg	Thr	Glu	Gly	Val	Pro	Ala	Glu	Val	His	Ala	Leu	Met	Asp
					145		150				155					160
	Asn	Gly	His	Phe	Ala	Asn	Asp	Pro	Met	Arg	Trp	Asn	Gln	Gly	Tyr	Pro
					165					170					175	
	Trp	Asn	Asn	Lys	Glu	Pro	Leu	Leu	Pro	Asn	Gly	Asn	His	Ala	Tyr	Thr
				180					185					190		
15	Gly	Cys	Val	Ala	Thr	Ala	Ala	Ala	Gln	Ile	Met	Arg	Tyr	His	Ser	Trp
			195					200					205			
	Pro	Leu	Gln	Gly	Glu	Gly	Ser	Phe	Asp	Tyr	His	Ala	Gly	Ser	Leu	Val
			210				215					220				
20	Gly	Asn	Trp	Ser	Gly	Thr	Phe	Gly	Glu	Met	Tyr	Asp	Trp	Ile	Asn	Met
					225		230				235					240
	Pro	Gly	Asn	Pro	Asp	Leu	Asp	Asn	Leu	Thr	Gln	Ser	Gln	Val	Asp	Ala
					245				250						255	
	Tyr	Ala	Thr	Leu	Met	Arg	Asp	Val	Ser	Ala	Ser	Val	Ser	Met	Ser	Phe
				260					265					270		
25	Tyr	Glu	Asn	Gly	Ser	Gly	Thr	Tyr	Ser	Val	Tyr	Val	Val	Gly	Ala	Leu
			275					280					285			
	Arg	Asn	Asn	Phe	Arg	Tyr	Lys	Arg	Ser	Leu	Gln	Leu	His	Val	Arg	Ala
			290				295					300				
30	Leu	Tyr	Thr	Ser	Gln	Glu	Trp	His	Asp	Met	Ile	Arg	Gly	Glu	Leu	Ala
					305		310				315					320
	Ser	Gly	Arg	Pro	Val	Tyr	Tyr	Ala	Gly	Asn	Asn	Gln	Ser	Ile	Gly	His
					325				330					335		
	Ala	Phe	Val	Cys	Asp	Gly	Tyr	Ala	Ser	Asp	Gly	Thr	Phe	His	Phe	Asn
				340					345					350		
35	Trp	Gly	Trp	Gly	Gly	Val	Ser	Asn	Gly	Phe	Tyr	Lys	Leu	Thr	Leu	Leu
				355				360					365			
	Ser	Pro	Thr	Ser	Leu	Gly	Ile	Gly	Gly	Glu	Gly	Ile	Gly	Phe	Thr	Ile
				370			375					380				
40	Tyr	Gln	Glu	Ile	Ile	Thr	Gly	Ile	Glu	Pro	Ala	Lys	Thr	Pro	Ala	Glu
					385		390				395					400
	Ala	Gly	Thr	Asp	Ala	Leu	Pro	Ile	Leu	Ala	Leu	Lys	Asp	Ile	Glu	Ala
					405				410					415		
	Glu	Tyr	Lys	Ser	Glu	Ser	Gly	Leu	Asn	Val	Gly	Tyr	Ser	Ile	Tyr	Asn
				420				425					430			
45	Thr	Gly	Glu	Glu	Gln	Ser	Asn	Leu	Asp	Leu	Gly	Tyr	Arg	Leu	Asn	Lys
			435					440					445			
	Ala	Asp	Gly	Glu	Val	Ile	Glu	Val	Lys	Thr	Ser	Ser	Ile	Asn	Ile	Ser
			450				455					460				
50	Trp	Tyr	Gly	Tyr	Gly	Glu	His	Pro	Glu	Ser	Phe	Ser	Leu	Ala	Pro	Asn
					465		470				475					480
	Gln	Leu	Ser	Gln	Gly	Ile	Asn	Thr	Ile	Thr	Leu	Leu	Tyr	Arg	Arg	Thr
					485					490					495	
	Gly	Thr	Glu	Gln	Trp	Glu	Pro	Val	Arg	His	Ala	Gln	Gly	Gly	Tyr	Val
				500				505					510			
55	Asn	Ser	Ile	Lys	Val	Asn	Thr	Thr	Asp	Pro	Asn	Asn	Val	Val	Val	Thr
			515					520					525			
	Val	Asp	Asn	Asn	Glu	Gly	Lys	Leu	Ser	Ile	Val	Pro	Asn	Ser	Phe	Val
				530			535					540				
60	Ala	Asp	Leu	Asn	Ser	Tyr	Glu	His	Ser	Thr	Ile	Thr	Val	Gln	Phe	Asn
					545		550				555					560
	Ser	Asp	Ser	Pro	Asp	Glu	Ile	Arg	Thr	Pro	Val	Ala	Phe	Ala	Leu	Ser
					565					570				575		
	Thr	Gly	Ala	Thr	Ala	Asp	Asp	Val	Ile	Ser	Leu	Gly	Trp	Val	Met	Ala
				580				585						590		
65	Glu	Val	Pro	Gly	Gly	Ser	Ser	Asn	Tyr	Pro	Val	Val	Trp	Ser	Lys	Asp
				595				600					605			
	Val	Leu	Thr	Leu	Ser	Glu	Gly	Asp	Tyr	Thr	Leu	Trp	Tyr	Arg	Phe	Ser
				610			615					620				
70	Ile	Asn	Asn	Gln	Lys	Asp	Glu	Trp	Lys	Lys	Ile	Gly	Ser	Val	Ser	Val
					625		630				635					640
	Lys	Thr	Pro	Thr	Glu	Tyr	Thr	His	Pro	Leu	Phe	Glu	Val	Gly	His	Asn
					645					650					655	
	Gln	Thr	Ser	Thr	Tyr	Thr	Leu	Asp	Met	Ala	His	Asn	Arg	Val	Leu	Pro
					660				665					670		
75	Asp	Phe	Thr	Leu	Lys	Asn	Leu	Gly	Leu	Pro	Phe	Asn	Gly	Glu	Leu	Val

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5 Val Val Phe Arg Gln Thr Gln Ser Ser Ser Gly Ser Leu Trp Ala Ala  
 675 690 695 700  
 Gln Glu Thr Val His Ile Lys Gln Gly Glu Thr Phe Val Tyr Lys Pro  
 705 710 715 720  
 Val Val Glu Gly Pro Ile Pro Asp Gly Ser Tyr Arg Ala Thr Leu His  
 725 730 735  
 Ala Phe Val Asn Gly Gln Gln Gln Tyr Leu Lys Gly Lys Arg Asn  
 740 745 750  
 10 Tyr Thr Val Lys Ile Val Asn Gly Thr Ala Val Glu Ala Ile Glu Ser  
 755 760 765  
 Ser Glu Glu Ile Arg Val Phe Pro Asn Pro Ala Arg Asp Tyr Val Glu  
 770 775 780  
 15 Ile Ser Ala Pro Cys Ile Pro Gln Glu Thr Ser Ile Ile Leu Phe Asp  
 785 790 795 800  
 Leu Ser Gly Lys Ile Val Met Lys Asn Ser Leu Ser Ala Gly His Gly  
 805 810 815  
 Arg Met Asp Val Ser Arg Leu Pro Asn Gly Ala Tyr Ile Leu Lys Val  
 820 825 830  
 20 Asp Gly Tyr Thr Thr Lys Ile Asn Ile Val His  
 835 840

(2) INFORMATION FOR SEQ ID NO:433

25 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 290 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
 30 (ii) MOLECULE TYPE: protein  
 (iii) HYPOTHETICAL: YES  
 (vi) ORIGINAL SOURCE:  
 35 (A) ORGANISM: Porphyromonas gingivalis  
 (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...290  
 40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:433

Met Lys Lys Leu Phe Leu Ser Leu Thr Ser Leu Val Met Val Phe Ala  
 1 5 10 15  
 45 Val Ala Ser Cys Asp Ile Ile Asp Lys Asp Gln Thr Leu Leu Pro Ala  
 20 25 30  
 Pro Thr Asn Val Thr Pro Asp Asn Pro Asp Asp Asn Pro Ser Glu Ile  
 35 40 45  
 50 Asp Ile Thr Gln Thr His Thr Glu Lys Tyr Val Leu Ala Glu Glu Phe  
 50 55 60  
 Thr Gly Gln Lys Cys Leu Asn Cys Pro Lys Gly His Arg Lys Leu Ala  
 65 70 75 80  
 Ala Leu Lys Glu Gln Tyr Gly Lys Arg Leu Thr Val Val Gly Ile His  
 85 90 95  
 55 Ala Gly Pro Gly Ser Leu Val Pro Pro Leu Phe Arg Thr Glu Ala Gly  
 100 105 110  
 Asp Ala Tyr Tyr Ser Lys Phe Ala Asn Asn Thr Pro Leu Pro Ala Leu  
 115 120 125  
 60 Met Val Ser Arg Lys Lys Phe Gly Ser Ser Tyr Val Tyr Asp Lys Ser  
 130 135 140  
 Tyr Lys Thr Trp Asp Val Pro Ile Ala Glu Gln Met Glu Gln Lys Ala  
 145 150 155 160  
 Lys Ile Asn Ile Phe Ala Val Ala Glu Tyr Thr Asp Thr Gln Lys Ile  
 165 170 175  
 65 Lys Val Thr Val Lys Gly Lys Ile Leu Glu Gly Asn Thr Leu Pro Lys  
 180 185 190  
 Ser Met Val Gln Val Tyr Leu Leu Glu Asp Lys Leu Ile Ala Pro Gln  
 195 200 205  
 70 Val Asp Gly Asn Thr Thr Val Glu Asn Tyr Glu His Asn His Val Leu  
 210 215 220  
 Arg Gly Ala Val Asn Gly Ile Trp Gly Glu Glu Phe Val Asn Leu Lys  
 225 230 235 240  
 Asp Tyr Leu Tyr Thr Tyr Ala Val Glu Pro Leu Ser Gly Met Ser Phe  
 245 250 255  
 75 Val Ala Glu Asn Tyr Ser Ile Val Ala Phe Val Tyr Asp Val Gln Thr

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Phe Glu Val Tyr Asp Val Val His Val Lys Ile Asn Pro Gln Ser Asp  
260 265 270  
Gly Lys  
275 280 285

5

(2) INFORMATION FOR SEQ ID NO: 434

10

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 223 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

15

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(71) ORIGINAL SOURCE:

20

(A) ORGANISM: *Porphyromonas gingivalis*

(ix) FEATURE:

(A) NAME/KEY: misc\_feature  
(B) LOCATION 1...223

25

(ri) SEQUENCE DESCRIPTION: SEQ ID NO:434

30

Met	Lys	Lys	Ser	Ser	Val	Val	Ala	Ser	Val	Leu	Ala	Val	Ala	Leu	Val
1			5						10					15	
Phe	Ala	Gly	Cys	Gly	Leu	Asn	Asn	Met	Ala	Lys	Gly	Gly	Leu	Ile	Gly
		20						25					30		
Ala	Gly	Val	Gly	Gly	Ala	Ile	Gly	Ala	Gly	Val	Gly	Asn	Val	Ala	Gly
		35					40					45			
Asn	Thr	Ala	Val	Gly	Ala	Ile	Val	Gly	Thr	Ala	Val	Gly	Gly	Ala	Ala
	50					55					60				
Gly	Ala	Leu	Ile	Gly	Lys	Lys	Met	Asp	Lys	Gln	Lys	Lys	Glu	Leu	Glu
65				70						75				80	
Ala	Ala	Val	Pro	Asp	Ala	Thr	Ile	Gln	Thr	Val	Asn	Asp	Gly	Glu	Ala
			85					90					95		
Ile	Leu	Val	Thr	Phe	Asp	Ser	Gly	Ile	Leu	Phe	Ala	Thr	Asn	Ser	Ser
		100						105					110		
Thr	Leu	Ser	Pro	Asn	Ser	Arg	Thr	Ala	Leu	Thr	Lys	Phe	Ala	Ala	Asn
		115					120					125			
Met	Asn	Lys	Asn	Pro	Asp	Thr	Asp	Ile	Arg	Ile	Val	Lys	His	Thr	Asp
	130					135					140				
Asn	Thr	Gly	Ser	Asp	Lys	Ile	Asn	Asp	Pro	Leu	Ser	Glu	Arg	Arg	Ala
145					150					155				160	
Ala	Ser	Val	Tyr	Ser	Phe	Leu	Asn	Ser	Gln	Gly	Val	Ser	Met	Ser	Arg
				165					170					175	
Met	Ala	Ala	Glu	Gly	Arg	Gly	Ser	His	Glu	Pro	Val	Ala	Asp	Asn	Ser
		180						185					190		
Thr	Val	Ala	Gly	Arg	Ser	Ala	Asn	Arg	Arg	Val	Glu	Val	Tyr	Ile	Leu
	195						200					205			
Pro	Asn	Ala	Lys	Met	Ile	Glu	Gln	Ala	Gln	Gln	Gly	Thr	Leu	Lys	
	210					215					220				

55

(2) INFORMATION FOR SEQ ID NO: 435

60

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 337 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

65

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Porphyromonas gingivalis

70

(ix) FEATURE:

(A) NAME/KEY: misc\_feature  
(B) LOCATION 1...337

75

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:435

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```

Met Ser Lys Lys Ser Ile Leu Leu Leu Cys Cys Ser Leu Cys Phe Ile
1      5      10      15
Ser Ala Thr Lys Ala Val Thr Pro Val Arg Asn Val Arg Asn Ser Gln
20      25      30
5 Val Asn Ser Lys Ala Lys Thr Glu Arg Thr Lys Pro Ser Asp Ser Val
35      40      45
Arg Tyr Ile Ser Asn Met Ile Ala Asp Arg Leu Glu Phe Arg Asn Lys
50      55      60
10 Ile Ser Ser Glu Lys Glu Val Arg Lys Ala Glu Tyr Glu Asn Arg Leu
65      70      75      80
Ala Met Glu Ala Leu Asn Tyr Pro Ala Ile Asp Leu Tyr Gly Glu Asp
85      90      95
Ser Trp Ser Glu Tyr Val Asn Pro Phe Val Gly Ala Gly Thr Asp Val
100      105      110
15 Glu Ile Pro Asn Ser Tyr Asp Ile Asp Cys Ser Ser Phe Val Met Pro
115      120      125
Val Glu Asp Lys Gln Val Thr Ser Gln Phe Gly Tyr Arg Arg Arg Phe
130      135      140
20 Gly Arg Met His Tyr Gly Ile Asp Leu Ser Val Asn Arg Gly Asp Thr
145      150      155      160
Ile Arg Ala Ala Phe Asp Gly Lys Val Arg Val Arg Ser Tyr Glu Ala
165      170      175
Arg Gly Tyr Gly Tyr Tyr Ile Val Leu Arg His Pro Asn Gly Leu Glu
180      185      190
25 Thr Val Tyr Gly His Met Ser Arg Gln Leu Val Asp Glu Asn Gln Ile
195      200      205
Val Arg Ala Gly Gln Pro Ile Gly Leu Gly Gly Ser Thr Gly Arg Ser
210      215      220
30 Thr Gly Pro His Leu His Phe Glu Thr Arg Phe Met Gly Ile Pro Ile
225      230      235      240
Asn Pro Ser Thr Ile Asp Phe Asp Asn Gly Val Pro Leu Arg Asp
245      250      255
Ile Tyr Thr Phe Lys Arg Gly Ser Asn Ser Arg Tyr Ala Lys Ala Ser
260      265      270
35 Lys Thr Ser Ser Arg Tyr Ala Lys Lys Gly Lys Lys Gly Arg Gln Ala
275      280      285
Ser Ser Pro Met Thr Tyr Arg Ile Lys Lys Gly Asp Thr Leu Glu Thr
290      295      300
40 Ile Ala Lys Arg His Gly Thr Ser Val Gln Lys Leu Cys Ala Thr Asn
305      310      315      320
Gly Ile Gly Lys Ser Lys Ile Leu Thr Pro Gly Lys Ala Leu Arg Ile
325      330      335
Lys

```

45

(2) INFORMATION FOR SEQ ID NO:436

```

50 (i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 151 amino acids
    (B) TYPE: amino acid
    (D) TOPOLOGY: linear

```

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

```

55 (vi) ORIGINAL SOURCE:
    (A) ORGANISM: Porphyromonas gingivalis

```

```

60 (ix) FEATURE:
    (A) NAME/KEY: misc_feature
    (B) LOCATION: 1...151

```

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:436

```

65 Met Ala Lys Ile Asn Phe Tyr Ala Glu Gly Val Ser Leu Pro Arg Ile
1      5      10      15
Arg Arg Arg Ile Val Gly Lys Trp Ile Ala Glu Val Cys Ser Arg Tyr
20      25      30
70 Gly Lys Ala Val Gly Glu Ile Ser Tyr Leu Phe Cys Asp Asp Glu Tyr
35      40      45
Ile Leu Lys Ala Asn Gln Glu Phe Leu Asp His Asp Tyr Tyr Thr Asp
50      55      60
75 Ile Ile Thr Phe Asp Ser Cys Glu Ala Asp Thr Val Asn Gly Asp Leu
65      70      75      80

```

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[illegible]

(2) INFORMATION FOR SEQ ID NO: 437

15 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 391 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) Hypothetical: YES

(vi) ORIGINAL SOURCE:  
(A) ORGANISM: Porphyromonas gingivalis

```
(ix) FEATURE:
      (A) NAME/KEY: misc_feature
      (B) LOCATION 1...391
```

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:437

35	Met 1	Lys	Val	Lys 5	Tyr	Leu	Met	Leu	Thr	Leu	Val	Gly	Ala	Ile	Ala	Leu
	Asn	Ala	Ser	Ala 20	Gln	Glu	Asn	Thr	Val	Pro	Ala	Thr	Gly	Gln	Leu	Pro
	Ala	Lys	Asn	Val	Ala	Phe	Ala	Arg	Asn	Lys	Ala	Gly	Ser	Asn	Trp	Phe
	Val	Thr	Leu	Gln	Gly	Gly	Val	Ala	Ala	Gln	Phe	Leu	Asn	Asp	Asn	Asn
40	Asn 65	Lys	Asp	Leu	Met	Asp	Arg	Leu	Gly	Ala	Ile	Gly	Ser	Leu	Ser	Val
	Gly	Lys	Tyr	His 85	Ser	Pro	Phe	Phe	Ala	Thr	Arg	Leu	Gln	Ile	Asn	Gly
45	Gly	Gln	Ala	His 100	Thr	Phe	Leu	Gly	Lys 105	Asn	Gly	Glu	Gln	Glu	Ile	Asn
	Thr	Asn	Phe	Gly	Ala	Ala	His	Phe	Asp	Phe	Met	Phe	Asp	Val	Val	Asn
	Tyr	Phe	Ala	Pro	Tyr	Arg	Glu	Asn	Arg	Phe	Phe	His	Leu	Ile	Pro	Trp
	Val	Gly	Val	Gly	Tyr	Gln	His	Lys	Phe	Ile	Gly	Ser	Glu	Trp	Ser	Lys
50	Asp	Asn	Val	Glu	Ser	Leu	Thr	Ala	Asn	Val	Gly	Val	Met	Met	Ala	Phe
	Arg	Leu	Gly	Lys 180	Arg	Val	Asp	Phe	Val	Ile	Glu	Ala	Gln	Ala	Ala	His
55	Ser	Asn	Leu	Asn	Leu	Ser	Arg	Ala	Tyr	Asn	Ala	Lys	Lys	Thr	Pro	Val
	Phe	Glu	Asp	Pro	Ala	Gly	Arg	Tyr	Tyr	Asn	Gly	Phe	Gln	Gly	Met	Ala
60	Thr	Ala	Gly	Leu	Asn	Phe	Arg	Leu	Gly	Ala	Val	Gly	Phe	Asn	Ala	Ile
	Unk	Pro	Met	Asp	Tyr	Ala	Leu	Ile	Asn	Asp	Leu	Asn	Gly	Gln	Ile	Asn
65	Arg	Leu	Arg	Ser	Glu	Val	Glu	Glu	Leu	Ser	Lys	Arg	Pro	Val	Ser	Cys
	Pro	Glu	Cys	Pro	Glu	Val	Thr	Pro	Val	Thr	Lys	Thr	Glu	Asn	Ile	Leu
70	Thr	Glu	Lys	Ala	Val	Leu	Phe	Arg	Phe	Asp	Ser	His	Val	Val	Asp	Lys
	Asp	Gln	Leu	Ile	Asn	Leu	Tyr	Asp	Val	Ala	Gln	Phe	Val	Lys	Glu	Thr
75	Asn	Glu	Pro	Ile	Thr	Val	Val	Gly	Tyr	Ala	Asp	Pro	Thr	Gly	Asn	Thr
	Gln	Tyr	Asn	Glu	Lys	Leu	Ser	Glu	Arg	Arg	Ala	Lys	Ala	Val	Val	Asp

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Val Leu Thr Gly Lys Tyr Gly Val Pro Ser Glu Leu Ile Ser Val Glu  
 355 360 365  
 Trp Lys Gly Asp Ser Thr Gln Pro Phe Ser Lys Lys Ala Trp Asn Arg  
 370 375 380  
 5 Val Val Ile Val Arg Ser Lys  
 385 390

(2) INFORMATION FOR SEQ ID NO:438

10 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 385 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

15 (ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

20 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...385

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:438

Met Thr Tyr Arg Ile Met Lys Ala Lys Ser Leu Leu Leu Ala Leu Ala  
 1 5 10 15  
 30 Gly Leu Ala Cys Thr Phe Ser Ala Thr Ala Gln Glu Ala Thr Thr Gln  
 20 25 30  
 Asn Lys Ala Gly Met His Thr Ala Phe Gln Arg Asp Lys Ala Ser Asp  
 35 40 45  
 35 His Trp Phe Ile Asp Ile Ala Gly Gly Ala Gly Met Ala Leu Ser Gly  
 50 55 60  
 Trp Asn Asn Asp Val Asp Phe Val Asp Arg Leu Ser Ile Val Pro Thr  
 65 70 75 80  
 Phe Gly Ile Gly Lys Trp His Glu Pro Tyr Phe Gly Thr Arg Leu Gln  
 85 90 95  
 40 Phe Thr Gly Phe Asp Ile Tyr Gly Phe Pro Gln Gly Ser Lys Glu Arg  
 100 105 110  
 Asn His Asn Tyr Phe Gly Asn Ala His Leu Asp Phe Met Phe Asp Leu  
 115 120 125  
 45 Thr Asn Tyr Phe Gly Val Tyr Arg Pro Asn Arg Val Phe His Ile Ile  
 130 135 140  
 Pro Trp Ala Gly Ile Gly Phe Gly Tyr Lys Phe His Ser Glu Asn Ala  
 145 150 155 160  
 Asn Gly Glu Lys Val Gly Ser Lys Asp Asp Met Thr Gly Thr Val Asn  
 165 170 175  
 50 Val Gly Leu Met Leu Lys Phe Arg Leu Ser Arg Val Val Asp Phe Asn  
 180 185 190  
 Ile Glu Gly Gln Ala Phe Ala Gly Lys Met Asn Phe Ile Gly Thr Lys  
 195 200 205  
 55 Arg Gly Lys Ala Asp Phe Pro Val Met Ala Thr Ala Gly Leu Thr Phe  
 210 215 220  
 Asn Leu Gly Lys Thr Glu Trp Thr Glu Ile Val Pro Met Asp Tyr Ala  
 225 230 235 240  
 Leu Val Asn Asp Leu Asn Asn Gln Ile Asn Ser Leu Arg Gly Gln Val  
 245 250 255  
 60 Glu Glu Leu Ser Arg Arg Pro Val Ser Cys Pro Glu Cys Pro Glu Pro  
 260 265 270  
 Thr Gln Pro Thr Val Thr Arg Val Val Val Asp Asn Val Val Tyr Phe  
 275 280 285  
 65 Arg Ile Asn Ser Ala Lys Ile Asp Arg Asn Gln Glu Ile Asn Val Tyr  
 290 295 300  
 Asn Thr Ala Glu Tyr Ala Lys Thr Asn Asn Ala Pro Ile Lys Val Val  
 305 310 315 320  
 Gly Tyr Ala Asp Glu Lys Thr Gly Thr Ala Ala Tyr Asn Met Lys Leu  
 325 330 335  
 70 Ser Glu Arg Arg Ala Lys Ala Val Ala Lys Met Leu Glu Lys Tyr Gly  
 340 345 350  
 Val Ser Ala Asp Arg Ile Thr Ile Glu Trp Lys Gly Ser Ser Glu Gln  
 355 360 365  
 75 Ile Tyr Glu Glu Asn Ala Trp Asn Arg Ile Val Val Met Thr Ala Ala  
 370 375 380

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Glu  
385

- 5 (2) INFORMATION FOR SEQ ID NO:439
- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 190 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear
- 10 (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- 15 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Porphyromonas gingivalis
- (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...190
- 20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:439

25 Met Glu Phe Phe Met Leu Phe Ile Ala Ala Val Phe Val Asn Asn Val  
 1 5 10 15  
 Val Leu Ser Gln Phe Leu Gly Ile Cys Pro Phe Leu Gly Val Ser Lys  
 20 25 30  
 Lys Val Asp Thr Ser Ile Gly Met Gly Ala Ala Val Thr Phe Val Leu  
 35 40 45  
 Ala Leu Ala Thr Leu Val Thr Phe Leu Ile Gln Lys Phe Val Leu Asp  
 50 55 60  
 Arg Phe Gly Leu Gly Phe Met Gln Thr Ile Ala Phe Ile Leu Val Ile  
 65 70 75 80  
 Ala Ala Leu Val Gln Met Val Glu Ile Ile Leu Lys Lys Val Ser Pro  
 85 90 95  
 Pro Leu Tyr Gln Ala Leu Gly Val Phe Leu Pro Leu Ile Thr Thr Asn  
 100 105 110  
 Cys Cys Val Leu Gly Val Ala Ile Leu Val Ile Gln Lys Asp Tyr Thr  
 115 120 125  
 40 Leu Leu Gln Ser Phe Val Tyr Ala Ile Ser Thr Ala Ile Gly Phe Thr  
 130 135 140  
 Leu Ala Met Val Thr Phe Ala Gly Ile Arg Glu Gln Leu Asp Met Thr  
 145 150 155 160  
 Asn Leu Pro Lys Ala Met Lys Gly Ile Pro Ser Ala Leu Leu Ala Ala  
 165 170 175  
 45 Gly Ile Leu Ala Met Ala Phe Met Gly Phe Ser Gly Ile Ala  
 180 185 190

- 50 (2) INFORMATION FOR SEQ ID NO:440
- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 186 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear
- 55 (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- 60 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Porphyromonas gingivalis
- (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...186
- 65

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:440

70 Met Leu Phe Ile Ala Ala Val Phe Val Asn Asn Val Val Leu Ser Gln  
 1 5 10 15  
 Phe Leu Gly Ile Cys Pro Phe Leu Gly Val Ser Lys Lys Val Asp Thr  
 20 25 30  
 Ser Ile Gly Met Gly Ala Ala Val Thr Phe Val Leu Ala Leu Ala Thr  
 35 40 45  
 75 Leu Val Thr Phe Leu Ile Gln Lys Phe Val Leu Asp Arg Phe Gly Leu

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```

      50      55      60
Gly Phe Met Gln Thr Ile Ala Phe Ile Leu Val Ile Ala Ala Leu Val
65      70      75      80
Gln Met Val Glu Ile Ile Leu Lys Lys Val Ser Pro Pro Leu Tyr Gln
5      85      90      95
Ala Leu Gly Val Phe Leu Pro Leu Ile Thr Thr Asn Cys Cys Val Leu
100      105      110
Gly Val Ala Ile Leu Val Ile Gln Lys Asp Tyr Thr Leu Leu Gln Ser
115      120      125
Phe Val Tyr Ala Ile Ser Thr Ala Ile Gly Phe Thr Leu Ala Met Val
130      135      140
Thr Phe Ala Gly Ile Arg Glu Gln Leu Asp Met Thr Asn Leu Pro Lys
145      150      155      160
Ala Met Lys Gly Ile Pro Ser Ala Leu Leu Ala Ala Gly Ile Leu Ala
15      165      170      175
Met Ala Phe Met Gly Phe Ser Gly Ile Ala
180      185

```

(2) INFORMATION FOR SEQ ID NO:441

20

```

(i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 833 amino acids
    (B) TYPE: amino acid
    (D) TOPOLOGY: linear

```

25

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

30

```

(vi) ORIGINAL SOURCE:
    (A) ORGANISM: Porphyromonas gingivalis

```

35

```

(ix) FEATURE:
    (A) NAME/KEY: misc_feature
    (B) LOCATION: 1...833

```

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:441

```

40      Met Lys Gln Leu Asn Ile Ile Ser Phe Ile Ile Ala Phe Leu Phe Leu
      1      5      10      15
      Gly Thr Ser Ala Ser Ala Gln Gln Ser Gly Gly Ser Val Thr Gly Thr
      20      25      30
      Val Val Asp Lys Ser Ser Lys Glu Pro Ile Ala Tyr Val Gln Val Phe
      35      40      45
45      Val Lys Gly Thr Thr Leu Gly Thr Ser Thr Asp Ala Asn Gly Asn Tyr
      50      55      60
      Ser Ile Lys Gly Ile Pro Ser Gly Asn Gln Thr Ile Val Ala Arg Leu
      65      70      75      80
      Met Gly Tyr Ser Thr Cys Glu Glu Lys Val His Ile Glu Lys Gly Gly
      85      90      95
50      Ser Arg His Val Asp Leu Tyr Leu Thr Glu Glu Ile Leu Ser Leu Asp
      100      105      110
      Gly Val Val Val Ser Ala Asn Arg Asn Glu Thr Phe Arg Arg Gln Ala
      115      120      125
55      Pro Ser Leu Val Thr Val Leu Ser Pro Glu Leu Phe Leu Lys Thr Asn
      130      135      140
      Ser Thr Asn Leu Ser Gln Gly Leu Lys Phe Gln Pro Gly Leu Arg Val
      145      150      155      160
60      Glu Asp Asn Cys Gln Asn Cys Gly Phe Asn Gln Val Arg Ile Asn Gly
      165      170      175
      Leu Glu Gly Ala Tyr Ser Gln Ile Leu Ile Asp Ser His Pro Ile Phe
      180      185      190
      Ser Ser Leu Ala Gly Val Tyr Gly Leu Glu Gln Met Pro Ala Asn Met
      195      200      205
65      Ile Glu Arg Val Glu Val Ile Arg Gly Gly Gly Ser Ala Leu Phe Gly
      210      215      220
      Ser Asn Ala Val Gly Gly Val Ile Asn Val Ile Thr Lys Glu Pro Leu
      225      230      235      240
70      Arg Asn Ser Ala Glu Ile Ser His Ser Thr Met Thr Phe Asp His Ala
      245      250      255
      Lys Gly Trp Gly Ser Phe Gln Asn Thr Thr Gln Phe Asn Gly Ser Met
      260      265      270
      Leu Thr Glu Asp Arg Lys Ala Gly Val Met Val Phe Gly Gln His Asn
      275      280      285
75      Tyr Arg Pro Gly Gln Asp Ile Asp Gly Asp Asn Phe Thr Glu Leu Pro

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290  
 Asn Leu Arg Asn Arg Ser Leu Gly Phe Arg Ser Tyr Tyr Lys Thr Gly  
 305  
 310  
 315  
 320  
 5 Leu Tyr Ser Lys Ala Thr Leu Glu Tyr His Ser Met Gln Glu Tyr Arg  
 325  
 330  
 335  
 Arg Gly Gly Asp Arg Leu Asp Asn Pro Pro Phe Glu Ala Gln Ile Ala  
 340  
 345  
 350  
 Glu Tyr Leu Gln His Tyr Ile Asn Gly Gly Ser Phe Lys Phe Asp Gln  
 355  
 360  
 365  
 10 Gly Phe Ser Gly Gly Lys Asp Phe Phe Ser Leu Tyr Ala Ser Ala Gln  
 370  
 375  
 380  
 Asp Val Gln Arg Arg Ser Tyr Tyr Gly Gly Gly Asp Tyr Thr Glu Asn  
 385  
 390  
 395  
 400  
 15 Leu Leu Asn Gly Ala Val Gln Ser Gly Ser Thr Glu Ser Asp Glu Tyr  
 405  
 410  
 415  
 Asn Asp Ala Phe Thr Ala Leu Thr Ser Tyr Gly Thr Thr Lys Gly Phe  
 420  
 425  
 430  
 Asp Leu Gln Gly Gly Gly Met Tyr Arg His Thr Phe Gly Glu Asn Trp  
 435  
 440  
 445  
 20 Asp Phe Thr Gly Gly Leu Glu Tyr Ile Tyr Gly Gln Leu Asp Asp Arg  
 450  
 455  
 460  
 Ser Gly Tyr Arg Pro Ser Lys Ile Asp Gln Asn Thr Ser Thr Phe Ser  
 465  
 470  
 475  
 480  
 25 Gln Tyr Asp Gln Leu Glu Tyr Lys Thr Glu Lys Leu Ser Ala Leu Ile  
 485  
 490  
 495  
 Gly Ala Arg Ile Asp Tyr Val Leu Leu Asn Gln Asp Gly Lys Arg Tyr  
 500  
 505  
 510  
 Ile Asp Pro Leu Phe Ile Phe Ser Pro Arg Ala Asn Val Arg Tyr Asn  
 515  
 520  
 525  
 30 Pro Asn Lys Asn Leu Ser Phe Arg Leu Ser Tyr Ser Glu Gly Phe Arg  
 530  
 535  
 540  
 Ala Pro Gln Tyr Phe Asp Glu Asp Leu His Val Glu Leu Ala Gly Gly  
 545  
 550  
 555  
 560  
 35 Thr Pro Ile Ser Arg Val Leu Ser Pro Asn Leu Lys Glu Glu Arg Ser  
 565  
 570  
 575  
 Arg Ser Ile Ser Ala Ser Phe Asp Tyr Tyr His Arg Ala Asp Glu Trp  
 580  
 585  
 590  
 Gln Phe Asn Ile Met Gly Glu Ala Phe Ser Thr Phe Ile Ser Asn Gln  
 595  
 600  
 605  
 40 Phe Lys Pro Ser Asp Lys Val Glu Thr Thr Ser Asp Gly Lys Glu Trp  
 610  
 615  
 620  
 Ile Ile Arg Thr Ile Tyr Asn Asp Lys Asp Gly Val Ser Lys Val Tyr  
 625  
 630  
 635  
 45 Gly Val Asn Leu Glu Gly Arg Ile Ala Tyr Asn Lys Ser Phe Asp Leu  
 645  
 650  
 655  
 Gln Leu Gly Gly Thr Trp Gln Arg Ser Arg Tyr Gly Ser Ile Tyr Thr  
 660  
 665  
 670  
 Ala Val Glu Ala Asp Lys Thr Thr Gly Gln Ala Glu Ile Ser Val Lys  
 675  
 680  
 685  
 50 Asp Tyr Val Arg Thr Pro Asn Leu Tyr Gly Tyr Phe Val Ala Thr Val  
 690  
 695  
 700  
 Arg Pro Thr Glu His Phe Ala Ile Asn Leu Ser Gly Thr Phe Thr Gly  
 705  
 710  
 715  
 720  
 55 Lys Met Asp Val Val His Glu Ala Tyr Glu Gly Asp Ile Pro Ala Glu  
 725  
 730  
 735  
 His Ile Ala Pro Asp Gly Ser Phe Asp Phe Glu Met Asn Gly Gln Gln  
 740  
 745  
 750  
 Phe Lys Gly Leu Ala Glu Gly His Ala Lys Leu Val Lys Thr Pro Ala  
 755  
 760  
 765  
 60 Phe Ala Asp Ile Asp Leu Lys Leu Ser His Asp Phe His Leu Ala Ser  
 770  
 775  
 780  
 Thr Met Thr Leu Glu Leu Asn Ala Gly Ile Gln Asn Ile Phe Asn Ser  
 785  
 790  
 795  
 800  
 65 Tyr Gln Lys Asp Thr Asp Lys Gly Pro Gly Arg Ala Ser Thr Tyr Val  
 805  
 810  
 815  
 Tyr Gly Pro Met Gln Pro Arg Arg Ile Phe Val Gly Thr Lys Ile Asn  
 820  
 825  
 830  
 Phe

70

(2) INFORMATION FOR SEQ ID NO:442

(1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 891 amino acids

(B) TYPE: amino acid

75



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(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

5 (iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Porphyromonas gingivalis*

10 (ix) FEATURE:

(A) NAME/KEY: misc\_feature

(B) LOCATION 1...891

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:442

15

Met Tyr Lys Lys Ile Ile Ala Val Ala Ala Leu Phe Cys Ala Ser Ile  
1 5 10 15

Gly Ile Leu Lys Gly Gln Ser Ser Asp Leu Thr Pro Gln Asp Thr Ile  
20 25 30

Tyr Ser Pro Glu Ile Ser Tyr Ala Lys Pro Ile His Lys Thr Ile Ala  
35 40 45

Ser Ile Glu Ile Glu Gly Met Arg Ser Phe Asp Asp Phe Val Leu Arg  
50 55 60

25 Asn Leu Ser Gly Leu Ala Val Gly Asp Glu Val Leu Ile Pro Gly Asp  
65 70 75 80

Ala Met Ser Ala Ala Val Asn Arg Ile Met Arg Gln Gly Tyr Phe Ser  
85 90 95

Asn Val Arg Ile Ile Ala Asp Lys Tyr Val Gly Asn Lys Val Tyr Leu  
100 105 110

30 Lys Ile Ile Val Thr Glu Arg Pro Arg Ile Ser Lys Val Thr Phe Ser  
115 120 125

Gly Val Lys Lys Ser Glu Arg Glu Asp Leu Glu Met Lys Ile Gly Leu  
130 135 140

Arg Glu Gly Ile Gln Met Thr Arg Asn Asn Glu Asp Lys Val Arg Gln  
145 150 155

35 Ile Val Gln Lys Tyr Phe Ser Glu Lys Gly Tyr Arg Asp Ala Ser Ile  
165 170 175

Arg Ile Thr Gln Glu Pro Asp Leu Ser Lys Asp Gly Phe Val Asn Val  
180 185 190

40 Leu Ile Ser Ile Glu Lys Lys Ser Lys Thr Lys Val Asn Glu Ile Tyr  
195 200 205

Phe Ser Gly Asn Lys Ala Leu Ser Asn His Lys Leu Arg Met Ala Met  
210 215 220

45 Lys Asn Thr Asn Ala Lys Phe Ser Leu Arg Lys His Ile Arg Ser Ser  
225 230 235 240

Phe Leu Lys Leu Phe Ser Thr His Lys Phe Val Glu Glu Ser Tyr Arg  
245 250 255

Glu Asp Leu Val Arg Leu Ile Glu Lys Tyr Gln Glu Tyr Gly Tyr Arg  
260 265 270

50 Asp Ala Glu Ile Leu Thr Asp Ser Val Val Lys Ala Pro Asp Gly Lys  
275 280 285

Arg Val Asp Ile Tyr Leu Asn Ile Glu Glu Gly Gln Lys Tyr Tyr Ile  
290 295 300

55 Lys Asp Val Asn Phe Val Gly Asn Ser Gln Tyr Pro Ser Glu Tyr Leu  
305 310 315 320

Glu Arg Val Leu Gly Ile Lys Ser Gly Asp Val Tyr Asn Gln Arg Arg  
325 330 335

Leu Ala Lys Arg Leu Asn Glu Asp Glu Asp Ala Val Gly Asn Leu Tyr  
340 345 350

60 Tyr Asn Asn Gly Tyr Ile Phe Ala Trp Val Asp Pro Val Glu Thr Asn  
355 360 365

Val Val Gly Asp Ser Val Ser Leu Asp Ile Arg Ile Ala Glu Gly Lys  
370 375 380

65 Gln Ala Asn Ile Asn Lys Val Ile Ile Lys Gly Asn Thr Val Val Tyr  
385 390 395 400

Glu Asp Val Val Arg Arg Glu Leu Tyr Thr Lys Pro Gly Gln Leu Phe  
405 410 415

Ser Arg Glu Asp Ile Ile Asn Ser Ile Arg Leu Ile Asn Gln Leu Gly  
420 425 430

70 His Phe Asp Ala Glu Lys Ser Ile Pro Arg Pro Ile Pro Asn Pro Glu  
435 440 445

Thr Gly Thr Val Asp Ile Glu Tyr Asp Leu Val Pro Arg Ser Ser Asp  
450 455 460

75 Gln Leu Glu Leu Ser Val Gly Trp Ser Gln Ser Gly Leu Leu Phe Arg  
465 470 475 480

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Gly Ala Ile Lys Phe Thr Asn Phe Ser Val Gly Asn Leu Leu His Pro  
 485 490 495  
 Ser Met Tyr Lys Lys Gly Ile Ile Pro Gln Gly Asp Gly Gln Thr Leu  
 500 505 510  
 5 Ser Leu Ser Ala Gln Thr Asn Gly Lys Tyr Tyr Gln Gln Tyr Ser Val  
 515 520 525  
 Thr Phe Met Asp Pro Trp Phe Gly Gly Lys Arg Pro Asp Met Phe Ser  
 530 535 540  
 10 Phe Ser Ala Phe Tyr Ser Lys Thr Thr Ala Ile Asp Ser Lys Phe Tyr  
 545 550 555 560  
 Asn Ser Asn Ala Gly Asn Tyr Tyr Asn Ala Tyr Tyr Asn Ser Tyr Tyr  
 565 570 575  
 Asn Asn Tyr Asn Ser Tyr Tyr Asn Gly Met Ser Asn Tyr Thr Gly Asp  
 580 585 590  
 15 Leu Tyr Thr Gln Ala Ser Asp Pro Asp Arg Ser Leu Gln Met Leu Gly  
 595 600 605  
 Thr Ser Ile Gly Tyr Gly Lys Arg Leu Thr Trp Pro Asp Asn Trp Phe  
 610 615 620  
 20 Gln Ile Tyr Thr Ser Leu Asn Tyr Thr Tyr Tyr Arg Leu Arg Asn Trp  
 625 630 635 640  
 Ser Tyr Asn Thr Phe Gln Asn Phe His His Gly Ser Ala Asn Asp Leu  
 645 650 655  
 Asn Leu Glu Leu Arg Leu Ser Arg Thr Ser Ile Asp Asn Pro Ile Tyr  
 660 665 670  
 25 Thr Arg Ser Gly Ser Asp Phe Met Val Ser Val Ala Ala Thr Leu Pro  
 675 680 685  
 Tyr Ser Leu Trp Asp Asn His Asp Tyr Ala Ser Gln Asn Leu Ser Val  
 690 695 700  
 30 Ser Asp Arg Tyr Arg Phe Ile Glu Tyr His Lys Trp Lys Phe Arg Gly  
 705 710 715 720  
 Arg Val Phe Thr Pro Leu Leu Asn Pro Ala Thr His Lys Tyr Thr Pro  
 725 730 735  
 Val Leu Met Ser Arg Val Glu Gly Ala Val Leu Gly Ser Tyr Asn Ser  
 740 745 750  
 35 Asn Lys Lys Ser Pro Phe Gly Thr Phe Tyr Met Gly Gly Asp Gly Met  
 755 760 765  
 Ser Ser Tyr Tyr Gly Gly Tyr Met Asn Glu Thr Ile Gly Leu Arg Gly  
 770 775 780  
 40 Tyr Lys Asn Gly Ser Ile Ala Gly Asn Asn Tyr Asp Tyr Ala Tyr Ala  
 785 790 795 800  
 Tyr Met Arg Leu Thr Met Glu Leu Arg Phe Pro Ile Leu Phe Glu Asn  
 805 810 815  
 Ser Phe Asn Ala Trp Leu Leu Ala Phe Ala Glu Ala Gly Asn Ala Trp  
 820 825 830  
 45 Arg Ser Ile Asp Asn Tyr Asn Pro Phe Asn Leu Lys Arg Ser Ala Gly  
 835 840 845  
 Val Gly Leu Arg Val Thr Leu Pro Met Val Gly Met Leu Gly Ile Asp  
 850 855 860  
 50 Trp Gly Tyr Gly Phe Asp Arg Pro Asp Asn Ser Leu Gln Arg Gly Gly  
 865 870 875 880  
 Ser Asn Val His Phe Val Leu Gly Gln Glu Phe  
 885 890

(2) INFORMATION FOR SEQ ID NO:443

55

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 174 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

60

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

65

- (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Porphyromonas gingivalis

70

- (ix) FEATURE:  
 (A) NAME/KEY: misc feature  
 (B) LOCATION 1...174

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:443

75

Met Asn Gly Asp Met Lys Arg Phe Leu Ile Leu Ile Gly Phe Ala Leu  
 1 5 10 15

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Ala Val Ala Phe Ser Gly Phe Ser Gln Lys Phe Ala Leu Val Asp Met  
 20 25 30  
 Glu Tyr Ile Leu Arg Asn Ile Pro Asp Tyr Glu Met Met Asn Glu Gln  
 35 40 45  
 5 Leu Glu Gln Val Ser Lys Lys Trp Gln Asn Glu Ile Glu Ala Leu Glu  
 50 55 60  
 Asn Glu Ala Gln Ser Met Tyr Lys Lys Tyr Gln Ser Asp Leu Val Phe  
 65 70 75 80  
 10 Leu Ser Ala Ala Gln Lys Lys Thr Gln Glu Ala Ile Val Lys Lys  
 85 90 95  
 Glu Gln Gln Ala Ser Glu Leu Lys Arg Lys Tyr Phe Gly Pro Glu Gly  
 100 105 110  
 Glu Leu Tyr Lys Lys Arg Ser Asp Leu Met Lys Pro Ile Gln Asp Glu  
 115 120 125  
 15 Ile Trp Asn Ala Ile Lys Glu Ile Ala Lys Arg Asn Asn Tyr Gln Met  
 130 135 140  
 Val Leu Asp Arg Gly Thr Ser Gly Ile Ile Phe Ala Ser Pro Ser Ile  
 145 150 155 160  
 20 Asp Ile Ser Asp Leu Val Leu Ser Lys Met Gly Phe Ser Lys  
 165 170

(2) INFORMATION FOR SEQ ID NO:444

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 170 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Porphyromonas gingivalis
- (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...170
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:444

Met Lys Arg Phe Leu Ile Leu Ile Gly Phe Ala Leu Ala Val Ala Phe  
 1 5 10 15  
 45 Ser Gly Phe Ser Gln Lys Phe Ala Leu Val Asp Met Glu Tyr Ile Leu  
 20 25 30  
 Arg Asn Ile Pro Asp Tyr Glu Met Met Asn Glu Gln Leu Glu Gln Val  
 35 40 45  
 Ser Lys Lys Trp Gln Asn Glu Ile Glu Ala Leu Glu Asn Glu Ala Gln  
 50 55 60  
 50 Ser Met Tyr Lys Lys Tyr Gln Ser Asp Leu Val Phe Leu Ser Ala Ala  
 65 70 75 80  
 Gln Lys Lys Thr Gln Glu Glu Ala Ile Val Lys Lys Glu Gln Gln Ala  
 85 90 95  
 55 Ser Glu Leu Lys Arg Lys Tyr Phe Gly Pro Glu Gly Glu Leu Tyr Lys  
 100 105 110  
 Lys Arg Ser Asp Leu Met Lys Pro Ile Gln Asp Glu Ile Trp Asn Ala  
 115 120 125  
 Ile Lys Glu Ile Ala Lys Arg Asn Asn Tyr Gln Met Val Leu Asp Arg  
 130 135 140  
 60 Gly Thr Ser Gly Ile Ile Phe Ala Ser Pro Ser Ile Asp Ile Ser Asp  
 145 150 155 160  
 Leu Val Leu Ser Lys Met Gly Phe Ser Lys  
 165 170

(2) INFORMATION FOR SEQ ID NO:445

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 163 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES

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(vi) ORIGINAL SOURCE:  
(A) ORGANISM: Porphyromonas gingivalis

5 (ix) FEATURE:  
(A) NAME/KEY: misc\_feature  
(B) LOCATION 1...163

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:445

```

10 Met Lys Lys Phe Phe Leu Met Leu Leu Met Ala Leu Pro Leu Ser Leu
    1      5      10      15
    Leu Ala Gln Lys Val Ala Val Val Asn Thr Glu Glu Ile Ile Ser Lys
        20      25      30
15 Met Pro Glu Gln Val Ala Ala Thr Lys Gln Leu Asn Glu Leu Ala Glu
    35      40      45
    Lys Tyr Arg Leu Asp Leu Lys Ser Met Asp Asp Glu Phe Ala Lys Lys
    50      55      60
    Thr Glu Glu Phe Val Lys Glu Lys Asp Ser Leu Leu Glu Asn Ile Arg
    65      70      75      80
20 Asn Arg Arg Gln Gln Glu Leu Gln Asp Ile Gln Thr Arg Tyr Gln Gln
    85      90      95
    Ser Tyr Gln Thr Met Gln Glu Asp Leu Gln Lys Arg Gln Gln Glu Leu
    100      105      110
    Phe Ala Pro Ile Gln Gln Lys Val Ala Asp Ala Ile Lys Lys Val Gly
    115      120      125
25 Asp Glu Glu Asn Cys Ala Tyr Ile Met Glu Ala Gly Met Met Leu Tyr
    130      135      140
    Thr Gly Ala Thr Ala Ile Asp Leu Thr Ala Lys Val Lys Ala Lys Leu
    145      150      155      160
30 Gly Ile Lys

```

(2) INFORMATION FOR SEQ ID NO:446

35 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 827 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

40 (ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

45 (vi) ORIGINAL SOURCE:  
(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:  
(A) NAME/KEY: misc\_feature  
(B) LOCATION 1...827

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:446

```

Met Lys Glu Ala Ile Pro Arg Lys Asn Lys Tyr Ile Lys Leu Asn Gly
1      5      10      15
55 Ile Tyr Arg Leu Ser Phe Ile Leu Leu Cys Cys Leu Leu Cys Ser Gln
    20      25      30
    Ala Ala Met Ala Gln Gly Val Arg Val Ser Gly Tyr Val Leu Asp Arg
    35      40      45
60 Gly Glu Lys Pro Ile Pro Phe Ala Gly Val Lys Val Arg Gly Thr Gly
    50      55      60
    Thr Gly Ala Thr Thr Asn Leu Lys Gly Tyr Tyr Glu Phe Arg Met Lys
    65      70      75      80
    Ala Thr Thr Asp Ser Ile Thr Ile Glu Phe Ser Ser Met Gly Tyr Gln
    85      90      95
65 Gly Val Ser Arg Ser Phe Pro Ser Leu Thr Lys Asp Thr Arg Leu Asn
    100      105      110
    Val Arg Leu Ala Glu Ala Glu Met Glu Leu Ser Ser Val Thr Val Gln
    115      120      125
70 Ala Thr Lys Arg Arg Leu Asn Thr Met Glu Arg Val Asn Thr Arg Asp
    130      135      140
    Leu Arg Val Asn Ala Gly Pro Thr Gly Gly Val Glu Ser Leu Ile Ser
    145      150      155      160
    Thr Tyr Ala Gly Val Thr Gln Asn Asn Glu Leu Ser Ser Gln Tyr Ser
    165      170      175
75 Val Arg Gly Gly Ser Tyr Asp Glu Asn Met Val Tyr Val Asn Gly Val

```



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Leu Phe Asn Leu Phe Asp Met Thr Asn Val Asn Ser Tyr Tyr Trp Val  
 785 790 795 800  
 Ser Asp Ala Tyr Gln Gln Tyr Ala Val Pro Asn Tyr Leu Thr Arg  
 805 810 815  
 5 Arg Gln Phe Asn Leu Arg Leu Leu Val Glu Phe  
 820 825

(2) INFORMATION FOR SEQ ID NO:447

10

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 672 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

15

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

20

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

(A) NAME/KEY: misc\_feature

(B) LOCATION 1...672

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:447

30

Met Tyr Ser Gly His His Lys Ile His Tyr Pro Phe Leu Ile Leu Leu  
 1 5 10 15

Val Cys Leu Ala Phe Ala Ala Cys Lys Ser Val Lys Leu Lys Asp Ala  
 20 25 30

Glu Lys Ala His Asp Arg Gln Glu Tyr Thr Lys Ala Ala Asp Met Tyr  
 35 40 45

35

Asn Thr Leu Tyr Arg Arg Thr Arg Arg Lys Gln Val Glu Met Lys Ala  
 50 55 60

Tyr Thr Ala Phe Arg Ser Gly Glu Asn Tyr Arg Ala Ala Gly Arg Gln  
 65 70 75 80

Ala Lys Ala Leu Arg Gly Tyr Leu Asn Ala Arg Arg Tyr Gly Tyr Pro  
 85 90 95

40

Asp Ser Val Val Leu Leu Arg Leu Ala Gln Thr Tyr Gln Gln Gly Gly  
 100 105 110

Asn Tyr Lys Glu Ala Glu Val Leu Phe Arg Gly Tyr Leu Glu Ala Tyr  
 115 120 125

45

Pro Lys Ser Tyr Phe Ala Ala Ile Gly Leu Glu Gly Cys Leu Phe Ala  
 130 135 140

Arg Gln Gln Lys Glu Tyr Pro Thr Arg Tyr Arg Ile Arg Arg Ala Ala  
 145 150 155 160

Glu Trp Asn Ser Ala Arg Gly Asp Phe Gly Pro Ala Tyr Ala Pro Asp  
 165 170 175

50

Ala Ser Ala Leu Tyr Phe Thr Ser Ser Arg Ser Lys Asp Asp Gly Leu  
 180 185 190

Asp Asn Ser Ser Ile Thr Gly Leu Lys Pro Asn Asp Ile Tyr Ile Ile  
 195 200 205

55

Lys Arg Asp Ala Gln Gly Arg Trp Gly Arg Pro Asp Ser Val Ser Gly  
 210 215 220

Gly Ile Asn Thr Pro Trp Asp Glu Gly Val Pro Thr Ile Thr Pro Asp  
 225 230 235 240

Gly Ser Thr Ile Tyr Tyr Thr Leu Ala Gln Gln Gly Ala Asp Tyr Asp  
 245 250 255

60

Arg Thr Val Gln Ile Tyr Ser Ala Ala Arg Ser Gly Glu Gly Gly Trp  
 260 265 270

Ser Asn Gly Ser Leu Val Asp Ile Met Arg Asp Ser Leu Arg Met Ala  
 275 280 285

65

Ala His Pro Ser Met Ser Ala Ser Gly Asp Tyr Leu Tyr Phe Val Ser  
 290 295 300

Asn Ile Gly Gly Ser Tyr Gly Gly Lys Asp Ile Tyr Arg Val Lys Val  
 305 310 315 320

Ser Asp Arg Ser Tyr Gly Ser Pro Glu Asn Leu Gly Pro Asp Ile Asn  
 325 330 335

70

Thr Pro Gly Asp Glu Met Phe Pro Phe Ile Asp Gly Asp Ser Thr Leu  
 340 345 350

Phe Phe Ala Ser Asp Gly His Ala Gly Leu Gly Gly Leu Asp Ile Phe  
 355 360 365

75

Lys Ala Thr Leu Asp Ser Thr Gly Gln Trp His Val Val Asn Met Gly  
 370 375 380

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Gln Pro Val Asn Ser Ser Ala Asp Asp Phe Gly Leu Ala Val Glu Pro  
 385 390 395 400  
 Lys Gly Lys Asn Lys Glu Glu Ala Leu Pro Asp Asn Gly Val Lys Gly  
 405 410 415  
 5 Val Phe Cys Ser Asn Arg Gly Asp Ala Arg Gly Trp Pro His Leu Phe  
 420 425 430  
 His Phe Glu Leu Pro Ala Ile Tyr Thr Glu Ile Gln Gly Tyr Val Met  
 435 440 445  
 10 Asp Arg Glu Glu Asn Pro Ile Ala Gly Ala Thr Val Arg Ile Val Gly  
 450 455 460  
 Glu Arg Gly Pro Val Gly Gln Gly Phe Val Thr Thr Arg Asp Asp Gly  
 465 470 475 480  
 Ser Tyr Lys Met Ser Val Gln Gly Asp Thr Arg Tyr Val Met Leu Ala  
 485 490 495  
 15 Gly Ala Ser Gly Tyr Leu Asn Gln Tyr Val Glu Leu Lys Thr Asp Thr  
 500 505 510  
 Ala Lys Gln Ser Glu Thr Tyr Tyr Val Asp Phe Phe Leu Ala Ser Arg  
 515 520 525  
 20 Glu Lys Ala Glu Gly Leu Gln Asn Ile Phe Tyr Asp Phe Asp Lys Ala  
 530 535 540  
 Thr Leu Arg Pro Glu Ser Met Lys Ser Leu Asp Glu Leu Ile Arg Ile  
 545 550 555 560  
 Leu Thr Asp Asn Pro Asp Ile Arg Ile Glu Leu Gly Ser His Ala Asp  
 565 570 575  
 25 Arg Lys Gly Pro Asp Ala Tyr Asn Leu Gly Leu Ser Asp Arg Arg Ala  
 580 585 590  
 Lys Ser Val Val Asp Tyr Leu Thr Ser Arg Gly Ile Ala Ala Asp Arg  
 595 600 605  
 30 Leu Thr Trp Lys Gly Tyr Gly Lys Ser Val Pro Lys Thr Val Thr Ala  
 610 615 620  
 Lys Ile Ala Glu Arg His Asp Phe Leu Lys Glu Gly Asp Val Leu Thr  
 625 630 635 640  
 Glu Glu Phe Val Ala Pro Leu Thr Glu Glu Gln Gln Ser Val Cys Asp  
 645 650 655  
 35 Gln Leu Asn Arg Arg Thr Glu Phe Arg Val Ile Glu Glu Glu Leu Arg  
 660 665 670

## (2) INFORMATION FOR SEQ ID NO:448

- 40 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 708 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
 45 (ii) MOLECULE TYPE: protein  
 (iii) HYPOTHETICAL: YES  
 (vi) ORIGINAL SOURCE:  
 50 (A) ORGANISM: Porphyromonas gingivalis  
 (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION: 1...708  
 55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:448

Met Lys Lys Phe Phe Phe Ala Leu Leu Ser Ile Gly Ile Ser Ala Gln  
 1 5 10 15  
 60 Ala Phe Ala Lys Thr Asp Asn Val Pro Thr Asp Ser Leu Arg Val His  
 20 25 30  
 Asn Leu Gln Thr Val Thr Val Tyr Ser Thr Arg Thr Ala Val Pro Leu  
 35 40 45  
 65 Lys Lys Ile Pro Ala Lys Met Glu Leu Ile Ser Ser Arg Asn Ile Lys  
 50 55 60  
 Gln Ser Gly Phe Asn Asn Met Thr Asp Ile Leu Lys Thr Gln Ser Ser  
 65 70 75 80  
 Leu Asp Val Ile Gln Tyr Pro Gly Phe Ser Ser Asn Ile Gly Ile Arg  
 85 90 95  
 70 Gly Phe Lys Pro Ser Gly Lys Tyr Val Thr Val Leu Val Asn Gly Ile  
 100 105 110  
 Pro Ala Gly Thr Asp Asn Ile Ser Thr Leu Asn Thr Ser Asn Ile Glu  
 115 120 125  
 75 Gln Ile Glu Ile Leu Lys Gly Pro Phe Ser Ser Ile Tyr Gly Thr Asn  
 130 135 140

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Ala Met Gly Gly Val Val Asn Ile Ile Thr His Lys Ser Lys Asp Lys  
 145 150 155 160  
 Ile His Gly Asn Val Ser Leu Phe Gly Gly Ser Tyr Gln Thr Met Ala  
 165 170 175  
 5 Gly Ser Phe Asn Leu Gly Gly Arg Phe Glu Asp Ile Phe Ser Phe Asp  
 180 185 190  
 Leu Ser Leu Gly Leu Asp Lys Gln Asn Lys Asp Tyr Lys Thr Gly Ser  
 195 200 205  
 10 Asn Asn Phe Leu Ser Leu Ser Lys Leu Glu Glu Ala Ile Val Asp Val  
 210 215 220  
 Asn Ala Thr Lys Asn Lys Lys Met Lys Gly Ser Asp Tyr Thr Val Ala  
 225 230 235 240  
 Thr Gly Arg Leu Arg Phe Gly Ile Asp Phe Thr Pro Glu Trp Ser Leu  
 245 250 255  
 15 Asn Leu Tyr Gln Asn Val Phe Leu Gly Asp Ala Ile Pro Val Gly Gly  
 260 265 270  
 Ser Ile Trp Gly Val Tyr Gly Glu Ser Lys Lys Asn Leu Asn Arg Ser  
 275 280 285  
 20 Ser Thr Ser Phe Glu Leu Leu Gly Lys His Gly Cys His Thr Leu Gln  
 290 295 300  
 Phe Ser Pro Tyr Phe Asn Ile Glu Lys Ser Glu Asn Tyr Asn Asn Ala  
 305 310 315 320  
 Asp Pro Thr Gly Phe Ile Asn Tyr Lys Ser Asp Tyr Tyr Thr Tyr Gly  
 325 330 335  
 25 Ala Leu Leu Gln Asp Lys Ile Ser Phe Gly Gly Gln Asn Ile Val Leu  
 340 345 350  
 Gly Val Asp Ser Arg Asn Met Thr Met Glu Ser Glu Arg Phe Glu Gln  
 355 360 365  
 30 Ala Gly Val Asn Thr Lys Pro Tyr Asn Pro Gly Tyr Ala Thr Asn Asn  
 370 375 380  
 Ile Gly Leu Phe Gly Gln Ala Asn Phe Tyr Leu Leu Asn Asp Ala Leu  
 385 390 395 400  
 Ser Ile Ser Ala Gly Ala Arg Ala Asp Phe Met Phe Phe Asp Leu Lys  
 405 410 415  
 35 Ala Asn Glu Tyr Leu Asn Asn Glu Ala Lys Gln Glu Thr His Asn Val  
 420 425 430  
 Ile Asn Pro Asn Val Gly Ile Lys Tyr Glu Phe Val Lys Gly Leu Thr  
 435 440 445  
 40 Ala His Gly Thr Phe Gly Ser Ala Phe Ser Ala Pro Asp Ala Phe Gln  
 450 455 460  
 Lys Ala Gly Gln Tyr Val Gly Pro Phe Gly Thr Thr Ile Gly Asn Pro  
 465 470 475 480  
 Asp Leu Lys Pro Glu Lys Ser Met Thr Trp Asp Phe Gly Ile Gly Tyr  
 485 490 495  
 45 Ser Asn Ala Arg Cys Gly Ile Gln Ala Asp Val Thr Leu Thr Tyr Phe  
 500 505 510  
 His Thr Asp His Lys Asp Leu Ile Leu Ser Ser Pro Asp Tyr Ala Asn  
 515 520 525  
 50 Asn Ile Thr Thr Tyr Ile Asn Ala Asp Lys Ala Arg Met Ser Gly Ile  
 530 535 540  
 Glu Ala Leu Leu Ser Tyr Asp Phe Gly Ser Leu Phe Ala Asn Lys Phe  
 545 550 555 560  
 Ser Leu Arg Ala Phe Ala Asn Ala Thr Ile Met Leu Asn Ser Glu Met  
 565 570 575 580  
 55 Lys Lys Ser Gln Thr Asp Ala Pro Trp Ser Glu Met Tyr Tyr Val Arg  
 580 585 590  
 Lys Gln Asn Ile Thr Phe Gly Ile Glu Tyr Arg Gly Lys Glu Gly Leu  
 595 600 605  
 60 Glu Val Met Leu Asn Gly Arg Phe Met Gly Arg Arg Ile Glu Gln Asn  
 610 615 620  
 Trp Tyr Ala Tyr Tyr Pro Glu Val Arg Pro Glu Leu Gln Gln Leu Leu  
 625 630 635 640  
 Ala Ala Glu Glu Pro Glu Leu Ala Ala Gln Gly Leu Leu Arg His Pro  
 645 650 655  
 65 Gln Ala Met Val Phe Asn Ala Ser Ala Tyr Tyr His Met Asn Lys Tyr  
 660 665 670  
 Leu Thr Phe Gly Val Asn Leu Asn Asn Ile Leu Asp Glu Leu Tyr Thr  
 675 680 685  
 70 Glu Lys Asp Gly Tyr His Met Pro Gly Arg Asn Ile Met Gly Lys Val  
 690 695 700  
 Met Val Asn Phe  
 705

(2) INFORMATION FOR SEQ ID NO:449

75



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(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 462 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION: 1...462

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:449

Met Asn Arg Phe Ser Asn His Trp Pro Cys Ile Leu Val Gly Phe Val  
 1 5 10 15  
 Leu Trp Phe Val Ser Ala Ser Arg Thr Val Ala Gln Asn Ala Ser Glu  
 20 25 30  
 Thr Thr Val Ser Tyr Asp Thr Asp Thr Ala Val Leu Ser Glu Ala Asp  
 35 40 45  
 Val Leu Arg Ile Ala Leu Ser Glu Asn Ala Thr Val Lys Val Ala Asp  
 50 55 60  
 Met Asp Val Arg Lys Gln Glu Tyr Ala Arg Arg Ala Ala Arg Ala Asp  
 65 70 75 80  
 Leu Phe Pro Lys Val Asp Leu Asn Gly Val Tyr Ser His Thr Leu Lys  
 85 90 95  
 Lys Gln Val Leu Tyr Ile Asp Met Pro Gly Phe Ser Ser Ser Glu Gly  
 100 105 110  
 Ile Glu Met Gly Arg Thr His Asn Thr Gln Gly Gly Val Asn Val Ser  
 115 120 125  
 Met Pro Leu Val Ser Ala Gln Leu Trp Lys Ser Ile Ala Met Thr Gly  
 130 135 140  
 Glu Gln Leu Asp Leu Ala Leu Glu Lys Ala Arg Ser Ser Arg Ile Asp  
 145 150 155 160  
 Leu Val Ala Glu Val Lys Lys Ala Tyr Leu Ser Val Leu Leu Ala Glu  
 165 170 175  
 Asp Ser Tyr Gly Val Phe Lys Arg Ser Tyr Asp Asn Ala Leu Ala Asn  
 180 185 190  
 Tyr Lys Asn Ile Ser Asp Lys Phe Asp Arg Gly Leu Val Ala Glu Tyr  
 195 200 205  
 Asp Lys Ile Arg Ala Asn Val Gln Val Arg Asn Ile Glu Pro Asn Leu  
 210 215 220  
 Leu Gln Ala Gln Asn Ser Val Ala Leu Ala Leu Trp Gln Leu Lys Val  
 225 230 235 240  
 Leu Met Ser Met Glu Val Glu Thr Pro Ile Arg Leu Ser Gly Ser Leu  
 245 250 255  
 Ser Asp Tyr Lys Glu Gln Val Tyr Thr Gly Tyr Phe Ala Ala Asp Thr  
 260 265 270  
 Leu Ile Ser Asn Asn Ser Ser Leu Arg Gln Leu Asp Ile Gln Arg Arg  
 275 280 285  
 Leu Ala Val Ser Ala Asp Lys Leu Asn Lys Tyr Ser Phe Leu Pro Thr  
 290 295 300  
 Leu Asn Leu Gly Gly Gln Tyr Thr Tyr Ser Leu Asn Ser Asn Asp Ile  
 305 310 315 320  
 Lys Phe Trp Gly Glu Gly Gln Arg Trp Thr Pro Phe Ser Thr Ile Ser  
 325 330 335  
 Leu Ser Leu Tyr Ile Pro Ile Phe Asn Gly Gly Lys Arg Leu Tyr Asn  
 340 345 350  
 Val Lys Gln Ser Ala Leu Ser Ile Arg Gln Ile Asp Leu Gln Arg Arg  
 355 360 365  
 His Ile Glu Gln Ser Ile Arg Met Gly Ile Lys Asn Gln Asn Asp Arg  
 370 375 380  
 Leu Arg Thr Cys Met Gln Arg Phe Val Ala Ser Glu Glu Ala Val Arg  
 385 390 395 400  
 Ser Ala Glu Lys Gly Tyr Gln Ile Ala Glu Lys Arg Tyr Gln Thr Gly  
 405 410 415  
 Glu Gly Thr Leu Val Glu Leu Asn Asp Ala Asp Val Ala Leu Leu Gln  
 420 425 430  
 Ala Arg Leu Asn Tyr Asn Gln Ala Ile Phe Asp Phe Met Thr Ala Lys  
 435 440 445  
 Ala Glu Leu Asp Lys Met Asn Gly Met Gly Ile Pro Glu Gln

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450

455

460

(2) INFORMATION FOR SEQ ID NO:450

5

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 492 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

10

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

15

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

(A) NAME/KEY: misc feature

(B) LOCATION 1...492

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:450

	Met	Trp	Gly	Asp	Ser	His	Gly	Val	Ala	Pro	Asn	Gln	Val	Arg	Arg	Thr
	1				5					10				15		
25	Leu	Val	Lys	Val	Ala	Leu	Ser	Glu	Ser	Leu	Pro	Pro	Gly	Ala	Lys	Gln
				20					25					30		
	Ile	Arg	Ile	Gly	Phe	Ser	Leu	Pro	Lys	Glu	Thr	Glu	Glu	Lys	Val	Thr
				35				40					45			
30	Ala	Leu	Tyr	Leu	Leu	Val	Ser	Asp	Ser	Leu	Ala	Val	Arg	Asp	Leu	Pro
				50			55					60				
	Asp	Tyr	Lys	Gly	Arg	Val	Ser	Tyr	Asp	Ser	Phe	Pro	Ile	Ser	Lys	Glu
						70					75					80
	Asp	Arg	Thr	Thr	Ala	Leu	Ser	Ala	Asp	Ser	Val	Ala	Gly	Arg	Arg	Phe
					85					90					95	
35	Phe	Tyr	Leu	Ala	Ala	Asp	Ile	Gly	Pro	Val	Ala	Ser	Phe	Ser	Arg	Ser
					100				105						110	
	Asp	Thr	Leu	Thr	Ala	Arg	Val	Glu	Glu	Val	Ala	Val	Asp	Gly	Arg	Pro
					115			120					125			
40	Leu	Pro	Leu	Lys	Glu	Leu	Ser	Pro	Ala	Ser	Arg	Arg	Leu	Tyr	Arg	Gly
					130			135					140			
	Tyr	Glu	Ala	Leu	Phe	Val	Pro	Gly	Asp	Gly	Gly	Ser	Arg	Asn	Tyr	Arg
					145			150				155				160
	Ile	Pro	Ala	Ile	Leu	Lys	Thr	Ala	Asn	Gly	Thr	Leu	Ile	Ala	Met	Ala
					165				170						175	
45	Asp	Arg	Arg	Lys	Tyr	Asn	Gln	Thr	Asp	Leu	Pro	Glu	Asp	Ile	Asp	Ile
					180				185						190	
	Val	Met	Arg	Arg	Ser	Thr	Asp	Gly	Gly	Lys	Ser	Trp	Ser	Asp	Pro	Arg
					195			200					205			
50	Ile	Ile	Val	Gln	Gly	Glu	Gly	Arg	Asn	His	Gly	Phe	Gly	Asp	Val	Ala
					210			215				220				
	Leu	Val	Gln	Thr	Gln	Ala	Gly	Lys	Leu	Leu	Met	Ile	Phe	Val	Gly	Gly
					225			230				235				240
	Val	Gly	Leu	Trp	Gln	Ser	Thr	Pro	Asp	Arg	Pro	Gln	Arg	Thr	Tyr	Ile
					245				250						255	
55	Ser	Glu	Ser	Arg	Asp	Glu	Gly	Leu	Thr	Trp	Ser	Pro	Pro	Arg	Asp	Ile
					260				265					270		
	Thr	His	Phe	Ile	Phe	Gly	Lys	Asp	Cys	Ala	Asp	Pro	Gly	Arg	Ser	Arg
					275			280					285			
60	Trp	Leu	Ala	Ser	Phe	Cys	Ala	Ser	Gly	Gln	Gly	Leu	Val	Leu	Pro	Ser
					290			295				300				
	Gly	Arg	Ile	Thr	Phe	Val	Ala	Ala	Ile	Arg	Glu	Ser	Gly	Gln	Glu	Tyr
					305			310				315				320
	Val	Leu	Asn	Asn	Tyr	Val	Leu	Tyr	Ser	Asp	Asp	Glu	Gly	Asp	Thr	Trp
					325					330					335	
65	Gln	Leu	Ser	Asp	Cys	Ala	Tyr	Arg	Arg	Gly	Asp	Glu	Ala	Lys	Leu	Ser
					340				345					350		
	Leu	Met	Pro	Asp	Gly	Arg	Val	Leu	Met	Ser	Ile	Arg	Asn	Gln	Gly	Arg
					355			360					365			
70	Gln	Glu	Ser	Arg	Gln	Arg	Phe	Phe	Ala	Leu	Ser	Ser	Asp	Asp	Gly	Leu
					370			375				380				
	Thr	Trp	Glu	Arg	Ala	Lys	Gln	Phe	Glu	Gly	Ile	His	Asp	Pro	Gly	Cys
					385			390				395				400
	Asn	Gly	Ala	Met	Leu	Gln	Val	Lys	Arg	Asn	Gly	Arg	Asp	Gln	Val	Leu
					405					410					415	
75	His	Ser	Leu	Pro	Leu	Gly	Pro	Asp	Gly	Arg	Arg	Asp	Gly	Ala	Val	Tyr

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420                      425                      430  
 Leu Phe Asp His Val Ser Gly Arg Trp Ser Ala Pro Val Val Val Asn  
                          435                      440                      445  
 Ser Gly Ser Ser Ala Tyr Ser Asp Met Thr Leu Leu Ala Asp Gly Thr  
 450                      455                      460  
 Ile Gly Tyr Phe Val Glu Glu Gly Asp Glu Ile Ser Leu Val Phe Ile  
 465                      470                      475                      480  
 Arg Phe Val Leu Asp Asp Leu Phe Asp Val Arg Gln  
                          485                      490

10

(2) INFORMATION FOR SEQ ID NO:451

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 245 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

15

(ii) MOLECULE TYPE: protein

20

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Porphyromonas gingivalis

25

(ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...245

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:451

Met Lys Lys Glu Lys Leu Trp Ile Ala Ile Val Ala Gly Leu Ala Phe  
 1                      5                      10                      15  
 Val Leu Gly Leu Tyr Ala Leu Gly Arg Ser Val Ala Gln Leu Arg Arg  
                          20                      25                      30  
 Ser Gln Pro Ser Val Thr Val Thr Gly Met Ala Glu Arg Asn Phe Lys  
 35                      35                      40                      45  
 Ser Asp Leu Ile Val Trp Thr Ala Ser Tyr Gln Leu Gln Met Met Asp  
 50                      55                      60  
 Leu Glu Ser Ala Tyr Lys Ala Leu Lys Glu Lys Gln Ile Leu Val Ala  
 65                      70                      75                      80  
 Asp Tyr Leu Lys Asn Lys Gln Leu Pro Asp Ser Ser Tyr Ile Phe Ser  
                          85                      90                      95  
 Ser Val Ala Ile Ser Lys Glu Tyr Asn Tyr Tyr Tyr Asp Pro Arg Gln  
                          100                      105                      110  
 Glu Gln Asn Val Arg Thr Phe Ala Gly Tyr Leu Leu Ser Gln Thr Val  
 45                      115                      120                      125  
 Thr Val Thr Ser Gln Asp Ile Glu His Val Glu Lys Ile Ser Arg Asp  
                          130                      135                      140  
 Ile Thr Glu Leu Ile Asn Gln Gly Val Glu Ile Thr Ser Asp Arg Pro  
 50                      145                      150                      155                      160  
 Ala Tyr Tyr Tyr Thr Lys Leu Asn Asp Leu Lys Val Glu Met Leu Arg  
                          165                      170                      175  
 Asn Ala Ser Glu Asp Ala Phe Asn Arg Ala Ser Val Ile Ala Glu Gly  
                          180                      185                      190  
 Ser Gly Ser Ser Val Gly Lys Met Leu Ser Ser Ser Met Gly Val Phe  
 55                      195                      200                      205  
 Gln Ile Val Gly Leu Asn Ser Asn Glu Asp Tyr Ser Trp Gly Gly Ser  
                          210                      215                      220  
 Phe Asn Thr Ser Ser Lys Met Lys Thr Ala Ser Ile Thr Val Lys Ala  
 60                      225                      230                      235                      240  
 Ser Phe Ala Leu Lys  
                          245

65

(2) INFORMATION FOR SEQ ID NO:452

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 276 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

70

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

75

(vi) ORIGINAL SOURCE:

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(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

(A) NAME/KEY: misc feature

(B) LOCATION: 1...276

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:452

10 Met Lys Lys Thr Ile Ala Ile Ile Ala Ser Ala Leu Leu Ala Leu Gly  
 1 5 10 15  
 Ala Val Gly Cys Lys Lys Asn Ala Asp Thr Thr Ala Val Ser Glu Lys  
 20 25 30  
 Asp Ser Ile Ala Leu Ser Met Gly Ile Leu Tyr Gly Gln Asp Phe Ala  
 35 40 45  
 15 Asn Gln Phe Glu Met Ser Arg Leu Gln Gly Gln Pro Ile Asp Ser Val  
 50 55 60  
 Ala Phe Leu Asp Gly Phe Lys Tyr Gly Ile Asp Thr Thr Arg Phe Ser  
 65 70 75 80  
 20 Tyr Asn Leu Gly Ala Ile Tyr Ala Ser Asn Ile Ala Arg Gln Leu Ala  
 85 90 95  
 His Asp Ser Ile Asp Ile Asp Lys Phe Tyr Ala Ala Met Arg Ala Ala  
 100 105 110  
 Leu Leu Lys Asp Thr Val Ser Ile Ala Met Lys Pro Ala Asp Ala Gln  
 115 120 125  
 25 Ala Phe Met Gln Arg Ile Gln Ala Lys Lys Gln Arg Glu Asn Asn Met  
 130 135 140  
 Lys Gln Phe Gly Gln Asn Ile Glu Lys Gly Asn Glu Tyr Ile Asp Thr  
 145 150 155 160  
 30 Phe Lys Lys Glu Asp Gly Val Thr Val Thr Thr Thr Gly Leu Ala Tyr  
 165 170 175  
 Lys Thr Leu Gln Glu Gly Thr Gly Ala Thr Pro Ser Leu Ala Asp Thr  
 180 185 190  
 Val Arg Val Lys Tyr Val Gly Thr Leu Val Asp Gly Lys Glu Phe Asp  
 195 200 205  
 35 Lys Asn Glu Glu Gly Ile Glu Phe Ala Val Thr Gly Val Ile Lys Gly  
 210 215 220  
 Trp Thr Glu Met Leu Gln Leu Met Lys Val Gly Gln Lys Val Arg Val  
 225 230 235 240  
 40 Val Ile Pro Gln Glu Leu Ala Tyr Gly Glu Thr Gly Asn Tyr Thr Ile  
 245 250 255  
 Glu Pro Phe Ser Thr Leu Thr Phe Glu Met Glu Leu Ile Gly Ile Lys  
 260 265 270  
 Pro Gly Lys Lys  
 275

(2) INFORMATION FOR SEQ ID NO:453

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 775 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

(A) NAME/KEY: misc feature

(B) LOCATION: 1...775

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:453

65 Met Lys Val Leu Arg Gln Val Phe Leu Pro Ile Leu Phe Val Leu Leu  
 1 5 10 15  
 Thr Gly Ala Cys Ser Thr Thr Lys Asn Leu Pro Glu Gly Glu Gln Leu  
 20 25 30  
 70 Tyr Ile Gly Met Gly Lys Thr Gln Ile Leu Arg Gln Asp Lys Ser His  
 35 40 45  
 Ala Gly Gln Gln Ala Leu Thr Glu Val Glu Ser Thr Leu Lys Val Thr  
 50 55 60  
 75 Pro Asn Gly Ala Ile Phe Gly Ser Ala Ser Ala Ser Leu Pro Lys Ile  
 65 70 75 80

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	Pro	Phe	Gly	Leu	Trp	Leu	Tyr	Asn	Ser	Phe	Val	Gly	Asp	Ser	Thr	Val
				85						90					95	
	Ile	Ser	Lys	Trp	Ile	Phe	Asp	Lys	Phe	Ala	Ala	Lys	Pro	Val	Phe	Ile
				100					105					110		
5	Ser	Gln	Val	Lys	Ser	Asp	Ser	Arg	Ala	Lys	Val	Ala	Thr	Asn	Ile	Leu
				115				120					125			
	Arg	Glu	His	Gly	Tyr	Phe	Asp	Ala	Lys	Val	Lys	Ser	Ser	Val	Thr	Thr
				130				135					140			
10	Leu	Lys	Lys	Asp	Ser	Leu	Lys	Ala	Lys	Ile	Ser	Tyr	Thr	Val	Asp	Met
				145				150				155				160
	Ala	Ser	Pro	Tyr	His	Tyr	Asp	Ser	Ile	Ile	Pro	Leu	Pro	Ile	Ser	Thr
					165					170					175	
	Phe	Pro	Asp	Ser	Ile	Leu	Ala	Tyr	Arg	Gln	Thr	Pro	Ser	Leu	Ile	Arg
				180					185					190		
15	Lys	Gly	Asp	Gln	Phe	Asn	Leu	Ala	Lys	Leu	His	Glu	Glu	Arg	Gln	Thr
				195				200					205			
	Ile	Ser	Ala	Leu	Leu	Arg	Asp	Asn	Gly	Tyr	Tyr	Tyr	Phe	Arg	Pro	Gln
				210				215					220			
20	Asp	Ile	Ile	Tyr	Glu	Ala	Asp	Thr	Leu	Leu	Val	Arg	Gly	Ala	Val	Cys
				225				230				235				240
	Leu	Arg	Ala	Lys	Leu	Ser	Glu	Asp	Thr	Pro	Pro	Gln	Ala	Met	Arg	Pro
					245					250					255	
	Trp	Arg	Ile	Gly	Lys	Arg	Thr	Ala	Val	Leu	Leu	Gly	Met	Asn	Gly	Glu
				260					265					270		
25	Ser	Pro	Thr	Asp	Ser	Leu	Glu	Val	Glu	Asp	Met	Lys	Val	Leu	Tyr	Tyr
				275					280				285			
	Arg	Lys	Met	Pro	Val	Arg	Pro	Lys	Ile	Leu	Ala	Lys	Arg	Phe	Arg	Phe
							295					300				
30	Phe	Ser	Gly	Asn	Leu	Tyr	Arg	Gln	Lys	Asp	Asp	Glu	Thr	Thr	Arg	Lys
				305				310				315				320
	Ser	Leu	Ala	Arg	Leu	Gly	Ala	Phe	Ser	Val	Ile	Asp	Leu	Asn	Phe	Leu
					325					330					335	
	Gln	Arg	Asp	Ser	Ile	Ser	Gly	Leu	Leu	Asp	Val	Arg	Leu	Leu	Thr	Thr
				340					345					350		
35	Leu	Asp	Lys	Pro	Trp	Asp	Ala	Ser	Leu	Glu	Thr	Leu	Phe	Thr	Ser	Lys
				355				360					365			
	Ser	Asn	Asp	Phe	Ile	Gly	Pro	Gly	Leu	Asn	Phe	Ala	Leu	Ala	Arg	Arg
				370				375				380				
40	Asn	Val	Phe	Gly	Gly	Gly	Glu	Asn	Leu	Ser	Trp	Asn	Ile	Gly	Gly	Ser
				385				390				395				400
	Tyr	Glu	Trp	Glu	Thr	Gly	Asn	Arg	Pro	Glu	Asn	Ser	Ser	Asn	Arg	Leu
					405					410					415	
	Ile	Asp	Ile	Asn	Ser	Tyr	Asn	Met	Asn	Thr	Ala	Val	Asn	Leu	Ser	Phe
				420					425					430		
45	Pro	Ser	Ile	Val	Phe	Pro	Gly	Leu	Leu	Asp	Lys	Tyr	Tyr	Tyr	Tyr	Pro
				435				440					445			
	Thr	Thr	Thr	Thr	Phe	Gln	Ala	Ser	Ala	Thr	Ala	Leu	Asn	Arg	Ala	His
				450				455				460				
50	Tyr	Phe	Ser	Met	Tyr	Ser	Phe	Gly	Phe	Ser	Thr	Thr	Tyr	Glu	Phe	Gln
				465				470				475				480
	Pro	Ser	Lys	Glu	His	Arg	His	Ala	Ile	Phe	Pro	Leu	Lys	Leu	Asn	Tyr
					485					490					495	
	Asn	Leu	Leu	Gly	His	Gln	Thr	Glu	Thr	Phe	Gln	Ala	Ile	Thr	Ala	Asn
				500					505					510		
55	Asn	Pro	Pro	Leu	Leu	Leu	Ser	Leu	Gln	Ser	Gln	Phe	Leu	Ala	Gln	Met
				515				520					525			
	Gly	Tyr	Ile	Tyr	Thr	Phe	Asn	Lys	Ser	Val	Ser	Glu	Lys	Ser	Pro	His
				530				535				540				
60	His	Leu	Trp	Met	Gln	Phe	Gly	Leu	Ser	Glu	Ala	Gly	Asn	Leu	Leu	Asn
				545				550				555				560
	Leu	Ile	Tyr	Leu	Ala	Ala	Gly	Lys	Lys	Tyr	Ser	Asp	Thr	Lys	Asn	Phe
					565					570					575	
	Val	Gly	Val	Pro	Phe	Ser	Gln	Phe	Ile	Lys	Ala	Thr	Gly	Glu	Leu	Arg
				580					585					590		
65	Tyr	Ser	Tyr	Thr	Ile	Asp	Arg	Asn	Gln	Ser	Leu	Ala	Thr	Arg	Phe	Gly
				595				600					605			
	Thr	Gly	Val	Ile	Tyr	Ser	Tyr	Gly	Asn	Met	Arg	Val	Ala	Pro	Tyr	Ser
				610				615				620				
70	Glu	Gln	Phe	Tyr	Val	Gly	Gly	Ala	Asn	Ser	Ile	Arg	Ala	Phe	Thr	Val
				625				630				635				640
	Arg	Ser	Ile	Gly	Pro	Gly	Arg	Phe	Asn	Pro	Asp	Ser	Asp	Asn	Gln	Tyr
					645					650					655	
	Ser	Tyr	Leu	Asp	Gln	Val	Gly	Glu	Phe	Lys	Leu	Glu	Ala	Asn	Val	Glu
				660					665					670		
75	Tyr	Arg	Gly	Lys	Leu	Phe	Gly	Asp	Leu	His	Ala	Ala	Val	Phe	Leu	Asp

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5                   675                                   680                                   685  
 Ala Gly Asn Val Trp Leu Leu Arg Glu Asp Ser Ser Arg Pro Gly Gly  
       690                                   695                                   700  
 Ala Leu Ser Glu Val Gly Ser Val Ser Asn Phe Leu Asn Ser Ile Ala  
 705                                   710                                   715                                   720  
 Leu Gly Thr Gly Val Gly Leu Arg Tyr Asp Leu Ala Phe Leu Val Val  
       725                                   730                                   735  
 Arg Val Asp Val Gly Phe Gly Leu His Leu Pro Tyr Asn Thr Gly Lys  
       740                                   745                                   750  
 10 Lys Gly Tyr Tyr Asn Ile Pro Arg Phe Lys Asp Ala Ile Gly Phe His  
       755                                   760                                   765  
 Leu Ala Val Gly Tyr Pro Phe  
       770                                   775  
 15       (2) INFORMATION FOR SEQ ID NO:454  
           (i) SEQUENCE CHARACTERISTICS:  
               (A) LENGTH: 774 amino acids  
               (B) TYPE: amino acid  
 20               (D) TOPOLOGY: linear  
           (ii) MOLECULE TYPE: protein  
           (iii) HYPOTHETICAL: YES  
 25           (vi) ORIGINAL SOURCE:  
               (A) ORGANISM: Porphyromonas gingivalis  
           (vii) FEATURE:  
 30               (A) NAME/KEY: misc feature  
               (B) LOCATION 1...774  
           (viii) SEQUENCE DESCRIPTION: SEQ ID NO:454  
 35 Met Ser Ser His Ser Val Arg Tyr Leu Ile Gly Ile Ala Gly Cys Leu  
       1                                   5                                   10                                   15  
 Leu Leu Met Leu Ala Ser Ser Cys Ser Val Thr Arg Tyr Val Pro Asp  
       20                                   25                                   30  
 40 Gly Ser Arg Leu Leu Asp Arg Val Thr Ile Ala Ser Glu Thr Gly Ser  
       35                                   40                                   45  
 Ile Ala Leu Pro Glu Asp Ile Arg Asp Tyr Thr Leu Gln Gln Pro Asn  
       50                                   55                                   60  
 Tyr Arg Leu Phe Gly Met Thr Arg Trp Leu Leu Arg Val Tyr Ser Ser  
       65                                   70                                   75                                   80  
 45 Ser Asn Pro Asn Ser Asn Ser Trp Trp Asn Arg Ser Leu Arg Lys Met  
       85                                   90                                   95  
 Gly Glu Pro Pro Val Leu Ile Asp Ser Val Leu Thr Asp Arg Thr Ala  
       100                                   105                                   110  
 50 Asn Arg Leu Ala Lys Ala Met Ala Gly Asp Gly Phe Leu Asp Ala Thr  
       115                                   120                                   125  
 Ala Arg Ala Val Val Asp Thr Gly Leu Tyr Lys Lys Ala Arg Ile Thr  
       130                                   135                                   140  
 Tyr Leu Ile Gln Pro Gly Ser Arg Tyr Tyr Ile Arg Asn Met Ala Leu  
       145                                   150                                   155                                   160  
 55 Asp Val Lys Asn Pro Leu Leu Pro Pro Val Ala Leu Gly Asn Ser Leu  
       165                                   170                                   175  
 Pro Ser Ala Tyr Lys Val Gly Ile Ser Glu Gly Ser Pro Leu Ser Pro  
       180                                   185                                   190  
 60 Ile Val Leu Asp Glu Glu Arg Lys Ala Ile Ala Arg His Met Arg Asn  
       195                                   200                                   205  
 Asn Gly Phe Trp Lys Phe Ser Ala Glu Asp Val Tyr Tyr Glu Ala Asp  
       210                                   215                                   220  
 Thr Thr Val Ser Gly Gly Ser Gly Thr Lys Ser Ala Asp Leu Lys Leu  
       225                                   230                                   235  
 65 Val Val Asn Gly Ile Gly Arg Tyr Pro Tyr Arg Ile Gly Arg Val Phe  
       245                                   250                                   255  
 Phe His Ala Asp Tyr Asp Pro Leu Glu Ser Asp Phe Arg Val Gln Glu  
       260                                   265                                   270  
 70 Leu Pro Arg Ile Asp Ser Ile Ser Arg Gly Asp Tyr Thr Val Tyr Tyr  
       275                                   280                                   285  
 Gly Ser Arg Gly Arg Tyr Ile Arg Ala Ser Ala Leu Thr Arg Ser Val  
       290                                   295                                   300  
 Ser Val Thr Pro Gly Ala Phe Phe Cys Glu Asp Val Glu Arg Ser  
       305                                   310                                   315                                   320  
 75 Tyr Ile Lys Leu Asn Ala Leu Pro Ile Val Arg Asn Val Asn Ile Arg

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5 Phe Val Glu His Asn Gly Lys Asp Glu Ile Ala Leu Ala Asp Ser Ser  
 Arg Leu Val Asp Cys Tyr Ile Leu Thr Val Pro Ala Lys Ser Lys Ser  
 Phe Glu Ala Glu Val Leu Gly Thr Asn Ser Ala Gly Asp Phe Gly Ala  
 Ala Leu Ser Leu Gly Phe Thr Asp Arg Asn Leu Phe Arg Gly Ala Glu  
 10 Met Phe Asn Ile Lys Leu Lys Gly Ala Tyr Glu Ala Ile Arg Lys Gly  
 Ser His Ser Phe Met Glu Tyr Gly Val Glu Ser Ser Leu Arg Phe Pro  
 Arg Leu Leu Phe Pro Phe Ile Ser Asp Glu Thr Arg Arg Arg Leu Arg  
 15 Ala Ser Thr Glu Trp Lys Ile Gly Tyr Asn Tyr Gln Thr Arg Pro Glu  
 Phe Asp Arg Val Ile Leu Ser Ala Gln Leu Asn Tyr Ser Trp Gln Thr  
 20 Tyr Leu His Asn Arg Leu Arg His Thr Ile Arg Leu Leu Asp Val Asp  
 Tyr Leu His Leu Pro Tyr Ile Asp Pro Asp Phe Ala Gln Ser Leu Pro  
 25 Pro Thr Thr Ala Leu Tyr Asn Tyr Thr Thr Ala Ser Ser Met Glu Arg Thr Val  
 Ala Tyr Ile Leu Asn Tyr Thr Thr Ala Ser Ser Met Glu Arg Thr Val  
 Ser Asn Pro Phe Thr Ala Arg Phe Ser Ile Gln Thr Ala Gly Asn Leu  
 30 Leu Gln Ala Ile Ser Tyr Leu Thr Asp Ser Pro Lys Asp Glu His Gly  
 Leu Tyr Lys Met Phe Gly Leu His Tyr Ala Gln Phe Val Lys Leu Asp  
 Leu Asp Leu Ala Lys Thr Val Leu Leu Glu Lys Asp Asn Thr Leu Ala  
 35 Leu His Leu Gly Phe Gly Leu Ala Phe Pro Tyr Gly Asn Ala Arg His  
 Ile Pro Phe Glu Leu Arg Tyr Phe Ala Gly Gly Ser Asn Ser Val Arg  
 40 Gly Trp Ser Val Arg Thr Leu Gly Pro Gly Ser Met Lys Met Thr Pro  
 Asp Lys Thr Phe Phe Asp Gln Met Gly Asp Ile Arg Leu Asp Leu Asn  
 Val Glu Tyr Arg Thr Lys Leu Phe Trp Lys Phe Arg Ala Ala Ala Phe  
 45 Val Asp Ala Gly Asn Val Trp Thr Ile Lys Glu Tyr Glu Asn Gln Glu  
 Asp Gly Leu Phe Arg Phe Asp Arg Phe Tyr Lys Glu Ile Ala Leu Ala  
 50 Tyr Gly Leu Gly Leu Arg Leu Asp Phe Asp Tyr Phe Leu Val Arg Leu  
 Asp Ala Gly Leu Lys Ala Tyr Asp Pro Gln Gln Thr Gly Arg Tyr Lys  
 55 Trp Ala Ile Thr Arg Pro Asn Leu Ser Ser Asn Phe Ala Trp His Ile  
 Ala Val Gly Tyr Pro Phe

(2) INFORMATION FOR SEQ ID NO:455

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 867 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(iv) ORIGINAL SOURCE:

(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

(A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...867

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:455

5	Met	Arg	Lys	Arg	Ile	Leu	Gln	Leu	Phe	Leu	Thr	Ala	Leu	Leu	Leu	Ala
	1				5					10					15	
	Leu	Gly	Ser	Ser	Leu	Ala	Ile	Ala	Gln	Thr	Val	Val	Thr	Gly	Lys	Val
					20				25					30		
	Ile	Asp	Ser	Glu	Thr	Ser	Glu	Pro	Leu	Ile	Gly	Val	Ser	Val	Ser	Thr
					35			40					45			
10	Gly	Gln	Gly	Ala	Ser	Leu	Arg	Gly	Val	Thr	Thr	Asp	Met	Asp	Gly	Gly
		50					55					60				
	Phe	Arg	Phe	Glu	Val	Pro	Ala	Lys	Ser	Val	Leu	Thr	Phe	Arg	Cys	Val
		65				70					75				80	
15	Gly	Tyr	Ala	Thr	Val	Thr	Arg	Ser	Ile	Gly	Arg	Gly	Ser	Gln	Glu	Asp
					85				90					95		
	Leu	Gly	Thr	Ile	Leu	Leu	Asp	Pro	Gln	Ala	Ile	Gly	Leu	Asp	Glu	Ile
					100				105					110		
	Gln	Val	Ile	Ala	Ser	Val	Val	Pro	Lys	Asp	Arg	Met	Thr	Pro	Val	Pro
					115			120						125		
20	Val	Ser	Asn	Ile	Arg	Val	Ala	Asp	Ile	Gln	Ala	Ala	Ser	Leu	Asn	Val
							135					140				
	Glu	Phe	Pro	Glu	Leu	Val	Lys	Ser	Thr	Pro	Ser	Thr	Tyr	Thr	Thr	Lys
		145				150					155					160
25	Gly	Ser	Gly	Gly	Phe	Gly	Asp	Gly	Arg	Thr	Asn	Val	Arg	Gly	Phe	Asp
					165					170					175	
	Thr	Tyr	Asn	Phe	Gly	Val	Leu	Ile	Asn	Gly	Val	Pro	Val	Asn	Gly	Met
					180				185					190		
	Glu	Asp	Gly	Lys	Val	Tyr	Trp	Ser	Asn	Trp	Ser	Gly	Leu	Met	Asn	Gln
					195				200				205			
30	Ala	Ser	Thr	Ile	Gln	Ile	Gln	Arg	Gly	Leu	Gly	Ala	Ser	Lys	Leu	Gly
							215					220				
	Ile	Ser	Ser	Val	Gly	Gly	Thr	Met	Asn	Ile	Ile	Thr	Lys	Thr	Thr	Asp
							230					235				240
35	Ala	Asn	Thr	Gly	Gly	Ser	Ala	Tyr	Val	Gly	Met	Gly	Asn	Asp	Gly	Leu
					245					250					255	
	His	Lys	Glu	Ser	Phe	Ser	Ile	Ser	Thr	Gly	Met	Asn	Asp	Gly	Trp	Ala
					260				265					270		
	Ile	Thr	Ile	Ala	Gly	Ser	His	Met	Thr	Gly	Leu	Gly	Tyr	Val	Lys	Gly
					275				280					285		
40	Leu	Lys	Gly	Arg	Ala	Phe	Ser	Tyr	Phe	Phe	Asn	Val	Ser	Lys	Lys	Phe
							295					300				
	Asn	Glu	Arg	His	Thr	Leu	Ser	Leu	Thr	Gly	Phe	Gly	Ala	Pro	Gln	Trp
							310				315					320
45	His	Asn	Gln	Arg	Ser	Ser	Lys	Tyr	Ser	Val	Ala	Asp	Tyr	Asp	Lys	Tyr
							325				330				335	
	Gly	Ile	Arg	His	Asn	Gln	Ser	Phe	Gly	Tyr	Leu	Arg	Gly	Glu	Leu	Thr
					340				345					350		
	Pro	Thr	Ala	Tyr	Ala	Tyr	Asn	Thr	Tyr	His	Lys	Pro	Gln	Phe	Ser	Leu
					355			360					365			
50	Asn	His	Phe	Thr	Lys	Met	Asp	Glu	Asn	Thr	Ser	Leu	Tyr	Thr	Ala	Unk
							375					380				
	Tyr	Ala	Ser	Leu	Ala	Thr	Gly	Gly	Gly	Arg	Arg	Ala	Tyr	Gly	Lys	Asn
							390				395					400
55	Ser	Lys	Trp	Val	Leu	Ile	Asn	Tyr	Asn	Thr	Gly	Gln	Pro	Tyr	Glu	Gln
					405					410					415	
	Thr	Lys	Val	Thr	Pro	Asp	Gly	Leu	Ile	Asp	Tyr	Asp	Ala	Val	Leu	Ala
					420				425					430		
	Ala	Asn	Ala	Ala	Ala	Ser	Asn	Gly	Ser	Glu	Ala	Ile	Phe	Ala	Leu	Gly
					435			440					445			
60	Ser	Asn	Ser	His	Lys	Trp	Phe	Gly	Leu	Leu	Ser	Ser	Phe	Lys	Lys	Lys
							455				460					
	Leu	Asn	Ser	Ser	Leu	Thr	Leu	Thr	Ala	Gly	Tyr	Asp	Gly	Arg	Tyr	Tyr
							470				475					480
65	Arg	Gly	Asp	His	Tyr	Asp	Lys	Ile	Thr	Asp	Leu	Leu	Gly	Gly	Ser	Tyr
							485				490				495	
	Tyr	Ile	Glu	Asp	Pro	Lys	Thr	Lys	Leu	Ala	Tyr	His	Ala	Glu	Gly	Gln
							500			505				510		
	Gln	Leu	Lys	Val	Gly	Asp	Ile	Val	Asn	Arg	Asp	Tyr	Thr	Gly	Glu	Ile
					515			520					525			
70	Met	Trp	His	Gly	Leu	Phe	Ala	Gln	Met	Glu	His	Ser	Ser	Glu	Trp	Ile
							535					540				
	Asp	Ala	Phe	Val	Ser	Gly	Ser	Ile	Asn	Tyr	Glu	Leu	Tyr	Arg	Asn	His
							550				555				560	
75	Asn	Tyr	Gly	Gly	Ser	Lys	Ser	Thr	Gly	Tyr	Leu	Pro	Gly	Val	Ser	Pro
							565			570					575	

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Trp Lys Ser Phe Leu Pro Trp Ser Gly Lys Ala Gly Leu Ser Tyr Lys  
 580 585 590  
 Phe Ala Gln Gly His Asn Val Phe Ala Asn Gly Gly Phe Phe Thr Arg  
 595 600 605  
 5 Ala Pro Leu Phe Gly Asn Ile Tyr Ala Ala Gly Ala Ile Ile Pro Asn  
 610 615 620  
 Asp Lys Ala Asn Met Glu Lys Val Leu Thr Gly Glu Val Gly Tyr Gly  
 625 630 635 640  
 10 Phe Thr Asn His Lys Asn Phe Glu Phe Asn Ile Asn Gly Tyr Tyr Thr  
 645 650 655  
 Lys Trp Met Asp Arg Val Thr Ser Lys Arg Ile Gly Asn Glu Tyr Val  
 660 665 670  
 Tyr Leu Asn Gly Val Asp Ala Val His Cys Gly Val Glu Ala Glu Val  
 675 680 685  
 15 Ser Tyr Arg Pro Ile Arg Gln Ile Asp Leu Arg Gly Met Phe Ser Leu  
 690 695 700  
 Gly Asp Trp Thr Trp Gln Asn Asn Val Ser Tyr Thr Ser Tyr Asp Glu  
 705 710 715 720  
 20 Ala Gly Asn Glu Thr Gly Gln Asp Ile Thr Tyr Ile Lys Gly Leu His  
 725 730 735  
 Val Gly Asp Ala Ala Gln Met Thr Ala Ala Val Ser Ala Asp Ile Glu  
 740 745 750  
 Leu Phe Lys Gly Phe His Val Ile Gly Lys Tyr Asn Phe Leu Gly Lys  
 755 760 765  
 25 Asn Tyr Ala Gly Phe Asn Pro Ala Thr Arg Asn Ala Gln Gln Tyr Glu  
 770 775 780  
 Ala Asp Gly Lys Glu Ile Val Glu Ser Trp Lys Leu Pro Asp Val Gly  
 785 790 795 800  
 30 Leu Phe Asp Leu Ser Ala Ser Tyr Asn Phe Lys Leu Gly Ser Leu Ser  
 805 810 815  
 Thr Thr Phe Tyr Phe Asn Met Asp Asn Val Ala Asp Lys Arg Tyr Val  
 820 825 830  
 Ser Asp Ala Asp Asp Asn Ile Ile Gly Lys Lys His Asp Glu Ala Ser  
 835 840 845  
 35 Ala Leu Val Trp Tyr Gly Phe Gly Arg Thr Trp Ser Thr Gly Ile Arg  
 850 855 860  
 Val Asn Phe  
 865

40 (2) INFORMATION FOR SEQ ID NO:456

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 431 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...431

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:456

60 Met Lys Phe Ser Ile Arg Leu Phe Leu Cys Ile Ile Phe Leu Leu Ser  
 1 5 10 15  
 Ala Phe Ile Leu Pro Ala Leu Gly Gln Lys Ser Lys Gln Val Gln Arg  
 20 25 30  
 65 Leu Glu Lys Gln Arg Lys Glu Ala Leu Lys Ala Ile Glu Lys Thr Asp  
 35 40 45  
 Arg Glu Leu Arg Asn Thr Lys Lys Asp Lys Gln Asp Lys Gln Lys His  
 50 55 60  
 Leu Asn Leu Leu Asn Lys Gln Val Ala Gln Arg Lys Gln Met Val Gln  
 65 70 75 80  
 70 Leu Leu Asp Asn Glu Val Lys Glu Leu Gln Ser Asp Ile Asp Ser Met  
 85 90 95  
 Thr Gly Val Cys His Gln Leu Ser Val Glu Glu Lys Ala Arg Ser Asp  
 100 105 110  
 Glu Tyr Ala Gln Ala Leu Gln Ser Met Gln Lys Arg Lys Arg Ser Leu  
 115 120 125

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Asp Arg Ile Leu Phe Ile Ser Ser Ala Lys Ser Phe Asp Glu Gly Met  
 130 135 140  
 Arg Arg Met Arg Phe Leu Glu Gln Tyr Ala Ser Ala Tyr Lys Leu Ala  
 145 150 155 160  
 5 Ser Val Arg Leu Arg Asp Thr Arg Ser Lys Leu Glu Thr Glu Arg Ala  
 165 170 175  
 Thr Val Glu Asp Ala Lys Lys Glu Lys Gly His Leu Leu Val Ile Arg  
 180 185 190  
 10 Glu Glu Glu Lys Lys Lys Leu Glu Gly Gln Gln Ala Glu Gln Arg Arg  
 195 200 205  
 Gln Val Gln Ala Leu Gly Ala Lys Gln Lys Asp Leu Glu Ala Gln Leu  
 210 215 220  
 Arg Lys Gln Lys Lys Gln Ala Glu Ala Leu Asn Arg Lys Ile Glu Lys  
 225 230 235 240  
 15 Gln Ile Ala Lys Glu Ile Glu Ala Ala Glu Arg Arg Ala Arg Glu Glu  
 245 250 255  
 Arg Glu Arg Leu Ala Arg Glu Ala Lys Ala Lys Gly Lys Pro Val Pro  
 260 265 270  
 20 Ala Glu Pro Glu Arg Lys Ala Glu Thr Lys Gly Gly Tyr Ala Met Asp  
 275 280 285  
 Ala Ser Glu Arg Ala Leu Ser Gly Ser Phe Ala Gln Asn Lys Gly Arg  
 290 295 300  
 Leu Pro Gly Pro Val Arg Gly Arg Tyr Arg Ile Val Ser Asp Phe Gly  
 305 310 315 320  
 25 Val His Gln His Ser Glu Leu Lys Lys Val Gln Val Asn Asn Gly Gly  
 325 330 335  
 Ile Asp Ile Ala Val Ala Thr Gly Ser Asp Ala Thr Ser Val Phe Asp  
 340 345 350  
 30 Gly Val Val Ser Ser Val Phe Val Ile Pro Gly Tyr Asn Ser Ala Val  
 355 360 365  
 Met Val Arg His Gly Asn Tyr Ile Thr Val Tyr Ala Asn Leu Ser Lys  
 370 375 380  
 Val Tyr Val Asn Ser Gly Thr Arg Val Lys Thr Gly Gln Ala Leu Gly  
 385 390 395 400  
 35 Arg Ala Tyr Thr Asp Pro Ser Asn Asn Gln Thr Ile Ile His Phe Glu  
 405 410 415  
 Ile Trp Lys Glu Arg Ser Lys Gln Asn Pro Arg Leu Trp Leu Arg  
 420 425 430

40 (2) INFORMATION FOR SEQ ID NO:457

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 333 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
 45  
 (ii) MOLECULE TYPE: protein  
 (iii) HYPOTHETICAL: YES  
 50  
 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Porphyromonas gingivalis  
 55  
 (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...333  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:457

60 Met Lys Lys Tyr Leu Leu Tyr Ala Ser Leu Leu Thr Ser Val Leu Leu  
 1 5 10 15  
 Phe Ser Cys Ser Lys Asn Asn Pro Asn Glu Pro Val Glu Asp Arg Ser  
 20 25 30  
 65 Ile Glu Ile Ser Ile Arg Val Asp Asp Phe Thr Lys Thr Gly Glu Ala  
 35 40 45  
 Val Arg Tyr Glu Arg Asn Gln Gly Ser Ala Ala Glu Arg Leu Ile Thr  
 50 55 60  
 Asn Leu Tyr Leu Leu Leu Phe Asp Gln Ser Gly Ala Asn Pro Ala Lys  
 65 70 75 80  
 70 Tyr Tyr Ile Thr Gly Asn Thr Phe Thr Gly Gly Thr Trp Leu Pro Asp  
 85 90 95  
 Asp Met Lys Val Lys Leu Asp Met Thr Gln Ser Glu Ala Gly Glu Arg  
 100 105 110  
 75 Lys Val Tyr Val Val Ala Asn Val Asp Asn Ala Val Lys Thr Ala Leu  
 115 120 125

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Asp Ala Val Ala Asn Glu Ser Asp Leu Gln Thr Val Lys Arg Thr Thr  
 130 135 140  
 Ala Met Pro Trp Ser Thr Asp Ile Ala Ser Pro Phe Leu Met Ser Gly  
 145 150 155 160  
 5 Asn Lys Thr His Asp Phe Leu Ala Asn Arg Leu Leu Asp Asn Val Pro  
 165 170 175  
 Leu Val Arg Ala Ile Ala Lys Val Glu Leu Asn Ile Ser Leu Ser Glu  
 180 185 190  
 10 Lys Phe Gln Ile Val Pro Ile Ile Val Asn Gly Ser Leu Ser Glu Phe  
 195 200 205  
 Lys Phe Arg Tyr Val Asn Phe Asp Lys Glu Thr Tyr Val Val Lys Pro  
 210 215 220  
 Thr Thr Lys Pro Asp Asn Leu Ile Ser Ser Ala Asn Gly Val Trp Pro  
 225 230 235 240  
 15 Gln Ile Thr Asp Trp Thr Val Trp Gly Ala Ser Leu Asn Thr Ser Pro  
 245 250 255  
 Ala Pro Asp Ala Gly Thr Gly Tyr Thr Leu Asp Ala Asn Gly Lys Val  
 260 265 270  
 20 Thr Ala Leu Arg Ile Val Thr Tyr Leu Asn Glu Arg Asp Ser Lys Gly  
 275 280 285  
 Ala Thr Val Glu Val Ala Leu Pro Arg Val Asp Asp Gly Thr Leu Pro  
 290 295 300  
 Pro Pro Glu Phe Gly Pro Glu Leu Tyr Arg Leu Pro Leu Pro Asp Lys  
 305 310 315 320  
 25 Ile Leu Arg Asn His Trp Tyr Lys Tyr Glu Val Glu Ile  
 325 330

(2) INFORMATION FOR SEQ ID NO:458

- 30 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 315 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
 35 (ii) MOLECULE TYPE: protein  
 (iii) HYPOTHETICAL: YES  
 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Porphyromonas gingivalis  
 40 (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...315  
 45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:458

Met Ile Arg Thr Ile Leu Ser Arg Tyr Val Ser Ser Asn Phe Trp Ser  
 1 5 10 15  
 50 Arg Gly Ala Thr Phe Phe Phe Thr Ile Phe Pro Ala Phe Ile Leu Ala  
 20 25 30  
 Ala Thr Ala Leu Pro Ala Cys Gly Gly Thr Ala Ser Gly Ser Asp  
 35 40 45  
 55 Arg Thr Leu Ala Val Thr Ile Glu Pro Gln Lys Tyr Phe Ile Glu Ser  
 50 55 60  
 Ile Ala Asp Lys Ser Val Gln Val Val Ala Leu Val Pro Ala Gly Ser  
 65 70 75 80  
 Asn Pro Glu Glu Tyr Asp Pro Ser Pro Thr Val Met Lys Arg Leu Ser  
 85 90 95  
 60 Glu Ala Asp Ala Tyr Phe Tyr Ile Gly Gly Leu Gly Phe Glu Gln Arg  
 100 105 110  
 Asn Leu Ala Ala Ile Arg Asp Asn Pro Lys Leu Pro Leu Phe Glu  
 115 120 125  
 65 Met Gly Lys Ala Leu Ala Asp Ala Gly Ser Ala Asp Leu His Gly Ser  
 130 135 140  
 Cys Thr Asp His Ser His Thr Asp Leu His Ala His Asp Pro His Tyr  
 145 150 155 160  
 Trp Ser Ser Val Val Gly Ala Lys Ala Leu Ser Arg Ala Ala Tyr Asp  
 165 170 175  
 70 Ala Leu Val Glu Leu Tyr Pro Asn Glu Lys Asp Lys Trp Asp Lys Gly  
 180 185 190  
 His Asp Arg Leu Asn Gly Arg Ile Asp Ser Val Lys Arg Leu Val Asp  
 195 200 205  
 75 Thr Met Phe Ala Asn Gly Lys Ala Asp Lys Ala Phe Val Ile Tyr His  
 210 215 220

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Pro Ser Leu Ser Phe Phe Ala Gln Glu Phe Gly Leu Arg Gln Ile Val  
 225 230 235 240  
 Ile Glu Glu Asp Gly Lys Glu Pro Thr Ala Ala His Leu Arg Arg Val  
 245 250 255  
 5 Ile Asp Gln Ala Arg Ala Asp Gly Val Arg Ile Val Phe Ile Gln Pro  
 260 265 270  
 Glu Phe Glu Thr Arg Gln Ala Glu Asp Ile Ala Arg Glu Ile Gly Ala  
 275 280 285  
 10 Arg Pro Val Arg Ile Asn Pro Leu Arg Ser Ser Trp Glu Glu Glu Ile  
 290 295 300  
 Leu His Ile Ala Arg Ala Leu Ala His Glu Arg  
 305 310 315

(2) INFORMATION FOR SEQ ID NO:459

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 848 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

(A) NAME/KEY: misc\_feature

(B) LOCATION 1...848

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:459

Met Ile Gly Lys Lys Ile Phe Phe Ile Leu Leu Ala Leu Ile Ala Phe  
 1 5 10 15  
 Ser Gly Leu Asn Ala Ala Thr Asp Thr Glu Phe Lys Tyr Pro Thr Asp  
 20 25 30  
 Ala Asn Ile Ile Gly His Val Lys Asp Ser Lys Thr Gly Glu His Leu  
 35 40 45  
 40 Val Gly Ile Thr Ile Ala Ile Lys Gly Thr Thr Phe Gly Thr Ser Thr  
 50 55 60  
 Asp Ala Thr Gly His Tyr Tyr Leu Arg Asn Leu Arg Pro Gly Glu Ile  
 65 70 75 80  
 45 Thr Leu Ile Met Arg Gly Met Gly Tyr Lys Ser Gln Glu Arg Val Val  
 85 90 95  
 Arg Val Glu Lys Asp Lys Thr Ile Glu Val Asn Phe Glu Ala Glu Glu  
 100 105 110  
 Asp Ala Ile Asn Leu Asp Glu Val Val Ile Ser Ala Asn Arg Glu Leu  
 115 120 125  
 50 Thr Leu Arg Arg Leu Ala Pro Thr Leu Val Asn Val Leu Asn Glu Lys  
 130 135 140  
 Val Phe Ser Gln Val Asn Ala Ser Asn Leu Ala Gln Gly Leu Ser Phe  
 145 150 155 160  
 55 Gln Pro Gly Val Arg Val Glu Asn Asn Cys Gln Asn Cys Gly Phe Asn  
 165 170 175  
 Gln Val Arg Ile Asn Gly Leu Asp Gly Arg Tyr Ala Gln Ile Leu Ile  
 180 185 190  
 Asp Ser Arg Pro Ile Met Ser Ala Leu Ala Gly Val Tyr Gly Leu Glu  
 195 200 205  
 60 Gln Ile Pro Ala Asn Met Ile Glu Arg Val Glu Val Val Arg Gly Gly  
 210 215 220  
 Gly Ser Ala Leu Tyr Gly Ser Ser Ala Ile Ala Gly Val Val Asn Ile  
 225 230 235 240  
 65 Ile Thr Lys Glu Pro Ser His Asn Ser Phe Thr Phe Asn Glu Ser Leu  
 245 250 255  
 Ser Phe Thr Gly Phe Ser Lys Leu Asp Asn Asn Thr Asn Phe Asn Ala  
 260 265 270  
 Ser Ile Val Ser Asp Asp Asn Arg Ala Gly Ala Met Val Phe Gly Gln  
 275 280 285  
 70 Ala Arg Tyr Arg Asn His Trp Asp Ala Asn Asn Asp Gly Tyr Ser Glu  
 290 295 300  
 Leu Gly Lys Ile Asp Ala Arg Ser Leu Gly Ala His Ser Tyr Leu Arg  
 305 310 315 320  
 75 Leu Ser Asp Tyr Ser Lys Leu Thr Gly Glu Phe His Thr Ile Ser Glu  
 325 330 335

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5 Phe Arg Arg Gly Gly Asp Arg Ile Asp Leu Pro Pro His Val Val Gly  
 Val Ala Glu Gln Thr Asp His Ser Val Phe Ser Gly Asn Leu Lys Tyr  
 Asp Leu Phe Ser Ser Asn Tyr Lys His His Phe Gln Ala Tyr Thr Ser  
 Gly Gln Ile Val Asn Arg Lys Ser Tyr Tyr Gly Gly Ile Gly Glu Ile  
 10 Asp Val Asn Gly His Pro Gly Gly Thr Glu Gly Tyr Pro Ile Pro Gln  
 Asp Gln Tyr Gly Asn Asn Tyr Gly Val Thr Lys Gly Lys Thr Tyr Met  
 Gly Gly Ile Gln Tyr Ser Tyr Asp Leu Asp Lys Phe Leu Leu Met Pro  
 15 Ser Gln Leu Leu Phe Gly Ala Glu Tyr Thr Arg Asp Glu Leu Asn Asp  
 Val Met Pro Ile Leu Ser Trp Gln Thr Gly Glu Asp Ala Asn Gly Asn  
 Thr Ile Pro Leu Tyr Pro Glu Leu Asp Gln Asn Ile Asn Asn Tyr Ser  
 20 Leu Phe Gly Gln Asn Glu Trp Lys Asn Asp Arg Trp Ser Ile Leu Val  
 Gly Ala Arg Leu Asp Lys His Ser Glu Val Lys Asp Met Ile Leu Ser  
 25 Pro Arg Thr Thr Leu Arg Phe Asn Val Asn Pro Asp Ile Asn Leu Arg  
 Ala Thr Tyr Ala Lys Gly Phe Arg Ala Pro Gln Val Phe Asp Glu Asp  
 Leu His Val Gly Val Val Gly Gly Glu Ala Gln Lys Val Phe Asn Asp  
 30 Pro Asn Leu Lys Pro Glu Ile Ser His Ala Phe Ser Leu Ser Ala Asp  
 Met Tyr His Arg Phe Gly Asn Val Gln Thr Asn Phe Leu Val Glu Gly  
 35 Phe Tyr Thr Arg Leu Leu Asp Val Phe Thr Asn Glu Glu Gln Pro Asp  
 Gln His Asp Gly Ile Lys Arg Tyr Thr Arg Ile Asn Gly Ser Gly Ala  
 40 Lys Val Phe Gly Leu Asn Leu Glu Gly Lys Val Ala Tyr Lys Ser Phe  
 Gln Leu Gln Ala Gly Leu Thr Leu Ala Ser Asn Lys Tyr Asp Glu Ala  
 Gln Glu Trp Gly Leu Asn Thr Val Lys Asp Thr Asn Gly Ala Phe Val  
 45 Thr Glu Ala Asn Ala Asn Gly Gln Gln Glu Tyr Lys Asn Glu Ser Met  
 Thr Asp Thr Gln Ile Thr Arg Thr Pro Ser Val Tyr Gly Tyr Phe Thr  
 50 Leu Ala Tyr Asn Pro Ala His Ser Trp Asn Ile Ala Leu Thr Gly Ala  
 Tyr Thr Gly Gln Met Tyr Val Pro His Ala Ile Glu Tyr Gly Val Lys  
 Ser Ala Glu Leu Asp Ile Met Gln Asn Asn Pro Glu Ile Thr Asp Glu  
 55 Thr Gly Lys Ala Pro Arg Ile Asp Glu Leu Lys Lys Thr Pro Ala Phe  
 Phe Asp Leu Gly Leu Lys Val Gly Tyr Asp Phe His Val Phe Gln Ala  
 Thr Glu Val Gln Leu Tyr Val Gly Met Asn Asn Ile Phe Asn Ser Phe  
 60 Gln Lys Asp Phe Asp Arg Gly Ala Ala Arg Asp Ser Gly Tyr Ile Tyr  
 Gly Pro Thr Gln Pro Arg Thr Gly Tyr Met Gly Leu Val Val Lys Phe  
 65

(2) INFORMATION FOR SEQ ID NO:460

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 202 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

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(vi) ORIGINAL SOURCE:  
(A) ORGANISM: Porphyromonas gingivalis

5 (ix) FEATURE:  
(A) NAME/KEY: misc\_feature  
(B) LOCATION 1...202

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:460

```

Met Thr Val Lys Arg Ala Val Arg Ile Ala Leu Leu Thr Leu Ile Gly
1      5      10
Ile Leu Phe Ser Ser Pro Ser Leu Val Arg Ala Gln Ser Leu Phe Ser
      20      25      30
15 Thr Glu His Val Leu Gln Leu Tyr Asn Lys Ile Leu Tyr Gly Glu Ser
      35      40      45
Ala Ala Asp Thr Val Ala Glu Lys Thr Ala Gly Glu Ser Ala Phe Pro
      50      55      60
20 Phe Ile Asp Lys Leu Ile Asn Leu Gly Arg Thr Phe Leu Gly Lys Pro
      65      70      75      80
Tyr Arg Tyr Arg Gly Pro Ser Pro Trp Pro Met Asp Cys Ser Gly Tyr
      85      90      95
Val Ser Tyr Leu Tyr Ser Lys Phe Asp Ile Lys Leu Pro Arg Gly Ala
      100      105      110
25 Ala Ala Gln Ser Gln Tyr Thr Asn Pro Ile Glu Arg Glu Asp Val Arg
      115      120      125
Pro Gly Asp Leu Leu Phe Phe Lys Gly Arg Asn Ala Arg Ser Asn Arg
      130      135      140
30 Ile Gly His Val Ala Leu Val Val Ser Val Asp Glu Asp Asp Ile Thr
      145      150      155      160
Met Met His Ser Arg Asn Ser Arg Gly Ile Val Ile Glu Lys Leu Asn
      165      170      175
Arg Ser Ala Tyr Phe Ser Arg Arg Leu Val Ser Tyr Gly Arg Val Pro
      180      185      190
35 Gly Ala Lys Arg Val Ile Pro Arg Lys Ser
      195      200

```

(2) INFORMATION FOR SEQ ID NO:461

40 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 455 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

45 (ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

50 (vi) ORIGINAL SOURCE:  
(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:  
(A) NAME/KEY: misc\_feature  
(B) LOCATION 1...455

55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:461

```

Met Lys Arg Thr Ile Leu Leu Thr Ala Leu Thr Val Leu Ser Ser Leu
1      5      10
60 Ser Leu Leu Arg Ala Gln Asn Glu Ser Glu Ala Ser Thr Asn Pro Met
      20      25      30
Ser Gly Leu Ser Leu Glu Asp Cys Ile Arg Ile Ala Lys Glu Arg Asn
      35      40      45
65 Leu Asn Leu Arg Arg Gln Glu Ile Glu Gln Glu Asn Arg Ile Ile Ser
      50      55      60
Leu Asp Ala Ala Arg His Ser Phe Leu Pro Ser Val Asn Ala Gly Ile
      65      70      75      80
Gly His Asn Tyr Ser Phe Gly Arg Ser Lys Asp Lys Thr Gly Val Thr
      85      90      95
70 Val Asp Arg Ser Ser Met Asn Thr Asn Leu Ser Ile Gly Ala Ser Val
      100      105      110
Glu Val Phe Ser Gly Thr Arg Arg Leu His Asp Leu Lys Gln Gln Lys
      115      120      125
75 Tyr Asn Val Glu Asp Gly Ile Ala Arg Leu Gln Lys Ala Arg Glu Asp
      130      135      140

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Leu Ser Leu Gln Ile Ala Ala Leu Tyr Ile Asn Leu Leu Phe Arg Gln  
 145 150 155 160  
 Glu Met Thr Arg Thr Ala Glu Thr Gln Leu Ala Leu Ile Arg Glu Gln  
 165 170 175  
 5 Arg Asn Arg Thr Ala Glu Met Val Arg Val Gly Lys Trp Ala Glu Gly  
 180 185 190  
 Lys Leu Leu Asp Ile Asn Ala Gln Met Ala Lys Asp Glu Gln Leu Leu  
 195 200 205  
 10 Val Gln Tyr Arg Ser Glu Glu Leu Ala Arg Leu Asp Leu Gly Gln  
 210 215 220  
 Ala Leu Glu Leu Glu His Pro Glu Ser Ile Ala Val Lys Ala Pro Asp  
 225 230 235 240  
 Thr Asp Val Leu Val Ala Glu Arg Leu Gly Ser Leu Leu Ala Pro Glu  
 245 250 255  
 15 Glu Ile Tyr Arg Thr Ala Leu Gly Leu Lys Pro Ala Leu His Ser Ser  
 260 265 270  
 Glu Leu Gln Ile Ala Ser Ala Arg Glu Gly Leu Ala Ser Ala Arg Ala  
 275 280 285  
 20 Ala Tyr Phe Pro Thr Leu Ser Leu Ser Ala Gly Tyr Ser Asn Gly Tyr  
 290 295 300  
 Phe Arg Asp Leu Gly Lys Glu Tyr Ala Ala Ile Asn Pro Ser Phe Ser  
 305 310 315 320  
 Glu Gln Trp Lys Asn Asn Gly Ser Tyr Ser Ile Gly Leu Ser Leu Asn  
 325 330 335  
 25 Ile Pro Ile Phe Ser Ala Met Gln Thr Gln Asp Arg Val Arg Ser Ser  
 340 345 350  
 Arg Leu Gln Ile Arg Ser Ser Glu Leu Arg Leu Val Glu Lys Lys  
 355 360 365  
 30 Ala Leu Tyr Lys Glu Ile Arg Gln Ala Tyr Ser Asn Ala Val Ala Ala  
 370 375 380  
 Asp Lys Ala Ile Ala Ala Glu Asn Ser Lys Ala Ala Thr Leu Lys  
 385 390 395 400  
 Ala Tyr Glu Tyr Ala Arg Asp Ser Phe Glu Ala Gly Arg Leu Ser Ala  
 405 410 415  
 35 Tyr Glu Tyr Ala Glu Ala Lys Thr Lys Tyr Ala Leu Ser Gln Val Glu  
 420 425 430  
 Glu Leu Arg Ala Lys Tyr Asp Phe Ile Tyr Lys Ala Lys Val Leu Asp  
 435 440 445  
 40 Phe Tyr Gln Gly Lys Asp Phe  
 450 455

(2) INFORMATION FOR SEQ ID NO:462

- 45 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 444 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
 50 (ii) MOLECULE TYPE: protein  
 (iii) HYPOTHETICAL: YES  
 (vi) ORIGINAL SOURCE:  
 55 (A) ORGANISM: Porphyromonas gingivalis  
 (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...444  
 60 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:462

Met Arg Phe Gln His Tyr Leu Ile Cys Thr Ala Ala Val Ala Ala Leu  
 1 5 10 15  
 65 Ala Ala Asn Pro Leu Thr Gly Gln Ser Asn Met Thr Leu Glu Cys  
 20 25 30  
 Ile Asp Tyr Ala Arg Arg His Ser Ser Ala Val Ala Leu Ser Ala Ala  
 35 40 45  
 Glu Leu Glu Gln Ser Lys Ala Asp Tyr Leu Gln Ala Val Gly Asn Phe  
 50 55 60  
 70 Leu Pro Arg Val Ser Ala Gly Thr Gly Ala Ser Trp Asn Phe Gly Arg  
 65 70 75 80  
 Gly Leu Asp Ala Glu Thr Asn Thr Tyr Thr Asp Ile Asn Ser Phe Asn  
 85 90 95  
 75 Asn Ser Tyr Ser Ile His Ala Thr Met Thr Leu Phe Asp Gly Leu Gln  
 100 105 110

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Ser Val Tyr Arg Leu Arg Met Ala His Ala Arg Arg Glu Ala Ser Arg  
 115 120 125  
 Leu Ser Val Arg Glu Gln Gln Glu Leu Ala Ala Leu Gly Thr Thr Glu  
 130 135 140  
 5 Ala Tyr Tyr Asp Leu Val Tyr Ala Arg Gln Met Gln Glu Leu Ala Met  
 145 150 155 160  
 Gln Lys Tyr Glu Glu Ser Ser Arg Leu His Arg Gln Thr Ala Arg Met  
 165 170 175  
 10 Glu Glu Leu Gly Met Lys Ser Arg Pro Asp Val Leu Glu Met Gln Ser  
 180 185 190  
 Arg Met Ala Gly Asp Arg Leu Ala Leu Thr Gln Ala Asp Asn Gln Cys  
 195 200 205  
 Ile Ile Ala Leu Ile Arg Leu Lys Glu Lys Met Asn Phe Pro Ile Asp  
 210 215 220  
 15 Asp Glu Leu Val Val Asp Asp Met Pro Ala Asp Ser Leu Ser Ala Asp  
 225 230 235 240  
 Met Ala Glu Ser Asp Ser Ser Ala Gly Val Phe Ala Arg Ala Ala His  
 245 250 255  
 20 His His Pro Val Leu Leu Arg Ala Lys Leu Asp Glu Gln Ala Ala Thr  
 260 265 270  
 Asp Arg Leu Arg Ala Ala Arg Gly Ala Phe Leu Pro Ser Val Ser Val  
 275 280 285  
 Ser Gly Gly Trp Asn Thr Gly Phe Ser Arg Phe Leu Asn Gly Ser Asp  
 290 295 300  
 25 Tyr Thr Pro Phe Ser Glu Gln Phe Arg Asn Arg Arg Gly Glu Tyr Val  
 305 310 315 320  
 Ser Leu Asn Leu Ser Ile Pro Ile Phe Ser Gly Phe Ser Leu Val Ser  
 325 330 335  
 30 His Leu Arg Gln Ala Arg Ala Glu Arg Arg Ala Ala Ile Val Arg Arg  
 340 345 350  
 Gly Glu Ala Glu Arg Arg Leu Tyr Ser Glu Ile Ala Gln Ala Met Ala  
 355 360 365  
 Asp Arg Asp Ala Ala Leu Ala Ser Tyr Arg Gln Ala Lys Glu His Thr  
 370 375 380  
 35 Asp Ala Met Gln Thr Ala Tyr Glu Ala Val Leu Gln Arg Tyr Glu Glu  
 385 390 395 400  
 Gly Leu Asn Thr Ala Ile Asp Leu Thr Thr Gln Ala Asn Arg Leu Leu  
 405 410 415  
 40 Asp Ala Arg Val Gln Arg Leu Arg Ala Ala Met Thr Tyr Arg Leu Lys  
 420 425 430  
 Cys Lys Leu Ile Ala Tyr Tyr Gly Cys Leu Ser Asp  
 435 440

## (2) INFORMATION FOR SEQ ID NO:463

45

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 940 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

50

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

55

- (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Porphyromonas gingivalis

- (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...940

60

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:463

65

Met Asn Lys Phe Tyr Lys Ser Leu Leu Gln Ser Gly Leu Ala Ala Phe  
 1 5 10 15  
 Val Ser Met Ala Thr Ala Leu Thr Ala Ser Ala Gln Ile Ser Phe Gly  
 20 25 30  
 Gly Glu Pro Leu Ser Phe Ser Ser Arg Ser Ala Gly Thr His Ser Phe  
 35 40 45  
 70 Asp Asp Ala Met Thr Ile Arg Leu Thr Pro Asp Phe Asn Pro Glu Asp  
 50 55 60  
 Leu Ile Ala Gln Ser Arg Trp Gln Ser Gln Arg Asp Gly Arg Pro Val  
 65 70 75 80  
 75 Arg Ile Gly Gln Val Ile Pro Val Asp Val Asp Phe Ala Ser Lys Ala  
 85 90 95



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	Ser	His	Ile	Ser	Ser	Ile	Gly	Asp	Val	Asp	Val	Tyr	Arg	Leu	Gln	Phe
			100						105					110		
	Lys	Leu	Glu	Gly	Ala	Lys	Ala	Ile	Thr	Leu	Tyr	Tyr	Asp	Ala	Phe	Asn
			115					120					125			
5	Ile	Pro	Glu	Gly	Gly	Arg	Leu	Tyr	Ile	Tyr	Thr	Pro	Asp	His	Glu	Ile
		130					135					140				
	Val	Leu	Gly	Ala	Tyr	Thr	Asn	Ala	Thr	His	Arg	Arg	Asn	Gly	Ala	Phe
	145					150					155				160	
10	Ala	Thr	Glu	Pro	Val	Pro	Gly	Ser	Glu	Leu	Ile	Met	Asp	Tyr	Glu	Val
					165					170					175	
	Ser	Arg	Gly	Gly	Thr	Leu	Pro	Asp	Ile	Lys	Ile	Ser	Gly	Ala	Gly	Tyr
					180					185				190		
	Ile	Phe	Asp	Lys	Val	Gly	Gly	Arg	Pro	Val	Thr	Asp	Asn	His	Tyr	Gly
		195						200					205			
15	Ile	Gly	Glu	Asp	Asp	Ser	Asp	Ser	Asp	Cys	Glu	Ile	Asn	Ile	Asn	Cys
		210					215					220				
	Pro	Glu	Gly	Ala	Asp	Trp	Gln	Ala	Glu	Lys	Asn	Gly	Val	Val	Gln	Met
	225					230					235				240	
20	Ile	Met	Val	Lys	Gly	Gln	Tyr	Ile	Ser	Met	Cys	Ser	Gly	Asn	Leu	Leu
					245					250				255		
	Asn	Asn	Thr	Lys	Gly	Asp	Phe	Thr	Pro	Leu	Ile	Ile	Ser	Ala	Gly	His
				260					265					270		
	Cys	Ala	Ser	Ile	Thr	Thr	Asn	Phe	Gly	Val	Thr	Gln	Ser	Glu	Leu	Asp
		275						280					285			
25	Lys	Trp	Ile	Phe	Thr	Phe	His	Tyr	Glu	Lys	Arg	Gly	Cys	Ser	Asn	Gly
		290					295					300				
	Thr	Leu	Ala	Ile	Phe	Arg	Gly	Asn	Ser	Ile	Ile	Gly	Ala	Ser	Met	Lys
	305					310					315				320	
30	Ala	Phe	Leu	Pro	Ile	Lys	Gly	Lys	Ser	Asp	Gly	Leu	Leu	Leu	Gln	Leu
					325					330					335	
	Asn	Asp	Glu	Val	Pro	Leu	Arg	Tyr	Arg	Val	Tyr	Tyr	Asn	Gly	Trp	Asp
				340					345					350		
	Ser	Thr	Pro	Asp	Ile	Pro	Ser	Ser	Gly	Ala	Gly	Ile	His	His	Pro	Ala
			355					360					365			
35	Gly	Asp	Ala	Met	Lys	Ile	Ser	Ile	Leu	Lys	Lys	Thr	Pro	Ala	Leu	Asn
		370					375					380				
	Thr	Trp	Ile	Ser	Ser	Ser	Gly	Ser	Gly	Gly	Thr	Asp	Asp	His	Phe	Tyr
	385					390					395				400	
40	Phe	Lys	Tyr	Asp	Gln	Gly	Gly	Thr	Glu	Gly	Gly	Ser	Ser	Gly	Ser	Ser
					405					410				415		
	Leu	Phe	Asn	Gln	Asn	Lys	His	Val	Val	Gly	Thr	Leu	Thr	Gly	Gly	Ala
				420					425					430		
	Gly	Asn	Cys	Gly	Gly	Thr	Glu	Phe	Tyr	Gly	Arg	Leu	Asn	Ser	His	Trp
		435						440					445			
45	Asn	Glu	Tyr	Ala	Ser	Asp	Gly	Asn	Thr	Ser	Arg	Met	Asp	Ile	Tyr	Leu
		450					455					460				
	Asp	Pro	Gln	Asn	Asn	Gly	Gln	Thr	Thr	Ile	Leu	Asn	Gly	Thr	Tyr	Arg
	465					470					475				480	
50	Asp	Gly	Tyr	Lys	Pro	Leu	Pro	Ser	Val	Pro	Arg	Leu	Leu	Leu	Gln	Ser
				485						490					495	
	Thr	Gly	Asp	Gln	Val	Glu	Leu	Asn	Trp	Thr	Ala	Val	Pro	Ala	Asp	Gln
				500					505					510		
	Tyr	Pro	Ser	Ser	Tyr	Gln	Val	Glu	Tyr	His	Ile	Phe	Arg	Asn	Gly	Lys
				515				520					525			
55	Glu	Ile	Ala	Thr	Thr	Lys	Glu	Leu	Ser	Tyr	Ser	Asp	Ala	Ile	Asp	Glu
		530					535					540				
	Ser	Ile	Ile	Gly	Ser	Gly	Ile	Ile	Arg	Tyr	Glu	Val	Ser	Ala	Arg	Phe
		545				550					555				560	
60	Ile	Tyr	Pro	Ser	Pro	Leu	Asp	Gly	Val	Glu	Ser	Tyr	Lys	Asp	Thr	Asp
				565						570					575	
	Lys	Thr	Ser	Ala	Asp	Leu	Ala	Ile	Gly	Asp	Ile	Gln	Thr	Lys	Leu	Lys
				580					585					590		
	Pro	Asp	Val	Thr	Pro	Leu	Pro	Gly	Gly	Gly	Val	Ser	Leu	Ser	Trp	Lys
				595				600					605			
65	Val	Pro	Phe	Leu	Ser	Gln	Leu	Val	Ser	Arg	Phe	Gly	Glu	Ser	Pro	Asn
		610					615					620				
	Pro	Val	Phe	Lys	Thr	Phe	Glu	Val	Pro	Tyr	Val	Ser	Ala	Ala	Ala	Ala
		625					630				635				640	
70	Gln	Thr	Pro	Asn	Pro	Pro	Val	Gly	Val	Val	Ile	Ala	Asp	Lys	Phe	Met
				645						650					655	
	Ala	Gly	Thr	Tyr	Pro	Glu	Lys	Ala	Ala	Ile	Ala	Ala	Val	Tyr	Val	Met
				660				665						670		
	Pro	Ser	Ala	Pro	Asp	Ser	Thr	Phe	His	Leu	Phe	Leu	Lys	Ser	Asn	Thr
				675				680					685			
75	Asn	Arg	Arg	Leu	Gln	Lys	Val	Thr	Thr	Pro	Ser	Asp	Trp	Gln	Ala	Gly

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5                   690                                   695                                   700  
 Thr Trp Leu Arg Ile Asn Leu Asp Lys Pro Phe Pro Val Asn Asn Asp  
 705                                   710                                   715                                   720  
 His Met Leu Phe Ala Gly Ile Arg Met Pro Asn Lys Tyr Lys Leu Asn  
 725                                   730                                   735  
 Arg Ala Ile Arg Tyr Val Arg Asn Pro Asp Asn Leu Phe Ser Ile Thr  
 740                                   745                                   750  
 Gly Lys Lys Ile Ser Tyr Asn Asn Gly Val Ser Phe Glu Gly Tyr Gly  
 755                                   760                                   765  
 10 Ile Pro Ser Leu Leu Gly Tyr Met Ala Ile Lys Tyr Leu Val Val Asn  
 770                                   775                                   780  
 Thr Asp Ala Pro Lys Ile Asp Met Ser Leu Val Gln Glu Pro Tyr Ala  
 785                                   790                                   795                                   800  
 Lys Gly Thr Asn Val Ala Pro Phe Pro Glu Leu Val Gly Ile Tyr Val  
 805                                   810                                   815  
 15 Tyr Lys Asn Gly Thr Phe Ile Gly Thr Gln Asp Pro Ser Val Thr Thr  
 820                                   825                                   830  
 Tyr Ser Val Ser Asp Gly Thr Glu Ser Asp Glu Tyr Glu Ile Lys Leu  
 835                                   840                                   845  
 20 Val Tyr Lys Gly Ser Gly Ile Ser Asn Gly Val Ala Gln Ile Glu Asn  
 850                                   855                                   860  
 Asn Asn Ala Val Val Ala Tyr Pro Ser Val Val Thr Asp Arg Phe Ser  
 865                                   870                                   875                                   880  
 Ile Lys Asn Ala His Met Val His Ala Ala Leu Tyr Ser Leu Asp  
 885                                   890                                   895  
 25 Gly Lys Gln Val Arg Ser Trp Asn Asn Leu Arg Asn Gly Val Thr Phe  
 900                                   905                                   910  
 Ser Val Gln Gly Leu Thr Ala Gly Thr Tyr Met Leu Val Met Gln Thr  
 915                                   920                                   925  
 30 Ala Asn Gly Pro Val Ser Gln Lys Ile Val Lys Gln  
 930                                   935                                   940

(2) INFORMATION FOR SEQ ID NO:464

- 35           (i) SEQUENCE CHARACTERISTICS:  
             (A) LENGTH: 670 amino acids  
             (B) TYPE: amino acid  
             (D) TOPOLOGY: linear  
  
 40           (ii) MOLECULE TYPE: protein  
             (iii) HYPOTHETICAL: YES  
  
 45           (vi) ORIGINAL SOURCE:  
               (A) ORGANISM: Porphyromonas gingivalis  
  
             (ix) FEATURE:  
                 (A) NAME/KEY: misc feature  
                 (B) LOCATION 1...670  
  
 50           (xi) SEQUENCE DESCRIPTION: SEQ ID NO:464

55 Met Lys Tyr Leu Ile Arg Leu Phe Leu Ser Leu Met Leu Leu Ser Leu  
 1                                   5                                   10                                   15  
 Trp Thr Gly Cys Thr His Glu Glu Leu Ser Ile Cys Asp Gly Glu Asn  
 20                                   25                                   30  
 Thr Leu Val Leu Arg Val Glu Thr Gly Lys Ala Pro Asn Ala Arg Ala  
 35                                   40                                   45  
 60 Thr Glu Pro Gly Gln Gly Ile Tyr Asn Glu Asn Lys Val Gly Ser Ile  
 50                                   55                                   60  
 Ser Val Leu Phe Tyr Leu Glu Gly Gln Leu Arg Trp Gln Val Lys Ser  
 65                                   70                                   75                                   80  
 Thr Asp Tyr Gln Ile His Glu Gly Ala Tyr Ile Ile Pro Val Lys Glu  
 85                                   90                                   95  
 65 Gln Met Arg Pro Leu Phe Asn Gly Asn Asn Asn Phe Ser Ile Tyr Val  
 100                                   105                                   110  
 Val Ala Asn Leu Asp Phe Asn Ala Pro Ala Thr Glu Ala Ala Leu Ser  
 115                                   120                                   125  
 70 Gln Phe Val Val Glu Lys Ser Ile Glu Val Ser Ser Thr Thr Ala Pro  
 130                                   135                                   140  
 Ala Asp Phe Val Met Leu Ala His Gly Asn Lys Gln Ile Asn Met Ala  
 145                                   150                                   155                                   160  
 Thr Thr Glu Gly Lys Leu Leu Gly Asp Tyr Lys Leu Lys Arg Val Ala  
 165                                   170                                   175  
 75 Ala Lys Ile Arg Met Ile Lys Pro Thr Ile Asn Val Gln Gly Tyr Glu

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				180					185					190
	Val	Val	Gly	Asn	Ile	Gln	Ala	Lys	Phe	Arg	Asn	Ser	Val	Thr
			195					200					205	
5	Phe	Leu	Thr	Thr	Glu	Ala	Gln	Glu	Ile	Pro	Ala	Ala	Ala	Ser
		210					215				220			
	Thr	Ser	Glu	Tyr	Leu	Asp	Ile	Ala	Glu	Ser	Ala	Pro	Ala	Asn
		225				230					235			240
	His	Phe	Tyr	Ser	Tyr	Tyr	Asn	Lys	Trp	Thr	Leu	Ser	Thr	Pro
					245						250			255
10	Arg	Pro	Glu	Phe	Phe	Ile	Met	Val	Lys	Phe	Lys	Lys	Thr	Gly
				260					265					270
	Asp	Asn	Thr	Ala	Lys	Pro	Tyr	Tyr	Tyr	Arg	Val	Pro	Leu	Glu
			275					280					285	
	Asp	Asn	Gln	Val	Lys	Ser	Asn	Val	Leu	Tyr	Asn	Leu	Asn	Val
15			290				295					300		Lys
	Glu	Ile	Leu	Gly	Ser	Leu	Gln	Glu	Pro	Glu	Ala	Val	Ser	Val
						310				315				320
	Thr	Leu	Ala	Ile	Glu	Glu	Trp	Ile	Leu	His	Gln	Asp	Ala	Phe
				325						330				335
20	Pro	Ala	Thr	Asn	Tyr	Leu	Ile	Val	Glu	Gln	His	Glu	Ile	Phe
				340					345					350
	Asn	Val	Asn	Thr	Tyr	Ser	Val	Lys	Tyr	Gln	Thr	Ser	Gln	Lys
			355					360					365	
25	Ser	Ile	Ser	Ile	Gln	Ser	Val	Thr	Phe	Ser	Tyr	Val	Ser	Ser
		370					375					380		Asp
	Thr	Gln	His	Asn	Asp	Leu	Val	Ala	Ser	Ser	Ser	Asp	Gln	Tyr
				385		390					395			400
	Ile	Thr	Ser	Asp	Asn	Thr	Ser	Ile	Ile	Ile	Thr	Ser	Lys	Ile
				405						410				415
30	Asn	Asn	Val	Pro	Lys	Lys	Ile	Val	Phe	Glu	Val	Thr	Asn	Gly
			420						425					430
	Gly	Leu	Lys	Glu	Thr	Val	Thr	Val	Leu	Gln	Tyr	Pro	Ala	Gln
			435					440					445	Phe
	Val	Asn	Thr	Leu	Gly	Thr	Ala	Ser	Ala	Trp	Arg	Pro	Asp	Gly
35			450				455					460		Ser
	Ala	Pro	Gly	Leu	Asn	Asn	Lys	Ala	Ile	Tyr	His	Val	Val	Val
			465			470					475			480
	Pro	Pro	Glu	Asn	Leu	Phe	Glu	Asp	Gly	Thr	Gln	Thr	Ile	Ile
				485						490				495
40	Pro	Pro	Thr	Glu	Thr	Ile	Ser	Phe	His	Lys	Lys	Glu	Asn	Asn
				500					505					510
	Pro	Ile	Val	Trp	Ser	Asp	Thr	Asn	Thr	Thr	Lys	Gln	Asp	Leu
			515					520					525	Glu
45	Ser	Arg	Met	Ile	Ser	Pro	Ser	Phe	Glu	Leu	Ala	Ser	Gln	Leu
			530				535					540		Gly
	Thr	Leu	Pro	Met	Pro	Tyr	Leu	Glu	Tyr	Trp	Pro	Gly	Thr	Ser
			545			550				555				560
	Leu	Asp	Tyr	Ser	Gly	Asn	Tyr	Asn	Asn	Lys	Arg	Tyr	Ala	Leu
				565						570				Phe
50	Cys	Ala	Phe	Tyr	Trp	Glu	Lys	Arg	Lys	Val	Asn	Asn	Glu	Glu
			580						585				590	Ile
	Phe	Asp	Asp	Trp	Arg	Leu	Pro	Thr	Glu	Ala	Glu	Ile	Lys	Leu
			595					600				605		Ile
55	Lys	Leu	Gln	His	Asn	Glu	Gln	Ser	Ala	Val	Gln	Ala	Ile	Met
			610				615					620		Thr
	Asn	Tyr	Tyr	Trp	Asp	Ser	Tyr	Ser	Ala	Asn	Gly	Ser	Tyr	Lys
			625			630					635			Met
	Gly	Gly	Gly	Gly	Gly	Asn	Ser	Ser	Lys	Ala	Tyr	Val	Arg	Cys
				645					650					Val
60	Arg	Asp	Val	Lys	Lys	Pro	Ile	Arg	Asp	Lys	Lys	Ser	Gly	Lys
			660						665					670

(2) INFORMATION FOR SEQ ID NO:465

- 65 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1282 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear
- 70 (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:  
 75 (A) ORGANISM: Porphyromonas gingivalis

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(ix) FEATURE:

(A) NAME/KEY: misc\_feature  
(B) LOCATION 1...1282

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:465

	Met	Arg	Lys	Ile	Leu	Ser	Phe	Leu	Met	Met	Cys	Ser	Leu	His	Leu	Gly
	1			5					10					15		
10	Leu	Gln	Ser	Gln	Thr	Trp	His	Gly	Asp	Pro	Asp	Ser	Val	Ala	Ala	Leu
			20					25					30			
	Pro	Ser	Ile	Gly	Ile	Gln	Glu	Ser	Ser	Cys	Thr	Arg	Ile	Thr	Phe	Glu
			35					40					45			
15	Val	Val	Phe	Pro	Gly	Phe	Tyr	Ser	Val	Glu	Lys	Arg	Glu	Gly	Asn	Gln
			50				55					60				
	Val	Phe	Gln	Arg	Ile	Ser	Met	Pro	Gly	Cys	Gly	Ser	Phe	Gly	Asn	Leu
	65					70				75					80	
	Gly	Glu	Ala	Glu	Leu	Pro	Val	Leu	Lys	Lys	Met	Ile	Ala	Val	Pro	Glu
				85					90					95		
20	Phe	Ser	Thr	Ala	Asn	Val	Ala	Val	Lys	Ile	Lys	Glu	Thr	Glu	Thr	Phe
				100					105					110		
	Asp	Asn	Tyr	Asn	Ile	Tyr	Pro	Asn	Pro	Thr	Tyr	Val	Val	Glu	Glu	Leu
			115					120					125			
25	Pro	Glu	Gly	Gly	Thr	Tyr	Leu	Val	Glu	Ala	Phe	Ala	Ile	Asn	Asn	Asp
			130				135					140				
	Tyr	Tyr	Ser	Gln	Asn	Val	Ser	Leu	Pro	Ser	Thr	His	Tyr	Val	Tyr	Ser
	145				150						155				160	
	Gln	Asp	Gly	Tyr	Phe	Arg	Ser	Gln	Arg	Phe	Ile	Glu	Val	Thr	Leu	Tyr
				165					170					175		
30	Pro	Phe	Arg	Tyr	Asn	Pro	Val	Arg	Gln	Glu	Ile	Leu	Phe	Ala	Lys	Lys
				180				185						190		
	Ile	Glu	Val	Thr	Ile	Thr	Phe	Asp	Asn	Pro	Gln	Pro	Pro	Leu	Gln	Lys
				195				200					205			
35	Asn	Thr	Gly	Ile	Phe	Asn	Lys	Val	Ala	Ser	Ser	Ala	Phe	Ile	Asn	Tyr
			210				215					220				
	Glu	Ala	Asp	Gly	Lys	Ser	Ala	Ile	Glu	Asn	Asp	Met	Val	Phe	Ser	Arg
	225				230						235				240	
	Gly	Thr	Thr	Thr	Tyr	Ile	Ser	Gly	Asn	Val	Ala	Ser	Asn	Leu	Pro	Gln
				245					250					255		
40	Asn	Cys	Asp	Tyr	Leu	Val	Ile	Tyr	Asp	Asp	Met	Phe	Asn	Val	Asn	Gln
				260				265					270			
	Gln	Pro	His	Asp	Glu	Ile	Lys	Arg	Leu	Cys	Glu	His	Arg	Ala	Phe	Tyr
			275					280					285			
45	Asn	Gly	Phe	Asp	Val	Ala	Ala	Val	Ser	Ile	Lys	Asp	Val	Leu	Asn	Ser
		290				295					300					
	Phe	Pro	Ser	Asn	Ala	Thr	Ser	Tyr	Ile	Asn	Glu	Thr	Lys	Leu	Lys	Asn
		305				310					315				320	
	Phe	Ile	Arg	Ser	Val	Tyr	Asn	Gln	Ser	Asn	Ala	Lys	Arg	Thr	Leu	Asp
				325						330				335		
50	Gly	Lys	Leu	Gly	Tyr	Val	Leu	Leu	Ile	Gly	Lys	Pro	Leu	Ser	Lys	Tyr
			340						345					350		
	Leu	Ala	Asp	Thr	Asp	Asn	Thr	Lys	Val	Pro	Thr	Ser	Phe	Ile	His	Asn
			355					360					365			
55	Val	Ser	Leu	Ile	Pro	Ser	His	Pro	Thr	Phe	Gly	Ser	Ile	Cys	Ala	Ser
		370					375					380				
	Asp	Tyr	Phe	Phe	Ser	Cys	Val	Ser	Pro	Leu	Asp	Thr	Val	Gly	Asp	Leu
		385				390					395				400	
	Phe	Ile	Gly	Arg	Phe	Ser	Val	Thr	Asn	Ala	His	Glu	Leu	His	Asn	Leu
				405					410					415		
60	Ile	Glu	Lys	Thr	Ile	Asn	Lys	Glu	Ile	Ser	Tyr	Asn	Pro	Ile	Ala	His
				420					425					430		
	Lys	Asn	Ile	Leu	Tyr	Ala	Glu	Gly	Lys	Gly	Cys	Asp	Ala	Pro	Ile	Leu
				435				440					445			
65	Arg	Leu	Phe	Leu	Lys	Glu	Ile	Ala	Ser	Gly	Tyr	Thr	Val	Asn	Ser	Ile
		450				455					460					
	Leu	Lys	Ser	Asn	Gln	Val	Ser	Ala	Ile	Asp	Ser	Ile	Phe	Asp	Cys	Leu
		465				470					475				480	
	Asn	Asn	Gly	Ser	His	His	Phe	Tyr	Phe	Asn	Thr	His	Gly	Met	Pro	Thr
				485					490					495		
70	Val	Trp	Gly	Ile	Gly	Gln	Gly	Leu	Asp	Val	Asn	Thr	Leu	Thr	Ala	Arg
				500					505					510		
	Leu	Asn	Asn	Thr	Ser	Ser	Gln	Gly	Leu	Cys	Thr	Ser	Leu	Ser	Cys	Ser
				515				520					525			
75	Ser	Ala	Val	Ala	Asp	Ser	Thr	Ile	Arg	Ser	Leu	Gly	Glu	Val	Leu	Thr
				530			535					540				

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	Thr	Tyr	Ala	Pro	Asn	Lys	Gly	Phe	Ser	Ala	Phe	Leu	Gly	Gly	Ser	Arg	
	545					550					555					560	
	Ala	Thr	Gln	Tyr	Ala	Val	Tyr	Leu	Glu	Gly	Pro	Cys	Pro	Pro	Ser	Glu	
					565					570						575	
5	Phe	Tyr	Glu	Tyr	Leu	Pro	Tyr	Ser	Leu	Tyr	His	Asn	Leu	Ser	Thr	Val	
				580					585					590			
	Val	Gly	Glu	Met	Leu	Leu	Ser	Ser	Ile	Ile	Asn	Thr	Asn	Ser	Val	Asp	
				595				600					605				
10	Thr	Tyr	Ser	Lys	Phe	Asn	Phe	Asn	Leu	Leu	Gly	Asp	Pro	Ala	Leu	Asn	
	610						615					620					
	Ile	Met	Ala	His	Gly	Met	Glu	Val	Ser	Asn	Cys	Ile	Thr	Leu	Pro	Asn	
	625					630					635					640	
	Asn	Thr	Ile	Ile	Ser	Ser	Pro	Ile	Thr	Ile	Lys	Asn	Gly	Gly	Cys	Leu	
					645					650					655		
15	Lys	Ile	Pro	Glu	Lys	Gly	Val	Leu	His	Phe	Thr	Asn	Asn	Gly	Ser	Ile	
				660					665					670			
	Gln	Val	Met	Ser	Gly	Gly	Thr	Leu	Glu	Ile	Gly	Asn	Gln	Ala	Lys	Ile	
				675				680					685				
20	Ser	Gly	Glu	Thr	Gly	Ala	Asn	Pro	Thr	Phe	Ile	Thr	Val	Tyr	Gly	Asp	
	690						695					700					
	Gly	Leu	Ala	Ile	Asn	Lys	Gln	Val	Glu	Ile	Asp	Asn	Ile	Asp	Arg	Leu	
	705					710					715					720	
	Asn	Leu	Phe	Ser	Thr	His	Ser	Val	Met	Pro	Lys	Phe	His	Phe	Asp	Ser	
					725					730					735		
25	Val	Lys	Phe	Asn	Ser	Ala	Pro	Leu	Tyr	Thr	Thr	Asn	Cys	Ile	Val	Glu	
				740					745					750			
	Ile	Ser	Asn	Cys	Glu	Phe	Thr	Asn	Arg	Ser	Asp	Ile	Ile	Ser	Lys	Asn	
				755				760					765				
30	Cys	Asp	Leu	Ser	Val	Glu	Asn	Ser	Met	Phe	Ser	Ser	Ser	Gly	Ile	Thr	
	770						775					780					
	Val	Phe	Lys	Pro	Met	Ala	Thr	Ser	Ser	Ile	Thr	Gly	Leu	Ser	Thr	Lys	
	785					790					795					800	
	Ala	Lys	Ile	Thr	Asp	Asn	Thr	Phe	Phe	Ala	Thr	Gly	Asn	Phe	Ala	Tyr	
					805					810					815		
35	His	Ile	Thr	Asn	Thr	Pro	Gly	Leu	Thr	Ala	Thr	Ser	Asn	Ala	Ala	Ile	
				820					825					830			
	Lys	Leu	Asp	Asn	Ile	Pro	Glu	Tyr	Tyr	Ile	Ser	Gly	Asn	Lys	Ile	Val	
				835				840					845				
40	Asn	Cys	Asp	Glu	Ala	Leu	Val	Leu	Asn	Asn	Ser	Gly	Asn	Arg	Thr	Asn	
	850						855					860					
	Arg	Leu	His	Asn	Ile	Thr	Arg	Asn	Val	Ile	Lys	Asn	Cys	Arg	Ile	Gly	
	865					870					875					880	
	Ser	Thr	Leu	Tyr	Asn	Ser	Tyr	Gly	Ile	Tyr	Asn	Arg	Asn	Lys	Ile	Ser	
					885					890					895		
45	Asn	Asn	His	Ile	Gly	Val	Arg	Leu	Leu	Asn	Asn	Ser	Cys	Phe	Tyr	Phe	
				900					905					910			
	Asp	Asn	Ala	Pro	Val	Ile	Asn	Glu	Glu	Asp	Lys	Gln	Thr	Phe	Ile	Ser	
				915				920					925				
50	Asn	Arg	Thr	Trp	Gln	Leu	Tyr	Ser	Ser	Asn	Gly	Thr	Phe	Pro	Leu	Asn	
	930						935					940					
	Phe	His	Tyr	Asn	Ser	Leu	Gln	Gly	Gly	Asp	Thr	Asp	Thr	Trp	Ile	Tyr	
	945					950				955						960	
	Asn	Asp	Thr	Tyr	Thr	Asn	Arg	Tyr	Ile	Asp	Val	Ser	Asn	Asn	His	Trp	
					965					970					975		
55	Gly	Asn	Asn	Asp	Leu	Phe	Asp	Pro	Asn	Gln	Val	Phe	Asn	Thr	Pro	Asp	
				980					985					990			
	Leu	Phe	Ile	Trp	Ile	Pro	Phe	Trp	Asp	Gly	Leu	Pro	Asn	Gly	Arg	Ser	
				995				1000						1005			
60	Gly	Asn	Ser	Ser	Ala	Glu	Ala	Val	Glu	Phe	Gln	Thr	Ala	Leu	Asp	Cys	
	1010						1015						1020				
	Ile	Gly	Asn	Ser	Asp	Tyr	Leu	Ser	Ala	Lys	Val	Ala	Leu	Lys	Met	Met	
	1025					1030					1035					1040	
	Val	Glu	Thr	Tyr	Pro	Glu	Ser	Asp	Phe	Ala	Ile	Ala	Ala	Leu	Lys	Glu	
					1045					1050					1055		
65	Leu	Phe	Arg	Ile	Glu	Lys	Met	Ser	Gly	Asn	Asp	Tyr	Glu	Gly	Leu	Lys	
				1060					1065					1070			
	Asp	Tyr	Phe	Arg	Ser	Asn	Pro	Thr	Ile	Ile	Ser	Ser	Gln	Asn	Leu	Phe	
				1075				1080					1085				
70	Pro	Thr	Ala	Asp	Phe	Leu	Ser	Ala	Arg	Cys	Asp	Ile	Val	Cys	Glu	Asn	
	1090						1095					1100					
	Tyr	Gln	Ser	Ala	Ile	Asp	Trp	Tyr	Glu	Asn	Arg	Leu	Asn	Ser	Glu	Ile	
	1105					1110					1115					1120	
	Ser	Tyr	Gln	Asp	Ser	Val	Phe	Ala	Val	Ile	Asp	Leu	Gly	Asp	Ile	Tyr	
					1125					1130					1135		
75	Trp	Asn	Met	Gln	Leu	Asp	Ser	Leu	Arg	Gly	Thr	Gly	Ile	Asp	Leu	Asn	

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1140 1145 1150  
 Ile Leu Ser Cys Glu Gln Arg Lys Ser Leu Glu Ser His Gln Asn Val  
 1155 1160 1165  
 Lys Asn Tyr Leu Leu Ser Thr Leu Pro Glu Ser Thr Gly Thr Leu Leu  
 1170 1175 1180  
 Pro Pro Leu Glu Cys Asn Lys Ser Ser Leu Asp Lys Ser Lys Ile Ile  
 1185 1190 1195 1200  
 Ser Ile Ser Pro Asn Pro Ala Lys Ala Val Val Thr Ile Ile Tyr Tyr  
 1205 1210 1215  
 Thr Asp Asn Pro Ser Cys Ser Val Ile Lys Ile Tyr Gly Ile Asn Gly  
 1220 1225 1230  
 Ala Ser Ala Asp Ile Thr Gly Leu Pro Lys His Leu Ser Glu Gly Tyr  
 1235 1240 1245  
 Tyr Ser Ile Gln Phe Asn Thr Ser Asn Phe Asp Pro Gly Phe Tyr Leu  
 1250 1255 1260  
 Val Thr Leu Asn Val Asp Gln Lys Ile Ile Asp Thr Glu Lys Leu Arg  
 1265 1270 1275 1280  
 Ile Lys

20

(2) INFORMATION FOR SEQ ID NO:466

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1274 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

(A) NAME/KEY: misc feature

(B) LOCATION 1...1274

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:466

40

Met Met Cys Ser Leu His Leu Gly Leu Gln Ser Gln Thr Trp His Gly  
 1 5 10 15  
 Asp Pro Asp Ser Val Ala Ala Leu Pro Ser Ile Gly Ile Gln Glu Ser  
 20 25 30  
 Ser Cys Thr Arg Ile Thr Phe Glu Val Val Phe Pro Gly Phe Tyr Ser  
 35 40 45  
 Val Glu Lys Arg Glu Gly Asn Gln Val Phe Gln Arg Ile Ser Met Pro  
 50 55 60  
 Gly Cys Gly Ser Phe Gly Asn Leu Gly Glu Ala Glu Leu Pro Val Leu  
 65 70 75 80  
 Lys Lys Met Ile Ala Val Pro Glu Phe Ser Thr Ala Asn Val Ala Val  
 85 90 95  
 Lys Ile Lys Glu Thr Glu Thr Phe Asp Asn Tyr Asn Ile Tyr Pro Asn  
 100 105 110  
 Pro Thr Tyr Val Val Glu Glu Leu Pro Glu Gly Gly Thr Tyr Leu Val  
 115 120 125  
 Glu Ala Phe Ala Ile Asn Asn Asp Tyr Tyr Ser Gln Asn Val Ser Leu  
 130 135 140  
 Pro Ser Thr His Tyr Val Tyr Ser Gln Asp Gly Tyr Phe Arg Ser Gln  
 145 150 155 160  
 Arg Phe Ile Glu Val Thr Leu Tyr Pro Phe Arg Tyr Asn Pro Val Arg  
 165 170 175  
 Gln Glu Ile Leu Phe Ala Lys Lys Ile Glu Val Thr Ile Thr Phe Asp  
 180 185 190  
 Asn Pro Gln Pro Pro Leu Gln Lys Asn Thr Gly Ile Phe Asn Lys Val  
 195 200 205  
 Ala Ser Ser Ala Phe Ile Asn Tyr Glu Ala Asp Gly Lys Ser Ala Ile  
 210 215 220  
 Glu Asn Asp Met Val Phe Ser Arg Gly Thr Thr Tyr Ile Ser Gly  
 225 230 235 240  
 Asn Val Ala Ser Asn Leu Pro Gln Asn Cys Asp Tyr Leu Val Ile Tyr  
 245 250 255  
 Asp Asp Met Phe Asn Val Asn Gln Gln Pro His Asp Glu Ile Lys Arg  
 260 265 270  
 Leu Cys Glu His Arg Ala Phe Tyr Asn Gly Phe Asp Val Ala Ala Val

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Ile Tyr Asn Arg Asn Lys Ile Ser Asn Asn His Ile Gly Val Arg Leu  
 885 890 895  
 Leu Asn Asn Ser Cys Phe Tyr Phe Asp Asn Ala Pro Val Ile Asn Glu  
 900 905 910  
 5 Glu Asp Lys Gln Thr Phe Ile Ser Asn Arg Thr Trp Gln Leu Tyr Ser  
 915 920 925  
 Ser Asn Gly Thr Phe Pro Leu Asn Phe His Tyr Asn Ser Leu Gln Gly  
 930 935 940  
 10 Gly Asp Thr Asp Thr Trp Ile Tyr Asn Asp Thr Tyr Thr Asn Arg Tyr  
 945 950 955 960  
 Ile Asp Val Ser Asn Asn His Trp Gly Asn Asn Asp Leu Phe Asp Pro  
 965 970 975  
 Asn Gln Val Phe Asn Thr Pro Asp Leu Phe Ile Trp Ile Pro Phe Trp  
 980 985 990  
 15 Asp Gly Leu Pro Asn Gly Arg Ser Gly Asn Ser Ser Ala Glu Ala Val  
 995 1000 1005  
 Glu Phe Gln Thr Ala Leu Asp Cys Ile Gly Asn Ser Asp Tyr Leu Ser  
 1010 1015 1020  
 20 Ala Lys Val Ala Leu Lys Met Met Val Glu Thr Tyr Pro Glu Ser Asp  
 1025 1030 1035 1040  
 Phe Ala Ile Ala Ala Leu Lys Glu Leu Phe Arg Ile Glu Lys Met Ser  
 1045 1050 1055  
 Gly Asn Asp Tyr Glu Gly Leu Lys Asp Tyr Phe Arg Ser Asn Pro Thr  
 1060 1065 1070  
 25 Ile Ile Ser Ser Gln Asn Leu Phe Pro Thr Ala Asp Phe Leu Ser Ala  
 1075 1080 1085  
 Arg Cys Asp Ile Val Cys Glu Asn Tyr Gln Ser Ala Ile Asp Trp Tyr  
 1090 1095 1100  
 30 Glu Asn Arg Leu Asn Ser Glu Ile Ser Tyr Gln Asp Ser Val Phe Ala  
 1105 1110 1115 1120  
 Val Ile Asp Leu Gly Asp Ile Tyr Trp Asn Met Gln Leu Asp Ser Leu  
 1125 1130 1135  
 Arg Gly Thr Gly Ile Asp Leu Asn Ile Leu Ser Cys Glu Gln Arg Lys  
 1140 1145 1150  
 35 Ser Leu Glu Ser His Gln Asn Val Lys Asn Tyr Leu Leu Ser Thr Leu  
 1155 1160 1165  
 Pro Glu Ser Thr Gly Thr Leu Leu Pro Pro Leu Glu Cys Asn Lys Ser  
 1170 1175 1180  
 40 Ser Leu Asp Lys Ser Lys Ile Ile Ser Ile Ser Pro Asn Pro Ala Lys  
 1185 1190 1195 1200  
 Ala Val Val Thr Ile Ile Tyr Tyr Thr Asp Asn Pro Ser Cys Ser Val  
 1205 1210 1215  
 Ile Lys Ile Tyr Gly Ile Asn Gly Ala Ser Ala Asp Ile Thr Gly Leu  
 1220 1225 1230  
 45 Pro Lys His Leu Ser Glu Gly Tyr Tyr Ser Ile Gln Phe Asn Thr Ser  
 1235 1240 1245  
 Asn Phe Asp Pro Gly Phe Tyr Leu Val Thr Leu Asn Val Asp Gln Lys  
 1250 1255 1260  
 50 Ile Ile Asp Thr Glu Lys Leu Arg Ile Lys  
 1265 1270

(2) INFORMATION FOR SEQ ID NO:467

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 925 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
 55  
 (ii) MOLECULE TYPE: protein  
 60  
 (iii) HYPOTHETICAL: YES  
 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Porphyromonas gingivalis  
 65  
 (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...925  
 70  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:467

Met Ala Ile Met Met Lys Ser Ile Val Phe Arg Ala Phe Leu Thr Ile  
 1 5 10 15  
 75 Leu Leu Ser Trp Ala Ala Ile Thr Asn Pro Thr Ala Gln Glu Ile Ser  
 20 25 30



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Gly Met Asn Ala Ser Cys Leu Ala Ala Pro Ala Gln Pro Asp Thr Ile  
 35 40 45  
 Leu Tyr Glu Ser Phe Glu Asn Gly Pro Val Pro Asn Gly Trp Leu Glu  
 50 55 60  
 5 Ile Asp Ala Asp Ala Asp Gly Ala Thr Trp Gly Ser Pro Ser Gly Ser  
 65 70 75 80  
 Phe Ser Val Pro Tyr Gly His Asn Gly Leu Cys Thr Tyr Ser His Ile  
 85 90 95  
 10 Arg Ser Gly Ile Ser Thr Ala Gly Asn Tyr Leu Ile Thr Pro Asn Ile  
 100 105 110  
 Glu Gly Ala Lys Arg Val Lys Tyr Trp Val Cys Asn Gln Tyr Ser Thr  
 115 120 125  
 Asn Pro Glu His Tyr Ala Val Met Val Ser Thr Thr Gly Thr Ala Ile  
 130 135 140  
 15 Glu Asp Phe Val Leu Leu Phe Asp Asp Ser Ile Thr Gly Lys Pro Thr  
 145 150 155 160  
 Pro Leu Val Trp Arg Arg Arg Ile Val Asp Leu Pro Glu Gly Thr Lys  
 165 170 175  
 20 Tyr Ile Ala Trp Arg His Tyr Lys Val Thr Asp Ser His Thr Glu Phe  
 180 185 190  
 Leu Lys Leu Asp Asp Val Thr Val Tyr Arg Ser Ile Glu Gly Pro Glu  
 195 200 205  
 Pro Ala Thr Asp Phe Thr Val Ile Asn Ile Gly Gln Asn Val Gly Arg  
 210 215 220  
 25 Leu Thr Trp Asn Tyr Pro Glu Asp Tyr Gln Pro Glu Gly Lys Gly Asn  
 225 230 235 240  
 Glu Glu Leu Gln Leu Ser Gly Tyr Asn Ile Tyr Ala Asn Gly Thr Leu  
 245 250 255  
 30 Leu Ala Gln Ile Lys Asp Val Ser Ile Leu Glu Tyr Val Asp Ser Thr  
 260 265 270  
 Tyr Ser Leu Arg Asp Asn Pro Leu Gln Val Glu Tyr Cys Val Thr Ala  
 275 280 285  
 Val Tyr Asp Glu Ser Ile Glu Ser Ser Thr Val Cys Gly Thr Leu His  
 290 295 300  
 35 Tyr Ala Thr Asp Ala Ile Leu Tyr Glu Asn Phe Glu Asn Gly Pro Val  
 305 310 315 320  
 Pro Asn Gly Trp Leu Val Ile Asp Ala Asp Gly Asp Gly Phe Ser Trp  
 325 330 335  
 40 Gly His Tyr Leu Asn Ala Tyr Asp Ala Phe Pro Gly His Asn Gly Gly  
 340 345 350  
 His Cys Ser Leu Ser Ala Ser Tyr Val Pro Gly Ile Gly Pro Val Thr  
 355 360 365  
 Pro Asp Asn Tyr Leu Ile Thr Pro Lys Val Glu Gly Ala Lys Arg Val  
 370 375 380  
 45 Lys Tyr Trp Val Ser Thr Gln Asp Ala Asn Trp Ala Ala Glu His Tyr  
 385 390 395 400  
 Ala Val Met Ala Ser Thr Thr Gly Thr Ala Val Gly Asp Phe Val Ile  
 405 410 415  
 50 Leu Phe Glu Glu Thr Met Thr Ala Lys Pro Thr Gly Ala Trp Tyr Glu  
 420 425 430  
 Arg Thr Ile Asn Leu Pro Glu Gly Thr Lys Tyr Ile Ala Trp Arg His  
 435 440 445  
 Tyr Asn Cys Thr Asp Ile Tyr Phe Leu Lys Leu Asp Asp Ile Thr Val  
 450 455 460  
 55 Phe Gly Thr Pro Ala Ser Glu Pro Glu Pro Val Thr Asp Phe Val Val  
 465 470 475 480  
 Ser Leu Ile Glu Asn Asn Lys Gly Arg Leu Lys Trp Asn Tyr Pro Asn  
 485 490 495  
 60 Gly Tyr Glu Pro Asp Lys Thr Asp Asp Lys Asp Pro Leu Gln Leu Ala  
 500 505 510  
 Gly Tyr Asn Ile Tyr Ala Asn Gly Ser Leu Leu Val His Ile Gln Asp  
 515 520 525  
 Pro Thr Val Leu Glu Tyr Ile Asp Glu Thr Tyr Ser Ser Arg Asp Asp  
 530 535 540  
 65 Gln Val Glu Val Glu Tyr Cys Val Thr Ala Val Tyr Asn Asp Asn Ile  
 545 550 555 560  
 Glu Ser Gln Ser Val Cys Asp Lys Leu Ile Tyr Asp Ser Gln Ser Asp  
 565 570 575  
 70 Ile Ile Leu Tyr Glu Gly Phe Glu Ala Gly Ser Ile Pro Glu Gly Trp  
 580 585 590  
 Leu Leu Ile Asp Ala Asp Gly Asp Asn Val Asn Trp Asp Tyr Tyr Pro  
 595 600 605  
 Trp Thr Met Tyr Gly His Asp Ser Glu Lys Cys Ile Ala Ser Pro Ser  
 610 615 620  
 75 Tyr Leu Pro Met Ile Gly Val Leu Thr Pro Asp Asn Tyr Leu Val Thr

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5 625 630 635 640  
 Pro Arg Leu Glu Gly Ala Lys Leu Val Lys Tyr Trp Val Ser Ala Gln  
 645 650 655  
 Asp Ala Val Tyr Ser Ala Glu His Tyr Ala Val Met Val Ser Thr Thr  
 660 665 670  
 Gly Thr Ala Val Glu Asp Phe Val Leu Leu Phe Glu Glu Thr Met Thr  
 675 680 685  
 Ala Lys Ala Asn Gly Ala Trp Tyr Glu Arg Thr Ile Thr Leu Pro Ala  
 690 695 700  
 10 Gly Thr Lys Tyr Ile Ala Trp Arg His Tyr Asp Cys Thr Asp Met Phe  
 705 710 715 720  
 Phe Leu Leu Leu Asp Asp Ile Thr Val Tyr Arg Ser Thr Glu Thr Val  
 725 730 735  
 15 Pro Glu Pro Val Thr Asp Phe Val Val Ser Leu Ile Glu Asn Asn Lys  
 740 745 750  
 Gly Arg Leu Lys Trp Asn Tyr Pro Asn Gly Tyr Glu Pro Asp Lys Thr  
 755 760 765  
 Asp Asp Lys Lys Pro Leu Gln Leu Thr Gly Tyr Asn Ile Tyr Ala Asn  
 770 775 780  
 20 Gly Ser Leu Leu Val His Ile Gln Asp Pro Thr Val Leu Glu Tyr Ile  
 785 790 795 800  
 Asp Glu Thr Tyr Ser Ser Arg Asp Gly Gln Val Glu Met Glu Tyr Cys  
 805 810 815  
 25 Val Thr Ala Val Tyr Asn Asp Asn Ile Glu Ser Gln Ser Val Cys Asp  
 820 825 830  
 Lys Leu Asn Tyr Thr Ile Thr Ser Leu Asp Asn Ile Gln Ser Asp Thr  
 835 840 845  
 Ser Leu Lys Ile Tyr Pro Asn Pro Ala Ser Tyr Val Val Arg Ile Glu  
 850 855 860  
 30 Gly Leu Ser Arg Ser Lys Ser Thr Ile Glu Leu Tyr Asn Ala Leu Gly  
 865 870 875 880  
 Ile Cys Ile Leu Arg Glu Glu Thr His Ser Glu Lys Thr Glu Ile Asp  
 885 890 895  
 35 Val Ser Arg Leu Asn Asp Gly Val Tyr Leu Ile Lys Val Val Gly Gly  
 900 905 910  
 Asn Lys Thr Thr Thr Glu Lys Val Glu Ile Lys Arg Pro  
 915 920 925

## (2) INFORMATION FOR SEQ ID NO:468

- 40 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 922 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
 45 (ii) MOLECULE TYPE: protein  
 (iii) HYPOTHETICAL: YES  
 50 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Porphyromonas gingivalis  
 (ix) FEATURE:  
 (A) NAME/KEY: misc feature  
 55 (B) LOCATION 1...922  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:468

60 Met Met Lys Ser Ile Val Phe Arg Ala Phe Leu Thr Ile Leu Leu Ser  
 1 5 10 15  
 Trp Ala Ala Ile Thr Asn Pro Thr Ala Gln Glu Ile Ser Gly Met Asn  
 20 25 30  
 Ala Ser Cys Leu Ala Ala Pro Ala Gln Pro Asp Thr Ile Leu Tyr Glu  
 35 40 45  
 65 Ser Phe Glu Asn Gly Pro Val Pro Asn Gly Trp Leu Glu Ile Asp Ala  
 50 55 60  
 Asp Ala Asp Gly Ala Thr Trp Gly Ser Pro Ser Gly Ser Phe Ser Val  
 65 70 75 80  
 70 Pro Tyr Gly His Asn Gly Leu Cys Thr Tyr Ser His Ile Arg Ser Gly  
 85 90 95  
 Ile Ser Thr Ala Gly Asn Tyr Leu Ile Thr Pro Asn Ile Glu Gly Ala  
 100 105 110  
 Lys Arg Val Lys Tyr Trp Val Cys Asn Gln Tyr Ser Thr Asn Pro Glu  
 115 120 125  
 75 His Tyr Ala Val Met Val Ser Thr Thr Gly Thr Ala Ile Glu Asp Phe



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Val Thr Asp Phe Val Val Ser Leu Ile Glu Asn Asn Lys Gly Arg Leu  
 740 745 750  
 Lys Trp Asn Tyr Pro Asn Gly Tyr Glu Pro Asp Lys Thr Asp Asp Lys  
 755 760 765  
 5 Lys Pro Leu Gln Leu Thr Gly Tyr Asn Ile Tyr Ala Asn Gly Ser Leu  
 770 775 780  
 Leu Val His Ile Gln Asp Pro Thr Val Leu Glu Tyr Ile Asp Glu Thr  
 785 790 795 800  
 10 Tyr Ser Ser Arg Asp Gly Gln Val Glu Met Glu Tyr Cys Val Thr Ala  
 805 810 815  
 Val Tyr Asn Asp Asn Ile Glu Ser Gln Ser Val Cys Asp Lys Leu Asn  
 820 825 830  
 Tyr Thr Ile Thr Ser Leu Asp Asn Ile Gln Ser Asp Thr Ser Leu Lys  
 835 840 845  
 15 Ile Tyr Pro Asn Pro Ala Ser Tyr Val Val Arg Ile Glu Gly Leu Ser  
 850 855 860  
 Arg Ser Lys Ser Thr Ile Glu Leu Tyr Asn Ala Leu Gly Ile Cys Ile  
 865 870 875 880  
 20 Leu Arg Glu Glu Thr His Ser Glu Lys Thr Glu Ile Asp Val Ser Arg  
 885 890 895  
 Leu Asn Asp Gly Val Tyr Leu Ile Lys Val Val Gly Gly Asn Lys Thr  
 900 905 910  
 Thr Thr Glu Lys Val Glu Ile Lys Arg Pro  
 915 920

25

(2) INFORMATION FOR SEQ ID NO:469

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 921 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

30

(ii) MOLECULE TYPE: protein

35

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Porphyromonas gingivalis

40

(ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...921

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:469

45

Met Lys Ser Ile Val Phe Arg Ala Phe Leu Thr Ile Leu Leu Ser Trp  
 1 5 10 15  
 Ala Ala Ile Thr Asn Pro Thr Ala Gln Glu Ile Ser Gly Met Asn Ala  
 20 25 30  
 50 Ser Cys Leu Ala Ala Pro Ala Gln Pro Asp Thr Ile Leu Tyr Glu Ser  
 35 40 45  
 Phe Glu Asn Gly Pro Val Pro Asn Gly Trp Leu Glu Ile Asp Ala Asp  
 50 55 60  
 55 Ala Asp Gly Ala Thr Trp Gly Ser Pro Ser Gly Ser Phe Ser Val Pro  
 65 70 75 80  
 Tyr Gly His Asn Gly Leu Cys Thr Tyr Ser His Ile Arg Ser Gly Ile  
 85 90 95  
 Ser Thr Ala Gly Asn Tyr Leu Ile Thr Pro Asn Ile Glu Gly Ala Lys  
 100 105 110  
 60 Arg Val Lys Tyr Trp Val Cys Asn Gln Tyr Ser Thr Asn Pro Glu His  
 115 120 125  
 Tyr Ala Val Met Val Ser Thr Thr Gly Thr Ala Ile Glu Asp Phe Val  
 130 135 140  
 65 Leu Leu Phe Asp Asp Ser Ile Thr Gly Lys Pro Thr Pro Leu Val Trp  
 145 150 155 160  
 Arg Arg Arg Ile Val Asp Leu Pro Glu Gly Thr Lys Tyr Ile Ala Trp  
 165 170 175  
 Arg His Tyr Lys Val Thr Asp Ser His Thr Glu Phe Leu Lys Leu Asp  
 180 185 190  
 70 Asp Val Thr Val Tyr Arg Ser Ile Glu Gly Pro Glu Pro Ala Thr Asp  
 195 200 205  
 Phe Thr Val Ile Asn Ile Gly Gln Asn Val Gly Arg Leu Thr Trp Asn  
 210 215 220  
 75 Tyr Pro Glu Asp Tyr Gln Pro Glu Gly Lys Gly Asn Glu Glu Leu Gln  
 225 230 235 240

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	Leu	Ser	Gly	Tyr	Asn	Ile	Tyr	Ala	Asn	Gly	Thr	Leu	Leu	Ala	Gln	Ile
				245						250					255	
	Lys	Asp	Val	Ser	Ile	Leu	Glu	Tyr	Val	Asp	Ser	Thr	Tyr	Ser	Leu	Arg
				260					265					270		
5	Asp	Asn	Pro	Leu	Gln	Val	Glu	Tyr	Cys	Val	Thr	Ala	Val	Tyr	Asp	Glu
			275						280				285			
	Ser	Ile	Glu	Ser	Ser	Thr	Val	Cys	Gly	Thr	Leu	His	Tyr	Ala	Thr	Asp
		290					295					300				
10	Ala	Ile	Leu	Tyr	Glu	Asn	Phe	Glu	Asn	Gly	Pro	Val	Pro	Asn	Gly	Trp
	305				310					315					320	
	Leu	Val	Ile	Asp	Ala	Asp	Gly	Asp	Gly	Phe	Ser	Trp	Gly	His	Tyr	Leu
				325						330					335	
	Asn	Ala	Tyr	Asp	Ala	Phe	Pro	Gly	His	Asn	Gly	Gly	His	Cys	Ser	Leu
			340					345						350		
15	Ser	Ala	Ser	Tyr	Val	Pro	Gly	Ile	Gly	Pro	Val	Thr	Pro	Asp	Asn	Tyr
			355					360					365			
	Leu	Ile	Thr	Pro	Lys	Val	Glu	Gly	Ala	Lys	Arg	Val	Lys	Tyr	Trp	Val
		370					375					380				
20	Ser	Thr	Gln	Asp	Ala	Asn	Trp	Ala	Ala	Glu	His	Tyr	Ala	Val	Met	Ala
	385					390					395				400	
	Ser	Thr	Thr	Gly	Thr	Ala	Val	Gly	Asp	Phe	Val	Ile	Leu	Phe	Glu	Glu
					405					410					415	
	Thr	Met	Thr	Ala	Lys	Pro	Thr	Gly	Ala	Trp	Tyr	Glu	Arg	Thr	Ile	Asn
				420					425					430		
25	Leu	Pro	Glu	Gly	Thr	Lys	Tyr	Ile	Ala	Trp	Arg	His	Tyr	Asn	Cys	Thr
			435					440					445			
	Asp	Ile	Tyr	Phe	Leu	Lys	Leu	Asp	Asp	Ile	Thr	Val	Phe	Gly	Thr	Pro
		450					455					460				
30	Ala	Ser	Glu	Pro	Glu	Pro	Val	Thr	Asp	Phe	Val	Val	Ser	Leu	Ile	Glu
	465					470					475				480	
	Asn	Asn	Lys	Gly	Arg	Leu	Lys	Trp	Asn	Tyr	Pro	Asn	Gly	Tyr	Glu	Pro
					485					490					495	
	Asp	Lys	Thr	Asp	Asp	Lys	Asp	Pro	Leu	Gln	Leu	Ala	Gly	Tyr	Asn	Ile
			500						505					510		
35	Tyr	Ala	Asn	Gly	Ser	Leu	Leu	Val	His	Ile	Gln	Asp	Pro	Thr	Val	Leu
			515					520					525			
	Glu	Tyr	Ile	Asp	Glu	Thr	Tyr	Ser	Ser	Arg	Asp	Asp	Gln	Val	Glu	Val
		530					535					540				
40	Glu	Tyr	Cys	Val	Thr	Ala	Val	Tyr	Asn	Asp	Asn	Ile	Glu	Ser	Gln	Ser
	545						550				555				560	
	Val	Cys	Asp	Lys	Leu	Ile	Tyr	Asp	Ser	Gln	Ser	Asp	Ile	Ile	Leu	Tyr
				565						570					575	
	Glu	Gly	Phe	Glu	Ala	Gly	Ser	Ile	Pro	Glu	Gly	Trp	Leu	Leu	Ile	Asp
				580					585					590		
45	Ala	Asp	Gly	Asp	Asn	Val	Asn	Trp	Asp	Tyr	Tyr	Pro	Trp	Thr	Met	Tyr
			595					600						605		
	Gly	His	Asp	Ser	Glu	Lys	Cys	Ile	Ala	Ser	Pro	Ser	Tyr	Leu	Pro	Met
		610					615					620				
50	Ile	Gly	Val	Leu	Thr	Pro	Asp	Asn	Tyr	Leu	Val	Thr	Pro	Arg	Leu	Glu
	625					630					635				640	
	Gly	Ala	Lys	Leu	Val	Lys	Tyr	Trp	Val	Ser	Ala	Gln	Asp	Ala	Val	Tyr
				645						650					655	
	Ser	Ala	Glu	His	Tyr	Ala	Val	Met	Val	Ser	Thr	Thr	Gly	Thr	Ala	Val
				660					665					670		
55	Glu	Asp	Phe	Val	Leu	Leu	Phe	Glu	Glu	Thr	Met	Thr	Ala	Lys	Ala	Asn
			675					680					685			
	Gly	Ala	Trp	Tyr	Glu	Arg	Thr	Ile	Thr	Leu	Pro	Ala	Gly	Thr	Lys	Tyr
		690					695					700				
60	Ile	Ala	Trp	Arg	His	Tyr	Asp	Cys	Thr	Asp	Met	Phe	Phe	Leu	Leu	Leu
	705					710					715				720	
	Asp	Asp	Ile	Thr	Val	Tyr	Arg	Ser	Thr	Glu	Thr	Val	Pro	Glu	Pro	Val
				725						730				735		
	Thr	Asp	Phe	Val	Val	Ser	Leu	Ile	Glu	Asn	Asn	Lys	Gly	Arg	Leu	Lys
				740					745					750		
65	Trp	Asn	Tyr	Pro	Asn	Gly	Tyr	Glu	Pro	Asp	Lys	Thr	Asp	Asp	Lys	Lys
			755					760					765			
	Pro	Leu	Gln	Leu	Thr	Gly	Tyr	Asn	Ile	Tyr	Ala	Asn	Gly	Ser	Leu	Leu
		770					775					780				
70	Val	His	Ile	Gln	Asp	Pro	Thr	Val	Leu	Glu	Tyr	Ile	Asp	Glu	Thr	Tyr
	785					790					795				800	
	Ser	Ser	Arg	Asp	Gly	Gln	Val	Glu	Met	Glu	Tyr	Cys	Val	Thr	Ala	Val
				805						810					815	
	Tyr	Asn	Asp	Asn	Ile	Glu	Ser	Gln	Ser	Val	Cys	Asp	Lys	Leu	Asn	Tyr
				820					825					830		
75	Thr	Ile	Thr	Ser	Leu	Asp	Asn	Ile	Gln	Ser	Asp	Thr	Ser	Leu	Lys	Ile

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835 840 845  
 Tyr Pro Asn Pro Ala Ser Tyr Val Val Arg Ile Glu Gly Leu Ser Arg  
 850 855 860  
 5 Ser Lys Ser Thr Ile Glu Leu Tyr Asn Ala Leu Gly Ile Cys Ile Leu  
 865 870 875 880  
 Arg Glu Glu Thr His Ser Glu Lys Thr Glu Ile Asp Val Ser Arg Leu  
 885 890 895  
 Asn Asp Gly Val Tyr Leu Ile Lys Val Val Gly Gly Asn Lys Thr Thr  
 900 905 910  
 10 Thr Glu Lys Val Glu Ile Lys Arg Pro  
 915 920

(2) INFORMATION FOR SEQ ID NO:470

- 15 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 593 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
 20 (ii) MOLECULE TYPE: protein  
 (iii) HYPOTHETICAL: YES  
 (vi) ORIGINAL SOURCE:  
 25 (A) ORGANISM: Porphyromonas gingivalis  
 (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...593  
 30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:470

Met Asn Ser Ile Met Lys Tyr Gln Leu Tyr Thr Ala Val Ile Met Ala  
 1 5 10 15  
 35 Leu Ser Val Ser Ser Val Cys Gly Gln Thr Pro Arg Asn Thr Glu Thr  
 20 25 30  
 Lys Arg Pro Asp Thr Leu Arg Arg Glu Leu Thr Ile Val Asn Asp Gln  
 35 40 45  
 40 Thr Val Glu Met Glu His Ala Asp Pro Leu Pro Ala Ala Tyr Lys Ala  
 50 55 60  
 Ile Glu Pro Arg Leu Lys Pro Phe Arg Pro Glu Tyr Asn Lys Arg Thr  
 65 70 75 80  
 Phe Gly Phe Val Pro Glu Val Ser Ser Ser Gly Arg Asn Asn Leu Pro  
 85 90 95  
 45 Asn Ile Leu Pro Thr Glu Gly His Met Lys His Arg Gly Tyr Leu Asn  
 100 105 110  
 Ile Gly Ile Gly His Thr Leu Asn Gln Arg Met Asp Ala Gly Tyr Arg  
 115 120 125  
 50 Leu Ile Asp Ala Glu Gln Glu Arg Leu Asn Leu Phe Leu Ser Tyr Arg  
 130 135 140  
 Gly Met Lys Ser Ala Phe Asn Thr Gly Asp Phe Asp Gly Asp Arg Lys  
 145 150 155 160  
 Asp Arg Arg Met Met Ala Gly Val Asp Tyr Glu Gln Arg Arg Pro Ser  
 165 170 175  
 55 Phe Val Leu Ala Thr Gly Leu Tyr Tyr Ser Asn His Tyr Phe Asn Asn  
 180 185 190  
 Tyr Gly Arg Gly Ala Thr Thr Asn Val Gly Ser Ile Pro Gln Leu Ser  
 195 200 205  
 60 Thr Pro Val Thr Pro Gln Met Asp Asn Gly Thr His Asn Val Arg Val  
 210 215 220  
 Tyr Leu Gly Ala Lys Asn Asp Val Ile Asp Ala Arg Ile Asp Tyr Arg  
 225 230 235 240  
 Phe Phe Arg Ser Ile Pro Tyr Leu Gly Thr Asp Pro Met Lys Ala Leu  
 245 250 255  
 65 Thr Glu His Thr Pro Glu Leu Asn Val Thr Met Ser Asn Glu Leu Ser  
 260 265 270  
 Asp Asp Ile Lys Leu Gly Val Glu Val Arg Thr Gly Gly Leu Phe Phe  
 275 280 285  
 70 Ala Lys Asn Ser Glu Met Ile Gln Thr Gly Val Leu Ser Glu Thr Asp  
 290 295 300  
 Arg Asn Leu Tyr Tyr Val Glu Gly Ala Pro Thr Ile Gly Phe Val Gly  
 305 310 315 320  
 Asp Ser Asp Asn Met Gln Trp Asn Ile Gln Ala Gly Val Gly Ile Ser  
 325 330 335  
 75 Ser His Phe Gly Ala Lys Gly Arg Leu Phe Phe Trp Pro Lys Leu Asp

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5                   340                   345                   350  
 Ala Ser Leu Ser Ile Phe Pro Ser Trp Arg Val Tyr Ala Lys Ala Phe  
                   355                   360                   365  
 Gly Gly Val Ile Arg Asn Gly Leu Ala Asp Val Met Gln Glu Glu Met  
                   370                   375                   380  
 Pro Tyr Leu Met Pro Asn Thr Ile Val Leu Pro Ser Arg Asn Ala Leu  
                   385                   390                   395                   400  
 Thr Ala Gln Leu Gly Val Lys Gly Asn Ile Ala Asp Val Val Arg Met  
                   405                   410                   415  
 10   Glu Val Tyr Gly Asp Phe Ser Lys Leu Thr Gly Val Pro Phe Tyr Thr  
                   420                   425                   430  
 Pro Thr Leu Pro Leu Tyr Asn Pro Ser Asp Leu Tyr Gln Tyr Asn Val  
                   435                   440                   445  
 15   Ser Phe Leu Pro Ile Tyr Ala Asp Gly Ser Arg Trp Arg Ala Gly Gly  
                   450                   455                   460  
 Lys Leu Glu Tyr Ser Tyr Arg Asp Met Leu Arg Phe Leu Val Asp Ala  
                   465                   470                   475                   480  
 Ser Tyr Gly Lys Trp Asn Leu Asp Gly Gly Leu Val Ala Ser Met Gln  
                   485                   490                   495  
 20   Pro Asp Leu Ile Leu Lys Ala Glu Val Gly Val His Pro Ile Ala Pro  
                   500                   505                   510  
 Leu Asp Val Arg Leu Arg Tyr Thr Gln Leu Asn Gly Arg Tyr Arg Tyr  
                   515                   520                   525  
 25   Ser Phe Gly Ser Ala Gly Ser Glu Ala Leu Gly Ile Gly Asn Val His  
                   530                   535                   540  
 Leu Leu Ser Ala Asp Val Ser Tyr Lys Leu Lys Lys Asn Leu Ser Leu  
                   545                   550                   555                   560  
 Tyr Leu Lys Ile Asp Asn Met Leu Ala Glu Thr Thr Glu Leu Ile Gly  
                   565                   570                   575  
 30   Tyr Tyr Pro Met Gln Pro Phe His Cys Phe Ala Gly Phe Ser Trp Thr  
                   580                   585                   590  
 Phe

35   (2) INFORMATION FOR SEQ ID NO:471

(i) SEQUENCE CHARACTERISTICS:  
       (A) LENGTH: 589 amino acids  
       (B) TYPE: amino acid  
       (D) TOPOLOGY: linear

40   (ii) MOLECULE TYPE: protein

45   (iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:  
       (A) ORGANISM: Porphyromonas gingivalis

50   (iix) FEATURE:  
       (A) NAME/KEY: misc\_feature  
       (B) LOCATION 1...589

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:471

55   Met Lys Tyr Gln Leu Tyr Thr Ala Val Ile Met Ala Leu Ser Val Ser  
       1                   5                   10                   15  
 Ser Val Cys Gly Gln Thr Pro Arg Asn Thr Glu Thr Lys Arg Pro Asp  
                   20                   25                   30  
 60   Thr Leu Arg Arg Glu Leu Thr Ile Val Asn Asp Gln Thr Val Glu Met  
                   35                   40                   45  
 Glu His Ala Asp Pro Leu Pro Ala Ala Tyr Lys Ala Ile Glu Pro Arg  
                   50                   55                   60  
 Leu Lys Pro Phe Arg Pro Glu Tyr Asn Lys Arg Thr Phe Gly Phe Val  
                   65                   70                   75                   80  
 65   Pro Glu Val Ser Ser Ser Gly Arg Asn Asn Leu Pro Asn Ile Leu Pro  
                   85                   90                   95  
 Thr Glu Gly His Met Lys His Arg Gly Tyr Leu Asn Ile Gly Ile Gly  
                   100                   105                   110  
 70   His Thr Leu Asn Gln Arg Met Asp Ala Gly Tyr Arg Leu Ile Asp Ala  
                   115                   120                   125  
 Glu Gln Glu Arg Leu Asn Leu Phe Leu Ser Tyr Arg Gly Met Lys Ser  
                   130                   135                   140  
 Ala Phe Asn Thr Gly Asp Phe Asp Gly Asp Lys Asp Arg Arg Met  
                   145                   150                   155                   160  
 75   Met Ala Gly Val Asp Tyr Glu Gln Arg Arg Pro Ser Phe Val Leu Ala

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165 170 175  
 Thr Gly Leu Tyr Tyr Ser Asn His Tyr Phe Asn Asn Tyr Gly Arg Gly  
 180 185 190  
 5 Ala Thr Thr Asn Val Gly Ser Ile Pro Gln Leu Ser Thr Pro Val Thr  
 195 200 205  
 Pro Gln Met Asp Asn Gly Thr His Asn Val Arg Val Tyr Leu Gly Ala  
 210 215 220  
 Lys Asn Asp Val Ile Asp Ala Arg Ile Asp Tyr Arg Phe Phe Arg Ser  
 225 230 235 240  
 10 Ile Pro Tyr Leu Gly Thr Asp Pro Met Lys Ala Leu Thr Glu His Thr  
 245 250 255  
 Pro Glu Leu Asn Val Thr Met Ser Asn Glu Leu Ser Asp Asp Ile Lys  
 260 265 270  
 15 Leu Gly Val Glu Val Arg Thr Gly Gly Leu Phe Phe Ala Lys Asn Ser  
 275 280 285  
 Glu Met Ile Gln Thr Gly Val Leu Ser Glu Thr Asp Arg Asn Leu Tyr  
 290 295 300  
 Tyr Val Glu Gly Ala Pro Thr Ile Gly Phe Val Gly Asp Ser Asp Asn  
 305 310 315 320  
 20 Met Gln Trp Asn Ile Gln Ala Gly Val Gly Ile Ser Ser His Phe Gly  
 325 330 335  
 Ala Lys Gly Arg Leu Phe Phe Trp Pro Lys Leu Asp Ala Ser Leu Ser  
 340 345 350  
 25 Ile Phe Pro Ser Trp Arg Val Tyr Ala Lys Ala Phe Gly Gly Val Ile  
 355 360 365  
 Arg Asn Gly Leu Ala Asp Val Met Gln Glu Glu Met Pro Tyr Leu Met  
 370 375 380  
 Pro Asn Thr Ile Val Leu Pro Ser Arg Asn Ala Leu Thr Ala Gln Leu  
 385 390 395 400  
 30 Gly Val Lys Gly Asn Ile Ala Asp Val Val Arg Met Glu Val Tyr Gly  
 405 410 415  
 Asp Phe Ser Lys Leu Thr Gly Val Pro Phe Tyr Thr Pro Thr Leu Pro  
 420 425 430  
 35 Leu Tyr Asn Pro Ser Asp Leu Tyr Gln Tyr Asn Val Ser Phe Leu Pro  
 435 440 445  
 Ile Tyr Ala Asp Gly Ser Arg Trp Arg Ala Gly Gly Lys Leu Glu Tyr  
 450 455 460  
 Ser Tyr Arg Asp Met Leu Arg Phe Leu Val Asp Ala Ser Tyr Gly Lys  
 465 470 475 480  
 40 Trp Asn Leu Asp Gly Gly Leu Val Ala Ser Met Gln Pro Asp Leu Ile  
 485 490 495  
 Leu Lys Ala Glu Val Gly Val His Pro Ile Ala Pro Leu Asp Val Arg  
 500 505 510  
 45 Leu Arg Tyr Thr Gln Leu Asn Gly Arg Tyr Arg Tyr Ser Phe Gly Ser  
 515 520 525  
 Ala Gly Ser Glu Ala Leu Gly Ile Gly Asn Val His Leu Leu Ser Ala  
 530 535 540  
 Asp Val Ser Tyr Lys Leu Lys Lys Asn Leu Ser Leu Tyr Leu Lys Ile  
 545 550 555 560  
 50 Asp Asn Met Leu Ala Glu Thr Thr Glu Leu Ile Gly Tyr Tyr Pro Met  
 565 570 575  
 Gln Pro Phe His Cys Phe Ala Gly Phe Ser Trp Thr Phe  
 580 585

55 (2) INFORMATION FOR SEQ ID NO:472

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 346 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

60

(ii) MOLECULE TYPE: protein

65

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Porphyromonas gingivalis

70

(ix) FEATURE:

(A) NAME/KEY: misc\_feature

(B) LOCATION: 1...346

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:472

75

Met Met Glu Lys Cys Ile Phe Ala His Tyr Pro His Asn Leu Val Phe



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	1				5					10					15		
	Met	Ile	Arg	Lys	His	Phe	Gly	Ile	Ile	Leu	Gly	Phe	Leu	Ser	Leu	Val	
				20					25					30			
5	Phe	Ser	Ala	Gly	Ala	Gln	Gln	Glu	Lys	Gln	Val	Phe	His	Phe	Leu	Asn	
			35					40					45				
	Leu	Pro	Ala	Thr	Ala	Gln	Ala	Leu	Ala	Ala	Gly	Gly	Lys	Ala	Ile	Thr	
			50				55					60					
	Ile	Val	Asp	Asp	Asn	Pro	Gly	Leu	Ala	Phe	Glu	Asn	Pro	Ala	Leu	Leu	
10			65			70					75					80	
	Gly	Tyr	Glu	Ser	Gly	Gly	Arg	Ala	Phe	Leu	Ser	Tyr	Leu	Tyr	Tyr	Met	
				85						90					95		
	Ser	Gly	Ser	His	Met	Gly	Asn	Ala	Cys	Tyr	Ala	Ser	Ser	Val	Gly	Glu	
				100					105					110			
15	Arg	Gly	Met	Trp	Gly	Val	Gly	Met	Arg	Phe	Leu	Asn	Tyr	Gly	Ser	Met	
				115				120					125				
	Gln	Gly	Tyr	Asp	Gln	Asn	Ala	Ile	Ala	Thr	Gly	Ser	Phe	Ser	Ala	Ser	
			130				135						140				
	Asp	Ile	Ala	Val	Gln	Gly	Phe	Tyr	Ser	His	Glu	Leu	Ser	Asn	His	Phe	
20						150					155					160	
	Arg	Gly	Gly	Val	Ser	Leu	Lys	Ala	Leu	Tyr	Ser	Ser	Ile	Glu	Thr	Tyr	
				165						170					175		
	Ser	Ser	Phe	Gly	Leu	Gly	Val	Asp	Val	Gly	Ile	Ser	Tyr	Tyr	Asp	Asp	
				180					185					190			
25	Asp	Lys	Gly	Tyr	Ser	Ala	Ser	Ala	Leu	Phe	Lys	Asn	Val	Gly	Ala	Gln	
				195				200					205				
	Leu	Lys	Gly	Tyr	Asn	Glu	Glu	Arg	Glu	Pro	Leu	Asp	Trp	Asp	Phe	Gln	
			210				215					220					
	Leu	Gly	Phe	Ser	Arg	Ser	Phe	Ile	Asn	Ala	Pro	Phe	Arg	Leu	His	Ile	
30						230					235					240	
	Thr	Leu	Phe	Asn	Leu	Asn	Pro	His	Tyr	Phe	Lys	Arg	Leu	Val	Pro	Arg	
				245						250					255		
	Asp	Leu	Ser	Lys	Met	Gln	Lys	Phe	Leu	Arg	His	Phe	Ser	Ile	Gly	Ala	
				260					265					270			
35	Glu	Phe	Thr	Pro	Ser	Glu	Arg	Phe	Trp	Val	Gly	Leu	Gly	Tyr	Thr	Pro	
			275					280					285				
	Gln	Ile	Ala	Gln	Asp	Phe	Glu	Val	Glu	Gly	Gly	Asn	Lys	Trp	Gly	Gly	
			290				295					300					
	Leu	Ser	Ala	Gly	Val	Gly	Phe	Thr	Ser	Gly	Val	Val	Arg	Val	Gly	Val	
40						310					315					320	
	Ser	Ala	Ala	Thr	Tyr	His	Pro	Ala	Ala	Leu	Ser	Phe	Met	Cys	Ser	Val	

45 (2) INFORMATION FOR SEQ ID NO: 473

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 345 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:  
(A) ORGANISM: Porphyromonas gingivalis

```
(ix) FEATURE:
      (A) NAME/KEY: misc_feature
      (B) LOCATION: 1...345
```

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:473

65	Met	Glu	Lys	Cys	Ile	Phe	Ala	His	Tyr	Pro	His	Asn	Leu	Val	Phe	Met
	1				5					10					15	
	Ile	Arg	Lys	His	Phe	Gly	Ile	Ile	Leu	Gly	Phe	Leu	Ser	Leu	Val	Phe
70				20					25					30		
	Ser	Ala	Gly	Ala	Gln	Gln	Glu	Lys	Gln	Val	Phe	His	Phe	Leu	Asn	Leu
			35					40					45			
	Pro	Ala	Thr	Ala	Gln	Ala	Leu	Ala	Ala	Gly	Gly	Lys	Ala	Ile	Thr	Ile
75				50			55					60				
	Val	Asp	Asp	Asn	Pro	Gly	Leu	Ala	Phe	Glu	Asn	Pro	Ala	Leu	Leu	Gly
	65					70					75				80	
	Tyr	Glu	Ser	Gly	Gly	Arg	Ala	Phe	Leu	Ser	Tyr	Leu	Tyr	Tyr	Met	Ser

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5 Gly Ser His Met Gly Asn Ala Cys Tyr Ala Ser Ser Val Gly Glu Arg  
 100 105 110  
 Gly Met Trp Gly Val Gly Met Arg Phe Leu Asn Tyr Gly Ser Met Gln  
 115 120 125  
 Gly Tyr Asp Gln Asn Ala Ile Ala Thr Gly Ser Phe Ser Ala Ser Asp  
 130 135 140  
 Ile Ala Val Gln Gly Phe Tyr Ser His Glu Leu Ser Asn His Phe Arg  
 145 150 155 160  
 10 Gly Gly Val Ser Leu Lys Ala Leu Tyr Ser Ser Ile Glu Thr Tyr Ser  
 165 170 175  
 Ser Phe Gly Leu Gly Val Asp Val Gly Ile Ser Tyr Tyr Asp Asp Asp  
 180 185 190  
 15 Lys Gly Tyr Ser Ala Ser Ala Leu Phe Lys Asn Val Gly Ala Gln Leu  
 195 200 205  
 Lys Gly Tyr Asn Glu Glu Arg Glu Pro Leu Asp Trp Asp Phe Gln Leu  
 210 215 220  
 Gly Phe Ser Arg Ser Phe Ile Asn Ala Pro Phe Arg Leu His Ile Thr  
 225 230 235 240  
 20 Leu Phe Asn Leu Asn Pro His Tyr Phe Lys Arg Leu Val Pro Arg Asp  
 245 250 255  
 Leu Ser Lys Met Gln Lys Phe Leu Arg His Phe Ser Ile Gly Ala Glu  
 260 265 270  
 25 Phe Thr Pro Ser Glu Arg Phe Trp Val Gly Leu Gly Tyr Thr Pro Gln  
 275 280 285  
 Ile Ala Gln Asp Phe Glu Val Glu Gly Gly Asn Lys Trp Gly Gly Leu  
 290 295 300  
 Ser Ala Gly Val Gly Phe Thr Ser Gly Val Val Arg Val Gly Val Ser  
 305 310 315 320  
 30 Ala Ala Thr Tyr His Pro Ala Ala Leu Ser Phe Met Cys Ser Val Gly  
 325 330 335  
 Ile Arg Leu Asp Asp Lys Ser Ile Phe  
 340 345

35 (2) INFORMATION FOR SEQ ID NO:474

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 330 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

(A) NAME/KEY: misc\_feature

(B) LOCATION: 1...330

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:474

55 Met Ile Arg Lys His Phe Gly Ile Ile Leu Gly Phe Leu Ser Leu Val  
 1 5 10 15  
 Phe Ser Ala Gly Ala Gln Gln Glu Lys Gln Val Phe His Phe Leu Asn  
 20 25 30  
 60 Leu Pro Ala Thr Ala Gln Ala Leu Ala Ala Gly Gly Lys Ala Ile Thr  
 35 40 45  
 Ile Val Asp Asp Asn Pro Gly Leu Ala Phe Glu Asn Pro Ala Leu Leu  
 50 55 60  
 Gly Tyr Glu Ser Gly Gly Arg Ala Phe Leu Ser Tyr Leu Tyr Tyr Met  
 65 70 75 80  
 Ser Gly Ser His Met Gly Asn Ala Cys Tyr Ala Ser Ser Val Gly Glu  
 85 90 95  
 Arg Gly Met Trp Gly Val Gly Met Arg Phe Leu Asn Tyr Gly Ser Met  
 100 105 110  
 70 Gln Gly Tyr Asp Gln Asn Ala Ile Ala Thr Gly Ser Phe Ser Ala Ser  
 115 120 125  
 Asp Ile Ala Val Gln Gly Phe Tyr Ser His Glu Leu Ser Asn His Phe  
 130 135 140  
 Arg Gly Gly Val Ser Leu Lys Ala Leu Tyr Ser Ser Ile Glu Thr Tyr  
 145 150 155 160  
 75 Ser Ser Phe Gly Leu Gly Val Asp Val Gly Ile Ser Tyr Tyr Asp Asp

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165 170 175  
 Asp Lys Gly Tyr Ser Ala Ser Ala Leu Phe Lys Asn Val Gly Ala Gln  
 180 185 190  
 5 Leu Lys Gly Tyr Asn Glu Glu Arg Glu Pro Leu Asp Trp Asp Phe Gln  
 195 200 205  
 Leu Gly Phe Ser Arg Ser Phe Ile Asn Ala Pro Phe Arg Leu His Ile  
 210 215 220  
 Thr Leu Phe Asn Leu Asn Pro His Tyr Phe Lys Arg Leu Val Pro Arg  
 225 230 235 240  
 10 Asp Leu Ser Lys Met Gln Lys Phe Leu Arg His Phe Ser Ile Gly Ala  
 245 250 255  
 Glu Phe Thr Pro Ser Glu Arg Phe Trp Val Gly Leu Gly Tyr Thr Pro  
 260 265 270  
 15 Gln Ile Ala Gln Asp Phe Glu Val Glu Gly Gly Asn Lys Trp Gly Gly  
 275 280 285  
 Leu Ser Ala Gly Val Gly Phe Thr Ser Gly Val Val Arg Val Gly Val  
 290 295 300  
 Ser Ala Ala Thr Tyr His Pro Ala Ala Leu Ser Phe Met Cys Ser Val  
 305 310 315 320  
 20 Gly Ile Arg Leu Asp Asp Lys Ser Ile Phe  
 325 330

(2) INFORMATION FOR SEQ ID NO:475

- 25 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 324 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
 30 (ii) MOLECULE TYPE: protein  
 (iii) HYPOTHETICAL: YES  
 (vi) ORIGINAL SOURCE:  
 35 (A) ORGANISM: Porphyromonas gingivalis  
 (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...324  
 40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:475

Met Cys Leu Glu Pro Ile Ile Ala Pro Ile Ser Ser Glu Leu Leu Glu  
 1 5 10 15  
 45 Gln Glu Leu Thr Ala Asp Arg Phe Leu Arg Met Thr Asn Lys Ala Gly  
 20 25 30  
 Asn Glu Ile Tyr Val Phe Thr Ala Glu Glu Ala Pro His Cys Met Lys  
 35 40 45  
 50 Glu Val Gly Arg Leu Arg Glu Glu Ala Phe Arg His Tyr Gly Gly Gly  
 50 55 60  
 Thr Gly Lys Ala Ile Asp Ile Asp Glu Phe Asp Thr Met Pro Gly Ser  
 65 70 75 80  
 Tyr Lys Gln Leu Ile Val Trp Asp Pro Gln Asn Lys Ala Ile Leu Gly  
 85 90 95  
 55 Gly Tyr Arg Phe Ile Tyr Gly Arg Asp Val Ala Phe Asp Thr Asp Gly  
 100 105 110  
 Lys Pro Leu Leu Ala Thr Ala Glu Met Phe Arg Phe Ser Asp Ala Phe  
 115 120 125  
 60 Leu His Asp Tyr Leu Pro Tyr Thr Val Glu Leu Gly Arg Ser Phe Val  
 130 135 140  
 Ser Leu Gln Tyr Gln Ser Thr Arg Met Gly Thr Lys Ala Ile Phe Val  
 145 150 155 160  
 Leu Asp Asn Leu Trp Asp Gly Ile Gly Ala Leu Thr Val Val Asn Pro  
 165 170 175  
 65 Glu Ala Leu Tyr Phe Tyr Gly Lys Val Thr Met Tyr Lys Asp Tyr Asp  
 180 185 190  
 Arg Arg Ala Arg Asn Leu Ile Leu Tyr Phe Leu Arg Lys His Phe Ser  
 195 200 205  
 70 Asp Pro Glu Gly Leu Val Lys Pro Ile His Pro Leu Pro Ile Glu Ile  
 210 215 220  
 Ser Ala Glu Asp Glu Ala Leu Phe Ser Ser Ser Asp Phe Asp Thr Asn  
 225 230 235 240  
 Tyr Lys Thr Leu Asn Ile Glu Val Arg Lys Leu Gly Ile Asn Ile Pro  
 245 250 255  
 75 Pro Leu Val Ser Ala Tyr Ile Ala Leu Ser Pro Glu Met Arg Val Phe

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[illegible]

(2) INFORMATION FOR SEQ ID NO:476

15 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 547 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

20 (iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:  
(A) ORGANISM: Porphyromonas gingivalis

25 (ix) FEATURE:  
(A) NAME/KEY: misc\_feature  
(B) LOCATION 1...547

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:476

	Met 1	Lys	Thr	Ile	Val	Arg	Tyr	Ser	Arg	Leu	Pro	Val	Ala	Leu	Phe	Phe
	Cys	Leu	Leu	Gly	Ala	Val	His	Leu	Ser	Val	Glu	Ala	Gln	Met	Leu	Asn
35	Thr	Pro	Phe	Glu	Leu	Ser	Asp	Gln	Ile	Val	Leu	Ser	Pro	Thr	Glu	Arg
	Gln	Tyr	Arg	Glu	Ile	Cys	Val	Gln	Thr	Lys	Glu	Lys	Arg	Gly	Ala	Asp
	Leu	Phe	Pro	Leu	Ser	Asp	Lys	Leu	Arg	Asp	Ser	Ala	Tyr	Val	Arg	Phe
40	Gly	Ser	Ala	Tyr	Gly	Asp	Ile	Ala	Gly	Asp	Tyr	Leu	Pro	Tyr	Asn	Gly
	Asn	Asn	Tyr	Ser	Ser	Leu	Ser	Leu	Glu	Ser	Gly	Gly	Arg	Ile	Ser	Val
45	Arg	Asn	Tyr	Gly	Thr	Leu	Gln	Gly	Ser	Ala	Ser	Tyr	Ser	Arg	Gly	Met
	His	Lys	Arg	Ile	Gly	Trp	Asn	Ala	Leu	Arg	Asn	Ala	Glu	Ala	Tyr	Tyr
	Pro	Tyr	Leu	Val	Ser	Asp	Ser	Thr	Gly	Gly	Asp	Tyr	His	Phe	Glu	Asp
50	Tyr	Arg	Leu	Ala	Gly	Tyr	Tyr	Ser	Phe	Arg	Ala	Gly	Arg	Leu	Pro	Leu
	Gly	Ile	Gly	Phe	Ser	Tyr	Arg	Gly	Glu	Val	Ala	Tyr	Arg	Leu	Thr	Asp
55	Pro	Arg	Thr	Thr	Asn	Thr	Thr	Gly	Ala	Leu	Glu	Leu	Ser	Cys	Ala	Thr
	Ser	Leu	Thr	Leu	Pro	Arg	Glu	Asn	Arg	Leu	Ser	Leu	Ser	Ala	Ala	Tyr
60	Leu	Tyr	His	Arg	Gln	His	Leu	Thr	Gln	Tyr	Asn	Trp	Arg	Pro	Gly	Gln
	Gln	Asp	Lys	Phe	Phe	Val	Ser	Tyr	Gly	Phe	Gly	Gln	Val	Asp	Val	Ser
	Asn	Ser	Pro	Ile	Trp	Phe	Gly	Ile	Ser	Arg	Met	Asn	Tyr	Val	Asn	Gly
65	Trp	Lys	Leu	Ser	Ser	Arg	Leu	Asp	Thr	Arg	Arg	Gly	Asp	Ala	Ile	Gly
	Leu	Asp	Tyr	Ser	Gly	Tyr	Phe	Leu	Asp	Thr	Glu	Glu	Arg	Ser	Ser	Ile
70	Asn	Leu	Phe	Ala	Leu	Leu	Tyr	Asn	Arg	Leu	Arg	Leu	Tyr	Gly	Ser	Trp
	His	Leu	Ser	Asp	Phe	Asp	Phe	Ser	Phe	Ser	Ala	Asp	Tyr	Ala	Leu	Arg
	Gln	Gly	Ile	Glu	Arg	Ile	Tyr	Glu	Asp	Tyr	Lys	Pro	Asp	Asp	Asn	Tyr
75	His	Ile	Tyr	Asp	Leu	Arg	Ile	Leu	Ala	Ile	Arg	Arg	Trp	Tyr	Met	Leu

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5                   355                   360                   365  
 Asn Glu Phe Ser Ala Gln Ala Gln Ala Ser Tyr Arg Ile Arg Thr Asp  
 370                   375                   380  
 Arg Gly Cys Ala Leu Arg Val Ser Ala Gly Ser Asp Phe Tyr Gly Tyr  
 385                   390                   395                   400  
 Asp Glu Thr Tyr Arg Lys His Gly His His Thr Met Ser Gly Met Leu  
 405                   410                   415  
 Arg Pro Phe Ala Gly Ile Ala Tyr Asp His Ala Gly Ser Lys Leu Asp  
 420                   425                   430  
 10 Phe Gly Leu Ser Leu Ser Ala Ala Tyr Arg Met Val Leu Thr His Ser  
 435                   440                   445  
 Tyr Lys Ile Arg Thr Ile Gln Lys Glu Gln Leu Asp Tyr Gln Leu Ala  
 450                   455                   460  
 15 Tyr Leu Pro Tyr Ala Tyr Arg Asn Arg Glu Gly Val Glu Val Arg Ser  
 465                   470                   475                   480  
 Ser Leu Tyr Val Ser Ile Pro Met Gln Asn Thr His Arg Leu Met Thr  
 485                   490                   495  
 Glu Leu Arg Leu Tyr Gly Asp Leu Met Lys Arg Lys Asp Gly Ile Ala  
 500                   505                   510  
 20 Tyr Gly Lys Thr Pro Gly Val Ile Ser His Ile Leu Ser Asp Pro Gln  
 515                   520                   525  
 Ala Glu Arg Thr Ser Gly His Thr Ile Gly Ala Ile Cys Asn Ile Ser  
 530                   535                   540  
 25 Tyr Leu Phe  
 545

(2) INFORMATION FOR SEQ ID NO:477

30       (i) SEQUENCE CHARACTERISTICS:  
           (A) LENGTH: 750 amino acids  
           (B) TYPE: amino acid  
           (D) TOPOLOGY: linear  
  
 35       (ii) MOLECULE TYPE: protein  
  
 (iii) HYPOTHETICAL: YES  
  
 (vi) ORIGINAL SOURCE:  
 40       (A) ORGANISM: Porphyromonas gingivalis  
  
 (ix) FEATURE:  
           (A) NAME/KEY: misc feature  
           (B) LOCATION 1...750  
  
 45       (xi) SEQUENCE DESCRIPTION: SEQ ID NO:477

Met Lys Lys Leu His Met Ile Ala Ala Leu Ala Val Leu Pro Phe Cys  
 1                   5                   10                   15  
 50 Leu Thr Ala Gln Ala Pro Val Ser Asn Ser Glu Ile Asp Ser Leu Ser  
                   20                   25                   30  
 Asn Val Gln Leu Gln Thr Val Gln Val Val Ala Thr Arg Ala Thr Ala  
 35                   40                   45  
 Lys Thr Pro Val Ala Tyr Thr Asn Val Arg Lys Ala Glu Leu Ser Lys  
 50                   55                   60  
 55 Ser Asn Tyr Gly Arg Asp Ile Pro Tyr Leu Leu Met Leu Thr Pro Ser  
 65                   70                   75                   80  
 Val Val Ala Thr Ser Asp Ala Gly Thr Gly Ile Gly Tyr Ser Gly Phe  
                   85                   90                   95  
 60 Arg Val Arg Gly Thr Asp Ala Asn Arg Ile Asn Ile Thr Thr Asn Gly  
                   100                   105                   110  
 Val Pro Leu Asn Asp Ser Glu Ser Gln Ser Val Phe Trp Val Asn Met  
                   115                   120                   125  
 Pro Asp Phe Ala Ser Ser Ile Glu Asp Leu Gln Val Gln Arg Gly Val  
                   130                   135                   140  
 65 Gly Thr Ser Thr Asn Gly Ala Gly Ala Phe Gly Ala Ser Val Asn Met  
 145                   150                   155                   160  
 Arg Thr Asp Asn Leu Gly Leu Ala Pro Tyr Gly Arg Val Asp Leu Ser  
                   165                   170                   175  
 70 Gly Gly Ser Phe Gly Thr Phe Arg Arg Ser Val Lys Leu Gly Ser Gly  
                   180                   185                   190  
 Arg Ile Gly Arg His Trp Ala Val Asp Ala Arg Leu Ser Lys Ile Gly  
                   195                   200                   205  
 Ser Asp Gly Tyr Val Asp Arg Gly Ser Val Asp Leu Lys Ser Tyr Phe  
 210                   215                   220  
 75 Ala Gln Val Gly Tyr Phe Gly Ser Asn Thr Ala Leu Arg Phe Ile Thr

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5	225											230											235											240
	Phe	Gly	Gly	Lys	Glu	Val	Thr	Gly	Ile	Ala	Trp	Asn	Gly	Leu	Ser	Lys	245	Val	Thr	Gly	Ile	Ala	Trp	Asn	Gly	Leu	Ser	Lys						
					245					250					255						255													
	Glu	Asp	Glu	Ala	Lys	Tyr	Gly	Arg	Arg	Tyr	Asn	Ser	Ala	Gly	Leu	Met	260	Tyr	Gly	Arg	Arg	Tyr	Asn	Ser	Ala	Gly	Leu	Met						
10	Tyr	Val	Asp	Ala	Gln	Gly	Val	Pro	His	Tyr	Tyr	His	Asn	Thr	Asn	265	Tyr	His	Ala	Ile	Met	Thr	His	Ser	Phe	Ser	Pro							
					265					270					275						280													
	Tyr	Glu	Gln	Arg	His	Tyr	His	Ala	Ile	Met	Thr	His	Ser	Phe	Ser	Pro	285	Tyr	His	Ala	Ile	Met	Thr	His	Ser	Phe	Ser							
					290						295					300						305												
15	Ser	Val	Ile	Leu	Asn	Leu	Thr	Ala	His	Tyr	Thr	Ala	Gly	Tyr	Gly	Tyr	310	Thr	Ala	His	Tyr	Thr	Ala	Gly	Tyr	Gly	Tyr							
					310					315					320						325													
	Thr	Asp	Glu	Tyr	Arg	Thr	Gly	Arg	Lys	Leu	Lys	Glu	Tyr	Ala	Leu	Gln	330	Thr	Ala	His	Tyr	Thr	Ala	Gly	Tyr	Gly	Tyr							
					325					330					335						340													
20	Pro	Tyr	Val	Glu	Asn	Ser	Val	Thr	Val	Lys	Lys	Thr	Asp	Leu	Ile	Arg	345	Thr	Ala	His	Tyr	Thr	Ala	Gly	Tyr	Gly	Tyr							
					340					345					350						355													
	Gln	Lys	Tyr	Leu	Asp	Asn	Asp	Phe	Gly	Gly	Leu	Ile	Gly	Ser	Leu	Asn	360	Thr	Ala	His	Tyr	Thr	Ala	Gly	Tyr	Gly	Tyr							
					355					360					365						370													
25	Trp	His	Thr	Gly	Ala	Trp	Asp	Leu	Gln	Phe	Gly	Ala	Ser	Gly	Asn	Ile	375	Thr	Ala	His	Tyr	Thr	Ala	Gly	Tyr	Gly	Tyr							
					370					375					380						385													
	Tyr	Lys	Gly	Asp	His	Phe	Gly	Arg	Ile	Thr	Tyr	Ile	Lys	Lys	Tyr	Asn	390	Thr	Ala	His	Tyr	Thr	Ala	Gly	Tyr	Gly	Tyr							
					390					395					400						405													
30	Gln	Pro	Leu	Ala	Pro	Asp	Phe	Glu	Tyr	Tyr	Arg	Asn	Arg	Ala	Asp	Lys	410	Thr	Ala	His	Tyr	Thr	Ala	Gly	Tyr	Gly	Tyr							
					405					410					415						420													
	Arg	Glu	Gly	Ala	Ala	Phe	Ala	Lys	Ala	Asn	Trp	Gln	Ile	Thr	Pro	Glu	425	Thr	Ala	His	Tyr	Thr	Ala	Gly	Tyr	Gly	Tyr							
					420					425					430						435													
35	Leu	Asn	Met	Tyr	Ala	Asp	Leu	Gln	Tyr	Arg	Thr	Ile	Gly	Tyr	Thr	Ile	440	Thr	Ala	His	Tyr	Thr	Ala	Gly	Tyr	Gly	Tyr							
					435					440					445						450													
	Asn	Gly	Ile	Thr	Asp	Glu	Tyr	Asp	Glu	Val	Gln	Gly	Ser	Met	Gln	His	455	Thr	Ala	His	Tyr	Thr												

(2) INFORMATION FOR SEQ ID NO: 478

70 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 494 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

75 (ii) MOLECULE TYPE: protein

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(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Porphyromonas gingivalis*

(ix) FEATURE:

(A) NAME/KEY: misc\_feature

(B) LOCATION 1...494

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:478

```

Met Lys Arg Arg Phe Leu Ser Leu Leu Leu Tyr Ile Leu Ser Ser
1      5      10      15
Ile Ser Leu Ser Ala Gln Arg Phe Pro Met Val Gln Gly Ile Glu Leu
15      20      25      30
Asp Thr Asp Ser Leu Phe Ser Leu Pro Lys Arg Pro Trp Arg Ala Ile
35      40      45
Gly Lys Thr Ile Gly Val Asn Leu Ala Val Trp Gly Phe Asp His Phe
50      55      60
Ile Met Asn Glu Asp Phe Ala Asp Ile Ser Trp Gln Thr Ile Lys Ser
20      65      70      75
Asn Phe Gln Thr Gly Phe Gly Trp Asp Asn Asp Lys Phe Val Thr Asn
85      90      95
Leu Phe Ala His Pro Tyr His Gly Ser Leu Tyr Phe Asn Ala Ala Arg
25      100      105      110
Ser Asn Gly Leu Ser Phe Arg His Ser Ala Pro Phe Ala Phe Phe Gly
115      120      125
Ser Leu Met Trp Glu Leu Leu Met Glu Asn Glu Pro Ser Ile Asn
130      135      140
Asp Leu Cys Ala Thr Thr Ile Gly Gly Ile Ala Leu Gly Glu Met Gly
145      150      155      160
His Arg Leu Ser Asp Leu Leu Ile Asp Asn Arg Thr Thr Gly Trp Glu
165      170      175
Arg Met Gly Arg Glu Val Ala Ile Ala Leu Ile Asn Pro Met Arg Phe
180      185      190
Leu Asn Arg Leu Thr Ala Gly Glu Val Thr Ser Val Gly Ser Arg Ser
195      200      205
Gly Gln Ile Phe Gln Ser Val Pro Ile Asn Ile Val Val Asp Ala Gly
210      215      220
Phe Arg Phe Leu Ala Asp Lys Arg His Ala Arg Thr Gly Ala Thr Ala
225      230      235      240
Leu Thr Leu Asn Leu Arg Phe Asp Tyr Gly Asp Pro Phe Arg Ser Glu
245      250      255
Thr Phe Ser Pro Tyr Asp Phe Phe Gln Phe Lys Ala Gly Leu Ser Phe
260      265      270
Ser Glu Ser Gln Pro Leu Leu Ser Gln Ile Asn Leu Ile Gly Ile Leu
275      280      285
Ser Gly Cys Gln Leu Leu Ala His Glu Arg Thr Val Leu Val Gly Gly
290      295      300
Leu Phe Gln His Phe Asp Tyr Tyr Asn Ser Glu Lys Arg Ile Ser Lys
305      310      315      320
Asn Ser Glu Glu Val Leu Val Thr Pro Tyr Arg Ile Ser Gln Val Ala
325      330      335
Ala Leu Gly Gly Gly Leu Ile Phe Gln His His Gly Lys Phe Arg Arg
340      345      350
Arg Pro Leu Glu Leu Tyr Ala Glu Thr Tyr Leu Asn Val Val Pro Met
355      360      365
Gly Ala Ser Leu Ser Asp His Tyr Asn Val Asp Asn Arg Asp Tyr Asn
370      375      380
Leu Gly Ser Gly Leu Ser Gly Lys Leu Tyr Leu Gly Ala Thr Tyr Asn
385      390      395      400
Asp Leu Trp Ser Trp Leu Leu Gly Val Glu Ser Tyr Arg Leu Tyr Thr
405      410      415
Trp Ile Gly Tyr Glu Glu Pro His Gln Lys Asn Thr Asp Val Ser Ser
420      425      430
Phe Met Val Gln Gly Asp Glu Ser Lys Ala Arg Leu Leu Val Thr Ser
435      440      445
Ser Glu Phe Ala Phe His Pro Gly Pro Trp His Val Ala Ile Val Ala
450      455      460
Arg Arg Phe Ile Arg Lys Thr Ala Tyr Gln Phe Tyr Pro Asn Val Ser
70      465      470      475      480
Phe Asp Thr Gly Asp Ile Gln Leu Arg Val Gly Phe His Phe
485      490

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75 (2) INFORMATION FOR SEQ ID NO:479

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- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 294 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: *Porphyromonas gingivalis*
- (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...294
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:479
- |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Lys | Arg | Leu | Ile | Val | Phe | Leu | Ala | Met | Gly | Gly | Leu | Leu | Phe | Thr |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Leu | Ala | Asn | Ala | Gln | Glu | Ala | Asn | Thr | Ala | Ser | Asp | Thr | Pro | Lys | Lys |
|     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |     |
| Asp | Trp | Thr | Ile | Lys | Gly | Val | Thr | Gly | Leu | Asn | Ala | Ser | Gln | Thr | Ser |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Leu | Thr | Asn | Trp | Ala | Ala | Gly | Gly | Glu | Asn | Thr | Val | Ala | Gly | Asn | Leu |
|     |     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Tyr | Leu | Asn | Ile | Asp | Ala | Asn | Tyr | Leu | Lys | Asp | Lys | Trp | Ser | Trp | Asp |
|     |     | 65  |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |     |
| Asn | Gly | Leu | Arg | Thr | Asp | Phe | Gly | Leu | Thr | Tyr | Thr | Thr | Ala | Asn | Lys |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     |     | 95  |     |
| Trp | Asn | Lys | Ser | Val | Asp | Lys | Ile | Glu | Leu | Phe | Thr | Lys | Ala | Gly | Tyr |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Glu | Ile | Gly | Lys | His | Trp | Tyr | Gly | Ser | Ala | Leu | Phe | Thr | Phe | Leu | Ser |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Gln | Tyr | Ala | Lys | Gly | Tyr | Glu | Lys | Pro | Ser | Asp | His | Leu | Thr | Gly | Val |
|     |     | 130 |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Lys | His | Ile | Ser | Asn | Phe | Phe | Ala | Pro | Ala | Tyr | Leu | Thr | Leu | Gly | Ile |
|     |     | 145 |     |     | 150 |     |     |     |     | 155 |     |     |     | 160 |     |
| Gly | Ala | Asp | Tyr | Lys | Pro | Asn | Glu | Lys | Phe | Ser | Leu | Tyr | Leu | Ser | Pro |
|     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |     |
| Thr | Thr | Gly | Lys | Leu | Thr | Val | Val | Ala | Asp | Asp | Tyr | Leu | Ser | Ser | Leu |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Gly | Ala | Phe | Gly | Val | Lys | Val | Gly | Glu | Lys | Thr | Met | Phe | Glu | Leu | Gly |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Ala | Leu | Val | Val | Gly | Ser | Ala | Asn | Ile | Asn | Leu | Met | Glu | Asn | Val | Asn |
|     |     | 210 |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Leu | Ile | Thr | Lys | Ala | Ser | Phe | Phe | Ser | Ala | Tyr | Thr | His | Asp | Phe | Gly |
|     |     | 225 |     |     | 230 |     |     |     |     | 235 |     |     |     | 240 |     |
| Asn | Ile | Asp | Ile | Asn | Trp | Glu | Ala | Met | Leu | Ala | Met | Lys | Ile | Asn | Lys |
|     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |     |
| Phe | Leu | Thr | Ala | Thr | Ile | Ala | Thr | Asn | Leu | Ile | Tyr | Asp | Asp | Asp | Val |
|     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |     |
| Lys | Ile | Asn | Asp | Gly | Pro | Lys | Ile | Gln | Phe | Lys | Glu | Val | Val | Gly | Val |
|     |     | 275 |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |
| Gly | Val | Ala | Tyr | Thr | Phe |     |     |     |     |     |     |     |     |     |     |
|     |     | 290 |     |     |     |     |     |     |     |     |     |     |     |     |     |
- (2) INFORMATION FOR SEQ ID NO:480
- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 204 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: *Porphyromonas gingivalis*
- (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...204



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## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:480

5 Met Lys Lys Met Ile Leu Ala Ala Thr Met Leu Leu Ala Thr Ile Gly  
 1 5 10 15  
 Phe Ala Asn Ala Gln Ser Arg Pro Ala Leu Arg Leu Asp Ala Asn Phe  
 20 25 30  
 Val Gly Ser Asn Leu Met Gln Lys Val Ala Asn Thr Ser Val Asn Asn  
 35 40 45  
 10 Lys Met Ile Val Gly Leu Arg Val Gly Ala Ala Ala Glu Phe Ala Leu  
 50 55 60  
 Ser Asn Asp Gly Phe Tyr Leu Ala Pro Gly Leu Ala Tyr Thr Met Arg  
 65 70 75 80  
 Gly Ala Lys Met Glu Ser Leu Ser Glu Thr Thr Thr Arg Leu His Tyr  
 85 90 95  
 15 Leu Gln Ile Pro Val Asn Ala Gly Met Arg Phe Ser Phe Ala Asp Asn  
 100 105 110  
 Met Ala Ile Ser Leu Glu Ala Gly Pro Tyr Phe Ala Tyr Gly Val Ala  
 115 120 125  
 20 Gly Thr Ile Lys Thr Lys Val Ala Gly Val Thr Ala Ser Val Asp Ala  
 130 135 140  
 Phe Gly Asp Asn Gly Tyr Asn Arg Phe Asp Leu Gly Leu Gly Leu Ser  
 145 150 155 160  
 Ala Ala Leu Ser Tyr Asp Arg Tyr Tyr Val Gln Ile Gly Tyr Glu His  
 165 170 175  
 25 Gly Leu Leu Asn Met Leu Lys Asp Ala Pro Asp Lys Thr Ser Leu Arg  
 180 185 190  
 Asn His Asp Phe Phe Val Gly Leu Gly Val Arg Phe  
 195 200

## (2) INFORMATION FOR SEQ ID NO:481

35 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 243 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
  
 (ii) MOLECULE TYPE: protein  
  
 40 (iii) HYPOTHETICAL: YES  
  
 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Porphyromonas gingivalis  
  
 45 (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION: 1...243

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:481

50 Met Lys Arg Ile Phe Thr Val Ala Leu Val Leu Leu Ala Ser Val Thr  
 1 5 10 15  
 Met Ala Ile Gly Gln Ser Arg Pro Ala Leu Arg Val Asp Ala Asn Phe  
 20 25 30  
 55 Val Gly Ser Asn Gln Ser Met Lys Arg Asp Gly Tyr Val Trp Asp Thr  
 35 40 45  
 Lys Met Asn Val Gly Leu Arg Val Gly Ala Ala Ala Glu Phe Met Ile  
 50 55 60  
 60 Gly Ser Arg Gly Phe Tyr Leu Ala Pro Gly Leu Asn Tyr Thr Met Lys  
 65 70 75 80  
 Gly Ser Lys Thr Glu Trp Asp Ile Pro Glu Met Val Pro Gly Thr Tyr  
 85 90 95  
 Ile Thr Met Val Ser Thr Arg Leu His Tyr Leu Gln Leu Pro Ile Asn  
 100 105 110  
 65 Ala Gly Met Arg Phe Asp Leu Met Asn Asp Met Ala Val Ser Ile Glu  
 115 120 125  
 Ala Gly Pro Phe Leu Ala Tyr Gly Ile Tyr Gly Thr Tyr Arg Gln Lys  
 130 135 140  
 70 Leu Glu Gly Trp Lys Pro Asn Asn Tyr Ser Thr Glu Phe Phe Gly Pro  
 145 150 155 160  
 Thr Leu Gly Gly Pro Thr Asn Ile Arg Trp Asp Ile Gly Ala Asn Ile  
 165 170 175  
 Ile Ala Ala Phe His Tyr Lys Arg Tyr Tyr Ile Gln Ile Gly Tyr Glu  
 180 185 190  
 75 His Gly Phe Val Asp Ile Val Ser Gly Gly Ser Asp Ile Pro Arg

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10

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 207 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

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(iii) Hypothetical: YES

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```
(ix) FEATURE:
      (A) NAME/KEY: misc_feature
      (B) LOCATION 1...207
```

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(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 951 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

60

(iii) HYPOTHETICAL: YES

65

(ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...951

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	Met	Arg	Val	Ser	Asp	Leu	Cys	Ser	Arg	Leu	Ser	Trp	Leu	Leu	Pro	Val
	1				5					10					15	
	Ile	Leu	Val	Gly	Leu	Leu	Cys	Ala	Thr	Leu	Val	Ala	Ala	Glu	Arg	Pro
				20					25					30		
5	Met	Ala	Gly	Ala	Val	Gly	Leu	His	His	Arg	Arg	His	Ala	Ala	Leu	Ser
			35					40					45			
	Asp	Ser	Thr	Ala	Lys	Asp	Thr	Val	Pro	Leu	Ala	Lys	Pro	Ile	Pro	Asp
		50				55						60				
10	Ser	Ala	Phe	Arg	Asp	Ser	Leu	Pro	Ala	Asp	Ser	Thr	Gly	Ser	Met	Arg
	65				70					75					80	
	Gln	Asp	Ser	Val	Tyr	Asp	Asp	Glu	Phe	Glu	Leu	Glu	Asp	Ile	Val	Glu
				85					90					95		
	Tyr	Glu	Ala	Ala	Asp	Ser	Ile	Val	Leu	Leu	Gly	Gln	Asn	Arg	Ala	Tyr
			100					105					110			
15	Leu	Phe	Gly	Lys	Ser	Tyr	Val	Ser	Tyr	Gln	Lys	Ser	Arg	Leu	Glu	Ala
			115					120					125			
	Asn	Phe	Met	Tyr	Leu	Asn	Thr	Asp	Ser	Ser	Thr	Val	Tyr	Thr	Arg	Tyr
		130				135						140				
20	Val	Leu	Asp	Thr	Ala	Gly	Tyr	Pro	Met	Ala	Phe	Pro	Val	Phe	Lys	Asp
	145					150					155				160	
	Gly	Glu	Gln	Ser	Phe	Glu	Ala	Lys	Asn	Phe	Thr	Tyr	Asn	Phe	Arg	Thr
				165					170					175		
	Glu	Lys	Gly	Ile	Ile	Ser	Gly	Val	Ile	Thr	Gln	Gln	Gly	Glu	Gly	Tyr
			180					185					190			
25	Leu	Thr	Ala	Gly	Lys	Thr	Lys	Lys	Met	Pro	Asp	Asn	Ile	Met	Phe	Met
			195					200					205			
	Gln	Gly	Gly	Arg	Tyr	Thr	Thr	Cys	Asp	Asn	His	Asp	His	Pro	His	Phe
		210					215					220				
30	Tyr	Ile	Asn	Leu	Ser	Lys	Ala	Lys	Val	His	Pro	Glu	Lys	Asp	Ile	Val
	225					230					235				240	
	Thr	Gly	Pro	Val	Asn	Leu	Val	Ile	Ala	Asp	Met	Pro	Leu	Pro	Ile	Gly
				245						250					255	
	Leu	Pro	Phe	Gly	Tyr	Phe	Pro	Phe	Ser	Asn	Lys	Tyr	Ser	Ser	Gly	Ile
			260					265					270			
35	Leu	Met	Pro	Thr	Tyr	Gly	Glu	Asp	Asn	Arg	Tyr	Gly	Phe	Tyr	Leu	Arg
			275					280					285			
	Asn	Gly	Gly	Tyr	Tyr	Phe	Ala	Phe	Ser	Asp	Tyr	Ile	Asp	Leu	Ala	Leu
		290				295						300				
40	Arg	Gly	Glu	Ile	Phe	Ser	Lys	Gly	Ser	Trp	Gly	Ile	Ser	Ala	Gln	Ser
	305					310					315				320	
	Lys	Tyr	Lys	Lys	Arg	Tyr	Lys	Tyr	Asn	Gly	Ser	Phe	Glu	Ala	Asn	Tyr
				325					330					335		
	Leu	Val	Ser	Lys	Ser	Gly	Asp	Lys	Tyr	Val	Pro	Gly	Asp	Tyr	Ser	Lys
			340					345					350			
45	Thr	Thr	Ser	Leu	Asn	Ile	Arg	Trp	Thr	His	Ser	Gln	Asp	Pro	Lys	Ala
			355					360					365			
	Asn	Pro	Leu	Gln	Thr	Leu	Ser	Ala	Asn	Val	Asn	Phe	Ala	Thr	Gly	Ser
		370				375						380				
50	Tyr	Phe	Gln	Asn	Ser	Leu	Asn	Thr	Thr	Tyr	Asp	Val	Asn	Ala	Arg	Thr
	385					390				395					400	
	Ala	Thr	Thr	Arg	Ser	Ser	Ala	Val	Ser	Tyr	Ser	Arg	Lys	Phe	Pro	Gly
				405						410					415	
	Thr	Pro	Phe	Ser	Ile	Thr	Gly	Ser	Met	Asp	Ile	Ser	Gln	Asn	Met	Arg
			420						425					430		
55	Asp	Thr	Thr	Val	Ser	Leu	Thr	Leu	Pro	Asn	Leu	Ser	Ile	Asn	Met	Ser
			435					440					445			
	Thr	Arg	Tyr	Pro	Phe	Lys	Arg	Lys	Thr	Arg	Val	Gly	Pro	Glu	Arg	Trp
		450				455						460				
60	Tyr	Glu	Lys	Leu	Ser	Val	Gly	Tyr	Ser	Gly	Gln	Leu	Arg	Asn	Ser	Ile
	465					470					475				480	
	Leu	Thr	Lys	Glu	Lys	Asp	Leu	Leu	Gln	Ser	Asn	Leu	Val	Arg	Asp	Trp
				485					490					495		
	Lys	Asn	Gly	Met	Arg	His	Ser	Val	Pro	Ile	Ser	Leu	Thr	Val	Pro	Leu
			500						505					510		
65	Leu	Asp	Tyr	Ile	Asn	Leu	Thr	Met	Gly	Val	Asn	Tyr	Asn	Glu	Trp	Trp
		515						520					525			
	Tyr	Thr	Lys	Gly	Ile	Arg	Lys	Ser	Trp	Asn	Glu	Asp	Lys	Lys	Thr	Phe
		530					535					540				
70	Leu	Pro	Ser	Asp	Thr	Thr	Tyr	Lys	Phe	Arg	Arg	Leu	Tyr	Asp	Tyr	Ser
	545					550					555				560	
	Leu	Ser	Ala	Gly	Leu	Ser	Thr	Thr	Leu	Tyr	Gly	Met	Phe	Lys	Pro	Trp
				565					570					575		
	Lys	Pro	Phe	Ser	Phe	Gly	Gly	Asn	Leu	Ile	Met	Ile	Arg	His	Arg	Phe
				580					585					590		
75	Thr	Pro	Thr	Val	Ser	Phe	Ser	Tyr	Met	Pro	Asp	Phe	Thr	Lys	Arg	Arg

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595 600 605  
 Tyr Gly Phe Trp Glu Leu Leu Glu His Thr Asp Gln Asn Gly Lys Leu  
 610 615 620  
 5 His Thr Leu Leu Tyr Ser Pro Tyr Phe Glu Gln Ile Phe Gly Ala Pro  
 625 630 635 640  
 15 Ser Met Gly Asn Ala Gly Ser Val Asn Phe Ser Phe Asp Asn Asn Leu  
 645 650 655  
 Glu Ala Lys Ile Lys Ser Lys Ser Asp Ser Thr Gly Ile Lys Lys Ile  
 660 665 670  
 10 Ser Leu Ile Asp Gln Phe Thr Trp Ser Thr Ser Tyr Asn Met Phe Ala  
 675 680 685  
 Asp Ser Ile Arg Trp Ser Asn Ile Ser Ala Ser Leu Ala Leu Arg Leu  
 690 695 700  
 15 Ser Lys Ser Phe Thr Leu Arg Leu Ser Gly Leu Phe Asp Pro Tyr Leu  
 705 710 715 720  
 Thr Lys Tyr Tyr Glu Gly Glu Asp Gly Lys Ile Ile Pro Tyr Lys Ser  
 725 730 735  
 Asn Asp Leu Arg Ile Phe Asn Gly Lys Gly Leu Ala Arg Leu Ile Ser  
 740 745 750  
 20 Thr Gly Thr Ser Phe Ser Tyr Thr Leu Asn Lys Glu Ser Leu Ser Gly  
 755 760 765  
 Leu Ile Ala Leu Phe Ser Gly Lys Lys Glu Arg Arg Asp Glu Lys Lys  
 770 775 780  
 25 Asn Thr Gly Ala Thr Pro His Glu Gly Asp Asp Ala Ala Asp Ile Leu  
 785 790 795 800  
 Glu Gly Gly Arg Pro Gln Asn Glu Ser Gly Gly Ser Leu Leu Glu Arg  
 805 810 815  
 Asn Arg Gln Gly Ala Val Asp Gln Asp Gly Tyr Phe Ala Tyr Ser  
 820 825 830  
 30 Ile Pro Trp Ser Leu Ser Phe Asp Tyr Ser Trp Asn Ile Ala Thr Asp  
 835 840 845  
 Tyr Asn Arg Tyr Asn Val Asn Lys Met Glu His Tyr Tyr Arg Val Thr  
 850 855 860  
 35 Gln Asn Leu Ser Phe Arg Gly Asn Ile Gln Pro Thr Pro Asn Trp Ser  
 865 870 875 880  
 Phe Gly Phe Asn Ala Asn Tyr Asn Phe Asp Leu Lys Lys Ile Thr Ser  
 885 890 895  
 Leu Thr Cys Asn Val Thr Arg Asp Met His Cys Trp Ala Ile Ser Ala  
 900 905 910  
 40 Ser Phe Ile Pro Ile Gly Ala Tyr Lys Ser Tyr Asn Phe Val Ile Ser  
 915 920 925  
 Val Lys Ser Ser Leu Leu Gln Asp Leu Lys Tyr Gln Gln Ser Asn Arg  
 930 935 940  
 45 Pro Ile Thr Asn Thr Trp Tyr  
 945 950

(2) INFORMATION FOR SEQ ID NO:484

- 50 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1226 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
  
 55 (ii) MOLECULE TYPE: protein  
 (iii) HYPOTHETICAL: YES  
 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Porphyromonas gingivalis  
 60 (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...1226  
 65 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:484

70 Met Met Lys Arg Tyr Thr Ile Ile Leu Ala Val Phe Leu Leu Phe Cys  
 1 5 10 15  
 Thr Val Phe Thr Phe Gln Ile Lys Ala Arg Pro Tyr Glu Arg Phe Ala  
 20 25 30  
 Asp Val Glu Lys Pro Trp Ile Gln Lys His Ser Met Asp Ser Lys Leu  
 35 40 45  
 Val Pro Ala Asn Lys Gly Asn Leu Ile Gln Ala Glu Ile Val Tyr Gln  
 50 55 60  
 75 Ser Val Ser Glu His Ser Asp Leu Val Ile Ser Pro Val Asn Glu Ile

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	65				70				75					80		
	Arg	Pro	Ala	Asn	Arg	Phe	Pro	Ser	His	Arg	Lys	Ser	Phe	Phe	Ala	Glu
					85					90					95	
5	Asn	Leu	Arg	Ala	Ser	Pro	Pro	Val	Val	Pro	Val	Ala	Val	Asp	Lys	Tyr
				100					105					110		
	Ala	Val	Pro	Val	Ala	Asn	Pro	Met	Asp	Pro	Glu	Asn	Pro	Asn	Ala	Trp
			115					120					125			
	Asp	Val	Thr	Leu	Lys	Ile	Thr	Thr	Lys	Ala	Val	Thr	Val	Pro	Val	Asp
		130					135					140				
10	Val	Val	Met	Val	Ile	Asp	Gln	Ser	Ser	Ser	Met	Gly	Gly	Gln	Asn	Ile
		145				150					155				160	
	Ala	Arg	Leu	Lys	Ser	Ala	Ile	Ala	Ser	Gly	Gln	Arg	Phe	Val	Lys	Lys
				165						170				175		
15	Met	Leu	Pro	Lys	Gly	Thr	Ala	Thr	Glu	Gly	Val	Arg	Ile	Ala	Leu	Val
			180						185					190		
	Ser	Tyr	Asp	His	Glu	Pro	His	Arg	Leu	Ser	Asp	Phe	Thr	Lys	Asp	Thr
		195					200					205				
	Ala	Phe	Leu	Cys	Gln	Lys	Ile	Arg	Ala	Leu	Thr	Pro	Ile	Trp	Gly	Thr
		210					215					220				
20	His	Thr	Gln	Gly	Gly	Leu	Lys	Met	Ala	Arg	Asn	Ile	Met	Ala	Thr	Ser
		225				230					235				240	
	Thr	Ala	Val	Asp	Lys	His	Ile	Ile	Leu	Met	Ser	Asp	Gly	Leu	Ala	Thr
				245					250					255		
25	Glu	Gln	Tyr	Pro	Val	Lys	Asn	Val	Thr	Thr	Ala	Asp	Phe	Ile	Gly	Lys
			260						265					270		
	Thr	Gly	Asn	Ala	Asn	Asp	Pro	Ile	Asp	Leu	Val	Ile	Gln	Gly	Ala	Ile
		275					280						285			
	Asn	Phe	Pro	Thr	Asn	Tyr	Val	Ser	Asn	Asn	Pro	Ser	Thr	Pro	Leu	Thr
		290					295					300				
30	Pro	Asn	Tyr	Pro	Thr	His	Ser	Ser	Lys	Val	Gly	Arg	Arg	Asn	Leu	Pro
		305				310					315				320	
	Glu	Ser	Lys	Phe	Asp	Tyr	Ser	Asn	Leu	Ser	Ala	Arg	Ile	Thr	Phe	Asp
				325						330				335		
35	Gly	Val	Ala	Gly	Ala	Leu	Val	Tyr	Glu	Pro	Arg	Phe	Pro	His	Pro	Tyr
			340						345					350		
	Tyr	Tyr	Tyr	Phe	Pro	Cys	Asn	Ala	Ala	Ile	Asn	Glu	Ala	Gln	Phe	Ala
		355						360				365				
	Lys	Asn	Ser	Gly	Tyr	Thr	Ile	His	Thr	Ile	Gly	Tyr	Asp	Leu	Gly	Asp
		370					375					380				
40	Phe	Ala	Leu	Ala	Asn	Asn	Ser	Leu	Lys	Leu	Thr	Ala	Thr	Asp	Glu	Asn
		385				390					395				400	
	His	Phe	Phe	Thr	Ala	Thr	Pro	Ala	Asn	Leu	Ala	Ala	Ala	Phe	Asp	Asn
				405						410				415		
45	Ile	Ala	Gln	Thr	Ile	Asn	Ile	Gly	Ile	Gln	Arg	Gly	Glu	Val	Thr	Asp
			420						425					430		
	Phe	Val	Ala	Pro	Gly	Phe	Ile	Val	Lys	Asn	Leu	Thr	Gln	Ser	Gly	Asp
		435						440					445			
	Val	Thr	His	Leu	Leu	Asn	Val	Ser	Asn	Gly	Thr	Val	His	Tyr	Asp	Val
		450				455						460				
50	Ser	Thr	Lys	Lys	Leu	Thr	Trp	Thr	Thr	Gly	Thr	Ile	Leu	Ser	Ser	Ser
		465				470					475				480	
	Glu	Ala	Thr	Ile	Thr	Tyr	Arg	Ile	Tyr	Ala	Asp	Leu	Asp	Tyr	Ile	Gln
				485						490				495		
55	Asn	Asn	Asp	Ile	Pro	Val	Asn	Thr	Thr	Ser	Ala	Ile	Gly	Pro	Asp	Leu
			500						505					510		
	Gly	Gly	Phe	Asp	Thr	Asn	Thr	Glu	Ala	Lys	Leu	Thr	Tyr	Thr	Asn	Ser
		515						520					525			
	Asn	Gly	Glu	Pro	Asn	Gln	Gln	Leu	Ile	Phe	Pro	Arg	Pro	Thr	Val	Lys
		530				535						540				
60	Leu	Gly	Tyr	Gly	Val	Ile	Lys	Arg	His	Tyr	Val	Leu	Val	Asn	Lys	Asp
		545				550					555				560	
	Gly	Gln	Pro	Ile	Gln	Ala	Asn	Gly	Thr	Val	Val	Ser	Ser	Leu	Ser	Glu
				565						570				575		
65	Ala	His	Val	Leu	Gln	Ser	Gln	Asp	Phe	Phe	Leu	Pro	Ser	Gly	Gly	Gly
			580						585					590		
	His	Ile	Val	Pro	Lys	Trp	Ile	Lys	Leu	Asp	Lys	Thr	Thr	Glu	Ala	Leu
		595						600					605			
	Gln	Tyr	Tyr	Ser	Val	Pro	Pro	Thr	Asn	Thr	Val	Ile	Thr	Thr	Ala	Asp
		610					615					620				
70	Gly	Lys	Arg	Tyr	Arg	Phe	Val	Glu	Val	Pro	Gly	Ser	Thr	Pro	Asn	Pro
		625				630					635				640	
	Gly	Gln	Ile	Gly	Ile	Ser	Trp	Lys	Lys	Pro	Ala	Gly	Asn	Ala	Tyr	Phe
				645						650				655		
75	Ala	Tyr	Lys	Leu	Leu	Asn	Tyr	Trp	Met	Gly	Gly	Thr	Thr	Asp	Gln	Gln
			660						665					670		

SUBSTITUTE SHEET (Rule 26) (RO/AU)

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Ser Glu Trp Asp Val Thr Ser Asn Trp Thr Gly Ala Gln Val Pro Leu  
 675 680 685  
 Thr Gly Glu Asp Val Glu Phe Ala Thr Thr Glu Asn Phe Gly Ser Pro  
 690 695 700  
 5 Ala Val Ala Asp Leu His Val Pro Thr Thr Asn Pro Lys Ile Ile Gly  
 705 710 715 720  
 Asn Leu Ile Asn Asn Ser Asp Lys Asp Leu Val Val Thr Thr Ser Ser  
 725 730 735  
 10 Gln Leu Thr Ile Asn Gly Val Val Glu Asp Asn Asn Pro Asn Val Gly  
 740 745 750  
 Thr Ile Val Val Lys Ser Ser Lys Asp Asn Pro Thr Gly Thr Leu Leu  
 755 760 765  
 Phe Ala Asn Pro Gly Tyr Asn Gln Asn Val Gly Gly Thr Val Glu Phe  
 770 775 780  
 15 Tyr Asn Gln Gly Tyr Asp Cys Ala Asp Cys Gly Met Tyr Arg Arg Ser  
 785 790 795 800  
 Trp Gln Tyr Phe Gly Ile Pro Val Asn Glu Ser Gly Phe Pro Ile Asn  
 805 810 815  
 20 Asp Val Gly Gly Asn Glu Thr Val Asn Gln Trp Val Glu Pro Phe Asn  
 820 825 830  
 Gly Asp Lys Trp Arg Pro Ala Pro Tyr Ala Pro Asp Thr Glu Leu Gln  
 835 840 845  
 Lys Phe Lys Gly Tyr Gln Ile Thr Asn Asp Val Gln Ala Gln Pro Thr  
 850 855 860  
 25 Gly Val Tyr Ser Phe Lys Gly Met Ile Cys Val Cys Asp Ala Phe Leu  
 865 870 875 880  
 Asn Leu Thr Arg Thr Ser Gly Val Asn Tyr Ser Gly Ala Asn Leu Ile  
 885 890 895  
 30 Gly Asn Ser Tyr Thr Gly Ala Ile Asp Ile Lys Gln Gly Ile Val Phe  
 900 905 910  
 Pro Pro Glu Val Glu Gln Thr Val Tyr Leu Phe Asn Thr Gly Thr Arg  
 915 920 925  
 Asp Gln Trp Arg Lys Leu Asn Gly Ser Thr Val Ser Gly Tyr Arg Ala  
 930 935 940  
 35 Gly Gln Tyr Leu Ser Val Pro Lys Asn Thr Ala Gly Gln Asp Asn Leu  
 945 950 955 960  
 Pro Asp Arg Ile Pro Ser Met His Ser Phe Leu Val Lys Met Gln Asn  
 965 970 975  
 40 Gly Ala Ser Cys Thr Leu Unk Ile Leu Tyr Asp Lys Leu Leu Lys Asn  
 980 985 990  
 Thr Thr Val Asn Asn Gly Asn Gly Thr Gln Ile Thr Trp Arg Ser Gly  
 995 1000 1005  
 Asn Ser Gly Ser Ala Asn Met Pro Ser Leu Val Met Asp Val Leu Gly  
 1010 1015 1020  
 45 Asn Glu Ser Ala Asp Arg Leu Trp Ile Phe Thr Asp Gly Gly Leu Ser  
 1025 1030 1035 1040  
 Phe Gly Phe Asp Asn Gly Trp Asp Gly Arg Lys Leu Thr Glu Lys Gly  
 1045 1050 1055  
 50 Leu Ser Gln Leu Tyr Ala Met Ser Asp Ile Gly Asn Asp Lys Phe Gln  
 1060 1065 1070  
 Val Ala Gly Val Pro Glu Leu Asn Asn Leu Leu Ile Gly Phe Asp Ala  
 1075 1080 1085  
 Asp Lys Asp Gly Gln Tyr Thr Leu Glu Phe Ala Leu Ser Asp His Phe  
 1090 1095 1100  
 55 Ala Lys Gly Ala Val Tyr Leu His Asp Leu Gln Ser Gly Ala Lys His  
 1105 1110 1115 1120  
 Arg Ile Thr Asn Ser Thr Ser Tyr Ser Phe Asp Ala Lys Arg Gly Asp  
 1125 1130 1135  
 60 Ser Gly Ala Arg Phe Arg Leu Ser Tyr Gly Cys Asp Glu Asn Val Asp  
 1140 1145 1150  
 Asp Ser His Val Val Ser Thr Asn Gly Arg Glu Ile Ile Ile Leu Asn  
 1155 1160 1165  
 Gln Asp Ala Leu Asp Cys Thr Val Thr Leu Phe Thr Ile Glu Gly Lys  
 1170 1175 1180  
 65 Leu Leu Arg Arg Leu Lys Val Leu Ala Gly His Arg Glu Val Met Lys  
 1185 1190 1195 1200  
 Val Gln Thr Gly Gly Ala Tyr Ile Val His Leu Gln Asn Ala Phe Thr  
 1205 1210 1215  
 70 Asn Asp Val His Lys Val Leu Val Glu Tyr  
 1220 1225

(2) INFORMATION FOR SEQ ID NO:485

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1225 amino acids

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(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein  
5

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:  
10 (A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:  
(A) NAME/KEY: misc\_feature  
(B) LOCATION 1...1225

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:485

```

Met Lys Arg Tyr Thr Ile Ile Leu Ala Val Phe Leu Leu Phe Cys Thr
1      5      10      15
Val Phe Thr Phe Gln Ile Lys Ala Arg Pro Tyr Glu Arg Phe Ala Asp
20      20      25      30
Val Glu Lys Pro Trp Ile Gln Lys His Ser Met Asp Ser Lys Leu Val
35      40      45
Pro Ala Asn Lys Gly Asn Leu Ile Gln Ala Glu Ile Val Tyr Gln Ser
50      55      60
Val Ser Glu His Ser Asp Leu Val Ile Ser Pro Val Asn Glu Ile Arg
25      65      70      75      80
Pro Ala Asn Arg Phe Pro Ser His Arg Lys Ser Phe Phe Ala Glu Asn
85      90      95
Leu Arg Ala Ser Pro Pro Val Val Pro Val Ala Val Asp Lys Tyr Ala
30      100      105      110
Val Pro Val Ala Asn Pro Met Asp Pro Glu Asn Pro Asn Ala Trp Asp
115      120      125
Val Thr Leu Lys Ile Thr Thr Lys Ala Val Thr Val Pro Val Asp Val
130      135      140
Val Met Val Ile Asp Gln Ser Ser Ser Met Gly Gly Gln Asn Ile Ala
35      145      150      155      160
Arg Leu Lys Ser Ala Ile Ala Ser Gly Gln Arg Phe Val Lys Lys Met
165      170      175
Leu Pro Lys Gly Thr Ala Thr Glu Gly Val Arg Ile Ala Leu Val Ser
40      180      185      190
Tyr Asp His Glu Pro His Arg Leu Ser Asp Phe Thr Lys Asp Thr Ala
195      200      205
Phe Leu Cys Gln Lys Ile Arg Ala Leu Thr Pro Ile Trp Gly Thr His
210      215      220
Thr Gln Gly Gly Leu Lys Met Ala Arg Asn Ile Met Ala Thr Ser Thr
45      225      230      235      240
Ala Val Asp Lys His Ile Leu Met Ser Asp Gly Leu Ala Thr Glu
245      250      255
Gln Tyr Pro Val Lys Asn Val Thr Thr Ala Asp Phe Ile Gly Lys Thr
50      260      265      270
Gly Asn Ala Asn Asp Pro Ile Asp Leu Val Ile Gln Gly Ala Ile Asn
275      280      285
Phe Pro Thr Asn Tyr Val Ser Asn Asn Pro Ser Thr Pro Leu Thr Pro
290      295      300
Asn Tyr Pro Thr His Ser Ser Lys Val Gly Arg Arg Asn Leu Pro Glu
55      305      310      315      320
Ser Lys Phe Asp Tyr Ser Asn Leu Ser Ala Arg Ile Thr Phe Asp Gly
325      330      335
Val Ala Gly Ala Leu Val Tyr Glu Pro Arg Phe Pro His Pro Tyr Tyr
60      340      345      350
Tyr Tyr Phe Pro Cys Asn Ala Ala Ile Asn Glu Ala Gln Phe Ala Lys
355      360      365
Asn Ser Gly Tyr Thr Ile His Thr Ile Gly Tyr Asp Leu Gly Asp Phe
370      375      380
Ala Leu Ala Asn Asn Ser Leu Lys Leu Thr Ala Thr Asp Glu Asn His
65      385      390      395      400
Phe Phe Thr Ala Thr Pro Ala Asn Leu Ala Ala Ala Phe Asp Asn Ile
405      410      415
Ala Gln Thr Ile Asn Ile Gly Ile Gln Arg Gly Glu Val Thr Asp Phe
70      420      425      430
Val Ala Pro Gly Phe Ile Val Lys Asn Leu Thr Gln Ser Gly Asp Val
435      440      445
Thr His Leu Leu Asn Val Ser Asn Gly Thr Val His Tyr Asp Val Ser
450      455      460
75 Thr Lys Lys Leu Thr Trp Thr Thr Gly Thr Ile Leu Ser Ser Ser Glu

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	465		470		475		480
	Ala Thr Ile Thr Tyr Arg Ile Tyr Ala Asp Leu Asp Tyr Ile Gln Asn						
		485			490		495
5	Asn Asp Ile Pro Val Asn Thr Thr Ser Ala Ile Gly Pro Asp Leu Gly						
		500			505		510
	Gly Phe Asp Thr Asn Thr Glu Ala Lys Leu Thr Tyr Thr Asn Ser Asn						
		515			520		525
	Gly Glu Pro Asn Gln Gln Leu Ile Phe Pro Arg Pro Thr Val Lys Leu						
		530			535		540
10	Gly Tyr Gly Val Ile Lys Arg His Tyr Val Leu Val Asn Lys Asp Gly						
		545			550		555
	Gln Pro Ile Gln Ala Asn Gly Thr Val Val Ser Ser Leu Ser Glu Ala						
		565			570		575
15	His Val Leu Gln Ser Gln Asp Phe Phe Leu Pro Ser Gly Gly Gly His						
		580			585		590
	Ile Val Pro Lys Trp Ile Lys Leu Asp Lys Thr Thr Glu Ala Leu Gln						
		595			600		605
	Tyr Tyr Ser Val Pro Pro Thr Asn Thr Val Ile Thr Thr Ala Asp Gly						
		610			615		620
20	Lys Arg Tyr Arg Phe Val Glu Val Pro Gly Ser Thr Pro Asn Pro Gly						
		625			630		635
	Gln Ile Gly Ile Ser Trp Lys Lys Pro Ala Gly Asn Ala Tyr Phe Ala						
		645			650		655
25	Tyr Lys Leu Leu Asn Tyr Trp Met Gly Gly Thr Thr Asp Gln Gln Ser						
		660			665		670
	Glu Trp Asp Val Thr Ser Asn Trp Thr Gly Ala Gln Val Pro Leu Thr						
		675			680		685
	Gly Glu Asp Val Glu Phe Ala Thr Thr Glu Asn Phe Gly Ser Pro Ala						
		690			695		700
30	Val Ala Asp Leu His Val Pro Thr Thr Asn Pro Lys Ile Ile Gly Asn						
		705			710		715
	Leu Ile Asn Asn Ser Asp Lys Asp Leu Val Val Thr Thr Ser Ser Gln						
		725			730		735
35	Leu Thr Ile Asn Gly Val Val Glu Asp Asn Asn Pro Asn Val Gly Thr						
		740			745		750
	Ile Val Val Lys Ser Ser Lys Asp Asn Pro Thr Gly Thr Leu Leu Phe						
		755			760		765
	Ala Asn Pro Gly Tyr Asn Gln Asn Val Gly Gly Thr Val Glu Phe Tyr						
		770			775		780
40	Asn Gln Gly Tyr Asp Cys Ala Asp Cys Gly Met Tyr Arg Arg Ser Trp						
		785			790		795
	Gln Tyr Phe Gly Ile Pro Val Asn Glu Ser Gly Phe Pro Ile Asn Asp						
		805			810		815
45	Val Gly Gly Asn Glu Thr Val Asn Gln Trp Val Glu Pro Phe Asn Gly						
		820			825		830
	Asp Lys Trp Arg Pro Ala Pro Tyr Ala Pro Asp Thr Glu Leu Gln Lys						
		835			840		845
	Phe Lys Gly Tyr Gln Ile Thr Asn Asp Val Gln Ala Gln Pro Thr Gly						
		850			855		860
50	Val Tyr Ser Phe Lys Gly Met Ile Cys Val Cys Asp Ala Phe Leu Asn						
		865			870		875
	Leu Thr Arg Thr Ser Gly Val Asn Tyr Ser Gly Ala Asn Leu Ile Gly						
		885			890		895
55	Asn Ser Tyr Thr Gly Ala Ile Asp Ile Lys Gln Gly Ile Val Phe Pro						
		900			905		910
	Pro Glu Val Glu Gln Thr Val Tyr Leu Phe Asn Thr Gly Thr Arg Asp						
		915			920		925
	Gln Trp Arg Lys Leu Asn Gly Ser Thr Val Ser Gly Tyr Arg Ala Gly						
		930			935		940
60	Gln Tyr Leu Ser Val Pro Lys Asn Thr Ala Gly Gln Asp Asn Leu Pro						
		945			950		955
	Asp Arg Ile Pro Ser Met His Ser Phe Leu Val Lys Met Gln Asn Gly						
		965			970		975
65	Ala Ser Cys Thr Leu Unk Ile Leu Tyr Asp Lys Leu Leu Lys Asn Thr						
		980			985		990
	Thr Val Asn Asn Gly Asn Gly Thr Gln Ile Thr Trp Arg Ser Gly Asn						
		995			1000		1005
	Ser Gly Ser Ala Asn Met Pro Ser Leu Val Met Asp Val Leu Gly Asn						
		1010			1015		1020
70	Glu Ser Ala Asp Arg Leu Trp Ile Phe Thr Asp Gly Gly Leu Ser Phe						
		1025			1030		1035
	Gly Phe Asp Asn Gly Trp Asp Gly Arg Lys Leu Thr Glu Lys Gly Leu						
		1045			1050		1055
75	Ser Gln Leu Tyr Ala Met Ser Asp Ile Gly Asn Asp Lys Phe Gln Val						
		1060			1065		1070

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Ala Gly Val Pro Glu Leu Asn Asn Leu Leu Ile Gly Phe Asp Ala Asp  
 1075 1080 1085  
 Lys Asp Gly Gln Tyr Thr Leu Glu Phe Ala Leu Ser Asp His Phe Ala  
 1090 1095 1100  
 5 Lys Gly Ala Val Tyr Leu His Asp Leu Gln Ser Gly Ala Lys His Arg  
 1105 1110 1115 1120  
 Ile Thr Asn Ser Thr Ser Tyr Ser Phe Asp Ala Lys Arg Gly Asp Ser  
 1125 1130 1135  
 10 Gly Ala Arg Phe Arg Leu Ser Tyr Gly Cys Asp Glu Asn Val Asp Asp  
 1140 1145 1150  
 Ser His Val Val Ser Thr Asn Gly Arg Glu Ile Ile Ile Leu Asn Gln  
 1155 1160 1165  
 Asp Ala Leu Asp Cys Thr Val Thr Leu Phe Thr Ile Glu Gly Lys Leu  
 1170 1175 1180  
 15 Leu Arg Arg Leu Lys Val Leu Ala Gly His Arg Glu Val Met Lys Val  
 1185 1190 1195 1200  
 Gln Thr Gly Gly Ala Tyr Ile Val His Leu Gln Asn Ala Phe Thr Asn  
 1205 1210 1215  
 20 Asp Val His Lys Val Leu Val Glu Tyr  
 1220 1225

(2) INFORMATION FOR SEQ ID NO:486

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 425 amino acids  
 (E) TYPE: amino acid  
 (D) TOPOLOGY: linear  
 (ii) MOLECULE TYPE: protein  
 (iii) HYPOTHETICAL: YES  
 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Porphyromonas gingivalis  
 (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...425  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:486

Met Glu Val Lys Lys Asn Thr Val Val Leu Arg Leu Leu Ile Trp Phe  
 1 5 10 15  
 45 Val Ala Ile Leu Leu Phe His Ser Ser Arg Leu Trp Gly Gln Glu Gly  
 20 25 30  
 Glu Gly Ser Ala Arg Tyr Arg Phe Lys Gly Phe Val Asp Thr Tyr His  
 35 40 45  
 Ala Val Arg Ser Ser Ser Pro Phe Asp Phe Met Ser Ser Arg Thr Arg  
 50 55 60  
 50 Val Arg Gly Glu Leu Glu Arg Ser Phe Gly Asn Ser Lys Val Ala Val  
 65 70 75 80  
 Ser Val Asn Ala Thr Tyr Asn Ala Leu Leu Lys Asp Glu Thr Gly Leu  
 85 90 95  
 55 Arg Leu Arg Glu Ala Phe Phe Glu His Gln Glu Glu His Trp Gly Leu  
 100 105 110  
 Arg Leu Gly Arg Gln Ile Val Ile Trp Gly Ala Ala Asp Gly Val Arg  
 115 120 125  
 Ile Thr Asp Leu Ile Ser Pro Met Asp Met Thr Glu Phe Leu Ala Gln  
 130 135 140  
 60 Asp Tyr Asp Asp Ile Arg Met Pro Val Asn Ala Leu Arg Phe Ser Val  
 145 150 155 160  
 Phe Asn Glu Ser Met Lys Val Glu Val Val Leu Pro Val Phe Glu  
 165 170 175  
 65 Gly Tyr Arg Leu Pro Val Asp Pro Arg Asn Pro Trp Asn Ile Phe Ser  
 180 185 190  
 Leu Ser Pro Ile Ala Gln Gly Met Asn Ile Val Trp Lys Glu Glu Ala  
 195 200 205  
 Gly Lys Pro Ala Phe Lys Val Ala Asn Ile Glu Tyr Gly Ala Arg Trp  
 210 215 220  
 70 Ser Thr Thr Leu Ser Gly Ile Asp Phe Ala Leu Ala Ala Leu His Thr  
 225 230 235 240  
 Trp Asn Lys Met Pro Val Ile Glu Val Gln Gly Ile Val Pro Thr Glu  
 245 250 255  
 75 Ile Ile Val Ser Pro Arg Tyr Tyr Arg Met Gly Phe Val Gly Gly Asp  
 260 265 270

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5 Leu Ser Val Pro Val Gly Gln Phe Val Phe Arg Gly Glu Ala Ala Phe  
 275 280 285  
 Asn Ile Asp Lys His Phe Thr Tyr Lys Ser His Ala Glu Gln Glu Gly  
 290 295 300  
 Phe Gln Thr Ile Asn Trp Leu Ala Gly Ala Asp Trp Tyr Ala Pro Gly  
 305 310 315 320  
 Glu Trp Met Ile Ser Gly Gln Phe Ser Met Glu Ser Ile Phe Arg Tyr  
 325 330 335  
 10 Arg Asp Phe Ile Ser Gln Arg Gln His Ser Thr Leu Ile Thr Leu Asn  
 340 345 350  
 Val Ser Lys Lys Phe Phe Gly Ser Thr Leu Gln Leu Ser Asp Phe Thr  
 355 360 365  
 Tyr Tyr Asp Leu Thr Gly Lys Gly Trp Phe Ser Arg Phe Ala Ala Asp  
 370 375 380  
 15 Tyr Ala Leu Asn Asp Gln Ile His Leu Met Ala Gly Tyr Asp Trp Phe  
 385 390 395 400  
 Ser Ser Lys Gly Ser Gly Ile Phe Asp Arg Tyr Lys Asp Asn Ser Glu  
 405 410 415  
 20 Leu Trp Phe Lys Ala Arg Tyr Ser Phe  
 420 425

(2) INFORMATION FOR SEQ ID NO:487

- 25 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 404 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
 30 (ii) MOLECULE TYPE: protein  
 (iii) HYPOTHETICAL: YES  
 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Porphyromonas gingivalis  
 35 (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...404  
 40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:487

Met Ser Ser Cys Glu Val Ala Tyr Phe Ser Leu Lys Pro Ile Asp Leu  
 1 5 10 15  
 45 Gln Asn Ile Arg Glu Arg Asn His Ser Ser Asp Ile Ala Leu Ser Asn  
 20 25 30  
 Leu Leu Asp Asn Ser Asn Gln Leu Ala Thr Ile Leu Ile Gly Asn  
 35 40 45  
 Asn Val Ile Asn Val Ala Ile Val Ile Leu Ser Asn Tyr Ala Ile Glu  
 50 55 60  
 Gln Thr Phe Val Phe Ser Ser Pro Ile Ile Gly Phe Leu Ile Gln Thr  
 65 70 75 80  
 Ile Leu Leu Thr Thr Val Leu Leu Leu Phe Gly Glu Ile Leu Pro Lys  
 85 90 95  
 55 Val Tyr Ala Arg Lys Asn Pro Leu Gln Tyr Ser Arg Phe Ser Ala Ala  
 100 105 110  
 Ala Met Ser Val Ile Tyr Lys Ile Leu Ser Pro Phe Ser Lys Leu Leu  
 115 120 125  
 Val Lys Ser Thr Gly Ile Val Thr Arg Gly Ile Ser Lys Lys Lys Tyr  
 130 135 140  
 60 Asp Met Ser Val Asp Glu Leu Ser Lys Ala Val Ala Leu Thr Thr Thr  
 145 150 155 160  
 Glu Gly Glu Pro Glu Lys Glu Met Ile Asn Glu Ile Ile Lys Phe  
 165 170 175  
 65 Tyr Asn Lys Thr Ala Cys Glu Ile Met Val Pro Arg Ile Asp Ile Val  
 180 185 190  
 Asp Val Asp Leu Ser Trp Pro Phe Arg Lys Met Leu Asp Phe Val Val  
 195 200 205  
 Ser Ser Gly Tyr Ser Arg Leu Pro Val Ser Glu Gly Ser Glu Asp Asn  
 210 215 220  
 70 Ile Lys Gly Val Ile Tyr Ile Lys Asp Leu Ile Pro His Met Asp Lys  
 225 230 235 240  
 Gly Asp Glu Phe Asp Trp His Pro Leu Ile Arg Lys Ala Tyr Phe Val  
 245 250 255  
 75 Pro Glu Asn Lys Arg Ile Asp Asp Leu Leu Glu Glu Phe Arg Ala Asn  
 260 265 270

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Lys Val His Val Ser Ile Val Val Asp Glu Phe Gly Gly Thr Cys Gly  
 275 280 285  
 Leu Ile Thr Met Glu Asp Ile Leu Glu Glu Ile Val Gly Glu Ile Thr  
 290 295 300  
 5 Asp Glu Tyr Asp Glu Glu Glu Leu Pro Phe Lys Val Leu Gly Asp Gly  
 305 310 315 320  
 Ser Tyr Leu Phe Glu Gly Lys Thr Ser Leu Ser Asp Val Arg His Tyr  
 325 330 335  
 10 Leu Asp Leu Pro Glu Asn Ala Phe Gly Glu Leu Gly Asp Glu Val Asp  
 340 345 350  
 Thr Leu Ser Gly Leu Phe Leu Glu Ile Lys Gln Glu Leu Pro His Val  
 355 360 365  
 Gly Asp Thr Ala Val Tyr Glu Pro Phe Arg Phe Gln Val Thr Gln Met  
 370 375 380  
 15 Asp Lys Arg Arg Ile Ile Glu Ile Lys Ile Phe Pro Phe Glu Arg Thr  
 385 390 395 400  
 Trp Glu Val Glu

20 (2) INFORMATION FOR SEQ ID NO:488

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 260 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

25 (ii) MOLECULE TYPE: protein  
 (iii) HYPOTHETICAL: YES

30 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Porphyromonas gingivalis

35 (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION: 1...260

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:488

40 Met Lys Leu Leu Leu Tyr Leu Leu Leu Val Leu Ser Thr Leu Ser Pro  
 1 5 10 15  
 Met Tyr Ser Gln Met Leu Phe Ser Glu Asn Leu Thr Met Asn Ile Asp  
 20 25 30  
 45 Ser Thr Lys Thr Ile Gln Gly Thr Ile Leu Pro Val Leu Asp Phe Lys  
 35 40 45  
 Thr Glu Lys Glu Asn Val Phe Thr Phe Lys Asn Thr Ala Asn Leu Asn  
 50 55 60  
 Leu Leu Ile Lys His Gly Gln Val Ile Asn Leu Ile Asn Lys Leu Glu  
 65 70 75 80  
 50 Phe Ser Thr Tyr Gly Asn Lys Val Thr Val Ser Gly Gly Tyr Val His  
 85 90 95  
 Thr Glu Tyr Arg Tyr Leu Leu His His Val Phe Glu Val Tyr Pro Tyr  
 100 105 110  
 55 Val Glu Ser Gln Trp Ala Glu Ser Arg Gly Met Lys Tyr Lys Val Ser  
 115 120 125  
 Thr Gly Leu Gln Ser Arg Tyr Arg Leu Val Asn Ser Asp Asn Cys Leu  
 130 135 140  
 Met Phe Ala Thr Leu Gly Val Phe Phe Glu Phe Glu Lys Trp Glu Gln  
 145 150 155 160  
 60 Pro Ala Thr Ser Leu Phe Ala Gly Thr Tyr Ala Tyr Ser Arg Ser Ile  
 165 170 175  
 Lys Ser His Leu Ser Ile Ser Phe Arg His Arg Leu Gly Glu His Trp  
 180 185 190  
 65 Glu Phe Thr Thr Thr Ala Ile His Gln Gly Lys Pro Asp Ser Tyr Phe  
 195 200 205  
 Lys Lys Ala Arg Phe Gly Gly Ala Ile Asp Leu Lys Tyr His Ile Thr  
 210 215 220  
 Pro Thr Ile Gly Ile Arg Gly Ala Tyr Arg Ile Ile Tyr Asp Thr Ala  
 225 230 235 240  
 70 Pro Ile Val Pro Val Arg Lys Asp Tyr Asn Thr Val Asp Val Gly Ile  
 245 250 255  
 Asp Ile Ser Phe  
 260

75 (2) INFORMATION FOR SEQ ID NO:489

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(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 834 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...834

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:489

1	Met	Lys	Arg	Ile	Val	Leu	Ser	Ser	Phe	Leu	Phe	Val	Leu	Ser	Ile	Leu
					5					10					15	
	Ser	Leu	Met	Ala	Gln	Asn	Asn	Thr	Leu	Asp	Val	His	Ile	Ser	Gly	Thr
			20						25					30		
25	Ile	Lys	Asp	Ala	Ser	Ser	Gly	Glu	Pro	Val	Pro	Tyr	Ala	Thr	Val	Ser
		35						40					45			
	Ile	Arg	Leu	Thr	Gly	Ala	Asp	Thr	Thr	Gln	Val	Phe	Arg	Gln	Val	Thr
		50				55						60				
	Asp	Gly	Asn	Gly	Tyr	Phe	Val	Ile	Gly	Leu	Pro	Ala	Ala	Pro	Ser	Tyr
	65					70					75				80	
30	His	Leu	Thr	Ala	Ser	Phe	Val	Gly	Met	Lys	Thr	His	Thr	Met	Gln	Ile
					85					90					95	
	Ser	Arg	Gly	Asn	Gly	Gln	His	Asp	Ile	Lys	Ser	Ile	Asp	Ile	Ser	Leu
			100						105					110		
35	Glu	Ser	Glu	Asp	Lys	Gln	Leu	Ser	Thr	Val	Thr	Val	Ser	Ala	Ala	Arg
		115						120					125			
	Pro	Leu	Val	Lys	Met	Glu	Ile	Asp	Arg	Leu	Ser	Tyr	Asn	Met	Lys	Asp
		130					135					140				
	Asp	Pro	Ala	Ala	Lys	Thr	Asn	Asn	Leu	Leu	Glu	Met	Leu	Arg	Asn	Val
	145					150					155				160	
40	Pro	Leu	Val	Thr	Val	Asp	Gly	Gln	Gly	Asn	Ile	Gln	Val	Lys	Gly	Ser
				165					170					175		
	Ser	Asn	Phe	Lys	Ile	His	Leu	Asn	Gly	Arg	Pro	Ser	Thr	Met	Val	Ser
			180						185					190		
45	Ser	Asn	Pro	Lys	Glu	Val	Phe	Arg	Ser	Ile	Pro	Ala	His	Thr	Ile	Lys
		195						200				205				
	Arg	Val	Glu	Val	Ile	Thr	Asp	Pro	Gly	Val	Lys	Tyr	Asp	Ala	Glu	Gly
		210				215						220				
	Thr	Ser	Ala	Ile	Leu	Asp	Ile	Val	Thr	Glu	Glu	Gly	Lys	Lys	Leu	Glu
	225					230					235				240	
50	Gly	Tyr	Ser	Gly	Ser	Ile	Thr	Ala	Ser	Val	Ser	Asn	Asn	Pro	Thr	Ala
				245					250					255		
	Asn	Gly	Ser	Ile	Phe	Leu	Thr	Ala	Lys	Ser	Gly	Lys	Val	Gly	Leu	Thr
			260						265					270		
55	Thr	Asn	Tyr	Asn	Tyr	Tyr	Gly	Gly	Lys	Asn	Lys	Gly	Ser	Arg	Tyr	Phe
		275						280					285			
	Thr	Glu	Arg	Thr	Thr	Ser	Met	Leu	Gln	Thr	Ile	Glu	Glu	Gly	Lys	Gly
		290				295						300				
	Gln	Glu	Thr	Phe	Gly	Gly	His	Phe	Gly	Asn	Ala	Leu	Leu	Ser	Phe	Glu
	305				310					315					320	
60	Ile	Asp	Ser	Leu	Asn	Leu	Phe	Thr	Val	Gly	Gly	Asn	Val	Arg	Leu	Trp
				325						330				335		
	Glu	Met	Thr	Thr	Asp	Arg	Asn	Ser	Val	Glu	Lys	Ser	Phe	Ala	Gly	Ser
			340					345					350			
65	Asn	Leu	Met	Ser	Tyr	Ile	Asp	Arg	Lys	Leu	Lys	Thr	Gln	Met	Asp	Ala
		355					360						365			
	Gly	Ser	Tyr	Glu	Leu	Asn	Ala	Asp	Tyr	Gln	His	Ser	Thr	Arg	Leu	Pro
		370				375					380					
	Gly	Glu	Leu	Leu	Thr	Val	Ser	Tyr	Arg	Phe	Thr	His	Asn	Pro	Asn	Asn
	385				390					395					400	
70	Ser	Glu	Thr	Phe	Ile	Asp	Gln	Trp	Lys	Arg	Asp	Pro	Leu	Asn	Thr	Ala
				405						410				415		
	Asn	Thr	Ile	Gln	Tyr	Ala	Gly	Gln	His	Ser	Lys	Ser	Asp	Ala	Gly	Met
			420					425					430			
75	Asp	Glu	His	Thr	Ala	Gln	Val	Asp	Tyr	Thr	Arg	Pro	Leu	Gly	Gln	Ala
		435					440						445			

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5 His Ser Leu Glu Ala Gly Leu Lys Tyr Ile Tyr Arg His Ala Thr Ser  
 450 455 460  
 Asp Pro Leu Tyr Glu Ile Arg Pro Ser Glu Asp Ala Pro Trp Gln Pro  
 465 470 475 480  
 Gly Ser Leu Tyr Ala Gln Asn Pro Ser Asn Gly Lys Phe Arg His Asp  
 485 490 495  
 10 Gln Tyr Ile Gly Ala Ala Tyr Ala Gly Tyr Asn Tyr Arg Lys Asp Gln  
 500 505 510  
 Tyr Ser Leu Gln Thr Gly Leu Arg Val Glu Ser Ser Arg Leu Lys Ala  
 515 520 525  
 Leu Phe Pro Glu Asn Ala Ala Ala Asp Phe Ser His Asn Ser Phe Asp  
 530 535 540  
 15 Trp Val Pro Gln Leu Thr Leu Gly Tyr Thr Pro Ser Pro Met Lys Gln  
 545 550 555 560  
 Leu Lys Leu Ala Tyr Asn Phe Arg Ile Gln Arg Pro Ala Ile Gly Gln  
 565 570 575  
 Leu Asn Pro Tyr Arg Leu Gln Thr Asn Asp Tyr Gln Val Gln Tyr Gly  
 580 585 590  
 20 Asn Pro Asp Leu Lys Ser Glu Lys Arg His His Val Gly Leu Ser Tyr  
 595 600 605  
 Asn Gln Tyr Gly Ala Lys Val Met Leu Thr Ala Ser Leu Asp Tyr Asp  
 610 615 620  
 Phe Cys Asn Asn Ala Ile Gln Asn Tyr Thr Phe Ser Asp Pro Ala Asn  
 625 630 635 640  
 25 Pro Asn Leu Phe His Gln Thr Tyr Gly Asn Ile Gly Arg Glu His Ser  
 645 650 655  
 Phe Ser Leu Asn Thr Tyr Ala Met Tyr Thr Pro Ala Val Trp Val Arg  
 660 665 670  
 30 Ile Met Leu Asn Gly Asn Ile Asp Arg Thr Phe Gln Lys Ser Glu Ala  
 675 680 685  
 Leu Gly Ile Asp Val Asn Ser Trp Ser Gly Met Val Tyr Ser Gly Leu  
 690 695 700  
 Met Phe Thr Leu Pro Lys Asp Trp Thr Val Asn Leu Phe Gly Gly Tyr  
 705 710 715 720  
 35 Tyr His Gly Gly Arg Ser Tyr Gln Thr Lys Tyr Asp Gly Asn Val Phe  
 725 730 735  
 Asn Asn Ile Gly Ile Ala Lys Gln Leu Phe Asp Lys Lys Leu Arg Val  
 740 745 750  
 40 Ser Leu Ser Ala Asn Asn Ile His Ala Lys Tyr Ser Thr Trp Lys Ser  
 755 760 765  
 Arg Thr Ile Gly Asn Gly Phe Thr Ile Tyr Ser Glu Asn Ala Gly Ile  
 770 775 780  
 Gln Arg Ser Val Ser Leu Ser Leu Thr Tyr Ser Phe Gly Lys Met Asn  
 785 790 795 800  
 45 Thr Gln Val Arg Lys Val Glu Arg Thr Ile Val Asn Asp Asp Leu Lys  
 805 810 815  
 Gln Thr Ser Ser Gln Gly Gln Gln Gly Gly Gln Gly Asn Pro Thr  
 820 825 830  
 50 Gly Asn

## (2) INFORMATION FOR SEQ ID NO:490

## 55 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 399 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

## 60 (ii) MOLECULE TYPE: protein

## (iii) HYPOTHETICAL: YES

## (vi) ORIGINAL SOURCE:

## 65 (A) ORGANISM: Porphyromonas gingivalis

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...399

## 70 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:490

Met Arg Leu Ser Ala Ile Leu Ile Ala Leu Ile Val Met Leu Pro Ala  
 1 5 10 15  
 75 Val Leu Ser Gly Gln His Tyr Tyr Ser Met Ala Gly Glu Arg Leu Glu  
 20 25 30

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Thr Asp Ser Ile Arg Pro Asn Glu Leu Ser Ala Ser Ile Arg Ser Ala  
 35 40 45  
 Leu Phe Phe Arg Asn Asn Glu Tyr Asn Ala Arg Ser Val Lys Gly Tyr  
 50 55 60  
 5 Thr Leu Pro Gly Ala Arg Val Ser Ala Phe Ala Ser Tyr Ser Leu Pro  
 65 70 75 80  
 Ala Ala His Gly Val Lys Leu Ser Leu Gly Val Ser Thr Leu Asn Tyr  
 85 90 95  
 10 Trp Gly Ala Ser Arg Tyr Pro Ala Gly Ile Ala Tyr Ser Asp Leu Pro  
 100 105 110  
 Tyr Trp Thr Asp Tyr Asn Asp Tyr Val Arg Leu Arg Ile Leu Pro Tyr  
 115 120 125  
 Val Gln Ala Met Leu Lys Pro Thr Ala Thr Thr Ala Leu Met Leu Gly  
 130 135 140  
 15 Asn Ile Ala Gly Gly Thr Ala His Gly Leu Ile Glu Pro Ile Tyr Asn  
 145 150 155 160  
 Pro Glu Leu Asp Leu Thr Ala Asp Pro Glu Ala Gly Val Gln Phe Arg  
 165 170 175  
 20 Gly Asp Trp Thr Arg Phe Arg Met Asp Val Trp Val Asn Trp Met Ser  
 180 185 190  
 Met Ile Phe Lys Asn Asp Asn His Gln Glu Ser Phe Val Phe Gly Leu  
 195 200 205  
 Ser Thr Thr Ser Lys Leu Leu Ser Gly Glu Gly Lys Trp Arg Leu Glu  
 210 215 220  
 25 Leu Pro Leu Gln Ala Ile Ala Thr His Arg Gly Gly Glu Tyr Asn Trp  
 225 230 235 240  
 Ala Gln Gln Asp Thr Val His Thr Trp Val Asn Gly Ala Val Gly Leu  
 245 250 255  
 30 Lys Leu Ser Tyr Arg Pro Arg Thr Asp Lys Pro Met Gln Ile Trp Gly  
 260 265 270  
 Ser Ala Tyr Gly Val Ala Ala Leu Ser Ser Gly Gly Tyr Phe Pro Tyr  
 275 280 285  
 Glu Arg Gly Trp Gly Gly Tyr Leu Ser Leu Gly Met Asp Leu Glu His  
 290 295 300  
 35 Phe Ala Phe Arg Thr Asp Tyr Trp Tyr Gly Arg His Tyr Val Ser Pro  
 305 310 315 320  
 Phe Ala Ala Pro Phe Ala Asn Ser Leu Thr Tyr Asp Lys Gln Pro Leu  
 325 330 335  
 40 Thr Asn Gly Trp Gly Asp Tyr Ile Arg Leu Tyr Ala Asp Tyr Ser Trp  
 340 345 350  
 Arg Met Ala Arg Ser Val Ser Leu Ala Ala Val Ala Arg Val Trp Phe  
 355 360 365  
 Gln Pro Ser Asp Arg Phe Ala Met Ser His Ala Leu Glu Leu Thr Met  
 370 375 380  
 45 Arg Ile Asp Pro Lys Phe Pro Ile Ala Phe Leu Lys Gly Asn His  
 385 390 395

## (C) INFORMATION FOR SEQ ID NO:491

- 50 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 382 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
 55 (ii) MOLECULE TYPE: protein  
 (iii) HYPOTHETICAL: YES  
 (vi) ORIGINAL SOURCE:  
 60 (A) ORGANISM: Porphyromonas gingivalis  
 (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (E) LOCATION 1...382  
 65 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:491

Met Asn Lys Ser Leu Leu Ser Leu Ala Cys Leu Ile Leu Cys Gly Met  
 1 5 10 15  
 70 Pro Ala Ile Ala Gln Gln Thr Gly Pro Ala Glu Arg Ser Gly Glu Pro  
 20 25 30  
 Ser Leu Ala Glu Arg Val Phe Gly Leu Glu Gln Lys Gln Lys Lys Leu  
 35 40 45  
 75 Lys Val Tyr Leu Gly Ile Gln Ser Phe Tyr Asp Gln Pro Leu Val Asp  
 50 55 60

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Asp Glu Ser His Ile Gly His Phe Lys Val Gln Glu Leu Arg Met Ser  
 65 70 75 80  
 Ala His Gly Glu Leu Asn Arg His Leu Ser Phe Asp Trp Arg Gln Arg  
 85 90 95  
 5 Leu Asn Arg Ala Ala Asp Gly Thr Ser Phe Ala Asp Asn Leu Ser Asn  
 100 105 110  
 Ala Ile Asp Ile Ala Gly Val Asp Trp His Pro Asn Asp Lys Val Ser  
 115 120 125  
 10 Phe Phe Phe Gly Arg Gln Tyr Ala Arg Phe Gly Gly Ile Glu Tyr Asp  
 130 135 140  
 Met Asn Pro Val Glu Ile Tyr Gln Tyr Ser Asp Leu Val Asp Tyr Met  
 145 150 155 160  
 Thr Cys Tyr Thr Ser Gly Val Asn Phe Ala Trp Asn Phe His Pro Glu  
 165 170 175  
 15 Gln Gln Leu Gln Leu Gln Val Leu Asn Ala Tyr Asn Asn Arg Phe Ala  
 180 185 190  
 Asp Arg Tyr His Val Thr Pro Asp Val Ala Thr Ala Thr Ser Tyr Pro  
 195 200 205  
 20 Leu Leu Tyr Ser Ala Gln Trp Asn Gly Thr Leu Leu Gly Gly Ala Leu  
 210 215 220  
 His Met Arg Tyr Ala Val Ser Met Ala His Gln Ala Gln Glu Arg Asn  
 225 230 235 240  
 Met Trp Tyr Phe Thr Ala Gly Asn Leu Phe Asn Pro Gly Lys Arg Ile  
 245 250 255  
 25 Asn Gly Tyr Leu Asp Leu Thr Tyr Ser Ile Glu Gly Leu Asp Asp Lys  
 260 265 270  
 Gly Ile Met Thr Ala Arg Tyr Gly Lys Gly Lys Thr Leu Thr Asp Val  
 275 280 285  
 30 Lys Tyr Tyr Ala Leu Val Ser Lys Trp Asn Phe Arg Ile Phe Asp Gln  
 290 295 300  
 Val Asn Leu Phe Leu Lys Gly Met Tyr Glu Asn Gly Tyr Ala Pro Ala  
 305 310 315 320  
 Gln Tyr Gly Glu Ser Ser His Thr Arg His Ser Tyr Gly Tyr Met Gly  
 325 330 335  
 35 Gly Val Glu Tyr Tyr Pro Thr Glu Thr Asn Phe Arg Leu Phe Val Thr  
 340 345 350  
 Tyr Ile Gly Arg His Tyr Arg Tyr Ser Ala Thr Glu Thr Glu Ser Thr  
 355 360 365  
 40 Asn Ala Leu Arg Ala Gly Leu Ile Tyr Gln Ile Pro Phe Leu  
 370 375 380

## (2) INFORMATION FOR SEQ ID NO:492

- 45 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 222 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
 50 (ii) MOLECULE TYPE: protein  
 (iii) HYPOTHETICAL: YES  
 (vi) ORIGINAL SOURCE:  
 55 (A) ORGANISM: Porphyromonas gingivalis  
 (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...222  
 60 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:492

Met Lys His Leu Phe Lys Ser Thr Leu Val Leu Leu Cys Ala Leu Ser  
 1 5 10 15  
 65 Phe Ser Gly Thr Tyr Thr Phe Ala Gln Asn Asn Thr Glu Lys Ser  
 20 25 30  
 Arg Phe Asp Phe Ser Val Arg Leu Gly Gln Gly Tyr Ile Ala Gly Ser  
 35 40 45  
 Thr Thr Asn Leu Met Tyr Gly Tyr Thr Ser Ala Asn Asp Arg Leu Leu  
 50 55 60  
 70 Ser Gly Ala Ile Tyr Leu Gly Leu Thr Pro Ser Lys Lys Glu Asn Ala  
 65 70 75 80  
 Thr Gly Val Ala Phe Arg Phe Leu Ser Pro Ser Pro Gly Tyr Tyr Val  
 85 90 95  
 75 Asp Ile Ser Gly Lys Glu Asn Thr Leu Asn Tyr Ala Phe Tyr Val Val  
 100 105 110

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Gly Ala Tyr Asn Arg Ile Ala Ile Pro Ile Arg Pro Ile Lys Asn Phe  
 115 120 125  
 Asn Phe Ile Phe Ser Thr Glu Val Gly Met Ala Trp Met Ser Arg His  
 130 135 140  
 5 Glu Gln Ile Tyr Asn Ser Thr Ser Gln Thr Trp Asp Lys Gln Arg Lys  
 145 150 155 160  
 Ser Arg Ser Gly Leu Asp Phe Gly Leu Gly Met His Leu Gln Unk His  
 165 170 175  
 10 Ile Asn Lys Thr Val Tyr Phe Met Ala Gly Thr Asp Leu Thr Ser Cys  
 180 185 190  
 Met Phe Gly Lys Arg Ile Asn Asp Tyr Gln Gln Lys Asp Arg Thr Phe  
 195 200 205  
 Ile Ala Leu Ile Asp Asn Ser Ile Gly Ile Gly Leu Asn Leu  
 210 215 220

(2) INFORMATION FOR SEQ ID NO:493

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 391 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

(A) NAME/KEY: misc\_feature

(B) LOCATION 1...391

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:493

35 Met Ile Ile Lys Lys Met Leu Lys Asn Lys Leu Ala Pro Leu Ala Ile  
 1 5 10 15  
 Leu Phe Leu Phe Ala Pro Lys Ala Met Lys Ala Gln Glu Gln Leu Asn  
 20 25 30  
 40 Val Val His Thr Ser Val Pro Ser Leu Asn Ile Ser Pro Asp Ala Arg  
 35 40 45  
 Ala Ala Gly Met Gly Asp Ile Gly Val Ala Thr Thr Pro Asp Ala Tyr  
 50 55 60  
 45 Ser Gln Tyr Trp Asn Pro Ser Lys Tyr Ala Phe Met Asp Thr Lys Ala  
 65 70 75 80  
 Gly Ile Ser Phe Ser Tyr Thr Pro Trp Leu Ser Lys Leu Val Asn Asp  
 85 90 95  
 Ile Ala Leu Met Gln Met Thr Gly Phe Tyr Lys Leu Gly Thr Asp Glu  
 100 105 110  
 50 Asn Gln Ala Ile Ser Ala Ser Leu Arg Tyr Phe Thr Leu Gly Lys Leu  
 115 120 125  
 Glu Thr Phe Asp Glu Leu Gly Glu Ser Met Gly Glu Ala His Pro Asn  
 130 135 140  
 55 Glu Phe Ala Val Asp Leu Gly Tyr Ser Arg Gln Leu Ser Glu Asn Phe  
 145 150 155 160  
 Ser Met Ala Val Ala Leu Arg Tyr Ile Arg Ser Asp Gln Ser Thr His  
 165 170 175  
 Asn Thr Gly Glu Asn Gln Ala Gly Asn Ala Phe Ala Ala Asp Ile Ala  
 180 185 190  
 60 Gly Tyr Leu Gln Lys Tyr Val Leu Leu Gly Asn Ala Glu Ser Leu Trp  
 195 200 205  
 Ser Leu Gly Phe Asn Val Lys Asn Ile Gly Thr Lys Ile Ser Tyr Asp  
 210 215 220  
 65 Gly Gly Val Thr Ser Phe Phe Ile Pro Thr Ser Leu Asn Leu Gly Thr  
 225 230 235 240  
 Gly Leu Leu Tyr Pro Ile Asp Asp Tyr Asn Ser Ile Asn Phe Asn Leu  
 245 250 255  
 Glu Leu Ser Lys Leu Leu Val Pro Thr Pro Pro Ile Met Asp Gln Asn  
 260 265 270  
 70 Asp Gln Ala Gly Tyr Glu Ala Ala Leu Lys Lys Tyr Gln Glu Thr Ser  
 275 280 285  
 Ser Ile Ser Gly Ile Phe Ser Ser Phe Gly Asp Ala Pro Gly Gly Leu  
 290 295 300  
 75 Lys Glu Glu Phe Arg Glu Ile Thr Trp Gly Leu Gly Ala Glu Tyr Ser  
 305 310 315 320



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Tyr Asp Asp Lys Phe Phe Val Arg Ala Gly Tyr Ser Tyr Leu His Pro  
 325 330 335  
 Thr Lys Gly Asn Leu Gln Tyr Phe Thr Ala Gly Ala Gly Phe Lys Met  
 340 345 350  
 5 Asn Ile Phe Arg Ile Asp Ala Ser Tyr Leu Leu Ser Thr Ile Gln Ser  
 355 360 365  
 Asn Pro Leu Asp Gln Thr Leu Arg Phe Thr Leu Ala Phe Asp Met Asp  
 370 375 380  
 10 Gly Leu Arg Asn Leu Phe His  
 385 390

(2) INFORMATION FOR SEQ ID NO:494

- 15 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 446 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
 (ii) MOLECULE TYPE: protein  
 20 (iii) HYPOTHETICAL: YES  
 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Porphyromonas gingivalis  
 25 (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...446  
 30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:494

Met Lys Thr Thr Val Gln Gln Ile Ile Leu Cys Leu Ala Leu Met Met  
 1 5 10 15  
 35 Ser Gly Val Leu Gly Gly Asn Ala Gln Ser Phe Trp Glu Glu Ile Ala  
 20 25 30  
 Pro Pro Phe Ile Ser Asn Glu Pro Asn Val Lys Tyr Ile Ile Pro Asn  
 35 40 45  
 Met Gly Ile Asp Ser Lys Gly Thr Ile Tyr Val Thr Val Thr Lys Arg  
 50 55 60  
 40 Ile Gln Gln Gly Ala Asn Tyr Thr Ser Glu Gln Leu Gly Met Tyr Tyr  
 65 70 75 80  
 Arg Pro Leu Gly Asp Asn Glu Gln Trp Trp Lys His Asp Pro Tyr Phe  
 85 90 95  
 45 Asp Asp Lys Ile Val Ala Asp Ile Gln Thr Asp Ala Tyr Gly Arg Val  
 100 105 110  
 Tyr Val Cys Thr Thr Ser Ser Arg Asp Gln Glu Tyr Gln Leu Tyr Ile  
 115 120 125  
 Asn Glu Gln Asn Glu Trp Arg Cys Ile Phe Lys Thr Ser Val Ser Thr  
 130 135 140  
 50 Tyr Glu His Gly Met Ala Val Phe Arg Ser Ser Thr Gly Val Thr Tyr  
 145 150 155 160  
 Ile Gly Thr Arg His His Ile Phe Ala Ser Gly Val Asn Asp Phe Glu  
 165 170 175  
 55 Phe Asn Thr Ile Tyr Glu Asp Ser Thr Pro Met Ser Cys Arg Phe Ala  
 180 185 190  
 Glu Ala Thr Asn Ser Gly Thr Ile Tyr Leu Ala Leu Met His Glu Thr  
 195 200 205  
 Thr Met Ser Thr Thr Ile Leu Thr Tyr Gln Asn Gly Glu Phe Val Asp  
 210 215 220  
 60 Ile Ser Glu Ser Glu Leu Ser Asn Ser Ile Ile Ala Ser Met Cys Ser  
 225 230 235 240  
 Asn Lys Glu Gly Asp Ile Ile Ala Leu Val Thr Ser Tyr Thr Gly Phe  
 245 250 255  
 65 Met Ser Gly Thr Leu Ala Ile Arg Lys Ala Asp Glu Gly Lys Trp Gln  
 260 265 270  
 Leu Val Gly Gly Asp Ile Gln Asn Ala Ile Val Gln Asn Ile Cys Met  
 275 280 285  
 Met Asp Asp Asn Lys Ile Ala Cys Glu Val Phe Gly Thr Pro Asn Gly  
 290 295 300  
 70 Val Asp Gly Arg Thr Arg Val Cys Val Ser Asp Ala Ser Val Phe Asp  
 305 310 315 320  
 Phe Glu Trp Tyr Glu Asp Glu Ile Tyr Gly Gly Leu Ile Phe Asp Thr  
 325 330 335  
 75 Phe Phe Tyr Ser Pro Trp Asp Lys Leu Leu Tyr Ala Lys Phe Gly Gly  
 340 345 350

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Ile Met Leu Arg Ser Lys Glu Ser Phe Ile Thr Ser Phe Ile Ser Pro  
 355 360 365  
 Thr Val Val Gln Gly Val Asp Val Tyr Thr Leu Ala Gly Lys Ile Arg  
 370 375 380  
 5 Ile Glu Ser Glu Thr Pro Val Ser Glu Val Leu Leu Phe Asp Leu Ala  
 385 390 395 400  
 Gly Arg Met Val Leu Arg Gln Thr Ile Asp Asn Lys Ile Tyr Ser Asp  
 405 410 415  
 10 Ile Asp Thr Asn Gly Leu Lys Arg Ser Gly Ile Tyr Val Val Ser Val  
 420 425 430  
 Arg Leu Ser Ser Gly Gln Val Phe Ser His Lys Val Gln Val  
 435 440 445

15 (2) INFORMATION FOR SEQ ID NO:495

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 308 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

20

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

25

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Porphyromonas gingivalis

30

(ix) FEATURE:

(A) NAME/KEY: misc\_feature

(B) LOCATION 1...308

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:495

35 Met Ile Ile Arg Cys Leu Ile Arg Arg Pro Arg Thr Val Leu Phe Gly  
 1 5 10 15  
 Leu Ile Phe Val Val Gly Leu Phe Ser Ala Met Ala Gln Glu Lys Lys  
 20 25 30  
 Asp Ser Leu Ser Thr Val Gln Pro Val Pro Asn Ser Ser Met Val Glu  
 35 40 45  
 40 Gln Thr Pro Leu Leu Ser Ile Asp His Pro Val Leu Pro Ala Ser Phe  
 50 55 60  
 Gln Asn Thr Arg Thr Leu Lys Arg Phe Arg Asp Lys His Leu Ser Asp  
 65 70 75 80  
 45 Ala Leu Leu Asn Gly Leu Lys Pro His Arg Ser Ser Leu Gln Leu Asn  
 85 90 95  
 Glu Glu Leu Asn Phe Ala Ala Glu Arg Asp Phe Val Ser Pro Leu  
 100 105 110  
 Leu Gln Thr Arg His Ala Ala Gly Val Leu Ser Trp Arg Pro Thr Asp  
 115 120 125  
 50 Arg Met His Phe Tyr Thr Ser Gly Asn Ile Gly Leu Gly His Asp Leu  
 130 135 140  
 Leu Thr Gly Val Arg Lys Asp Phe Gly Trp Asn Ala Gly Ala Asp Phe  
 145 150 155 160  
 55 Leu Leu Ser Gln Asn Leu Thr Ala His Val Gln Gly Gly Trp Gln Gln  
 165 170 175  
 Asn Phe Gly Phe Ile Pro Met Thr Ala Val Asn Gly Gln Leu Arg Trp  
 180 185 190  
 Gln Ala Thr Glu Arg Leu Ser Phe Thr Thr Gly Ile Asp Tyr Arg Gln  
 195 200 205  
 60 Val Gln Trp Asn Ala Phe Asp Asn Arg Thr Phe Ser Leu Lys Gly Ser  
 210 215 220  
 Ala Arg Tyr Glu Val Met Asp Asn Val Phe Val Asn Gly Phe Gly Ser  
 225 230 235 240  
 65 Tyr Pro Leu Tyr Ser Ser Thr Arg Ser Gly Leu Asn Met Ala Val Pro  
 245 250 255  
 Met His Gly Phe Gly Pro Gln Tyr Gly Gly Ser Leu Glu Leu Lys Val  
 260 265 270  
 Ser Glu Arg Phe Gly Phe Ala Val Gly Met Glu Arg Glu Tyr Asn Ile  
 275 280 285  
 70 Trp Thr Arg Arg Trp Glu Thr His Tyr Phe Ala Tyr Pro Val Phe Tyr  
 290 295 300  
 Gly Asp Lys Lys  
 305

75

(2) INFORMATION FOR SEQ ID NO:496

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(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 315 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...315

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:496

Met	Lys	Thr	Asn	Arg	Arg	Tyr	Ala	Phe	Val	Leu	Pro	Leu	Leu	Leu	Leu
1			5						10					15	
Thr	Gly	Leu	Leu	Ala	Trp	Gly	Gln	Asp	Ser	Ser	His	Gly	Ser	Asn	Thr
		20						25					30		
Ala	Phe	Ala	Thr	Asp	Ser	Ser	Ser	Arg	Glu	Leu	Pro	Thr	Glu	Gln	Ser
		35						40				45			
Ala	Tyr	Arg	Ile	His	Ser	Ala	Tyr	Met	Val	Gly	Gly	Gly	Gly	Ser	Ile
	50					55				60					
Thr	Arg	Asp	Thr	Tyr	Leu	Ser	Pro	Leu	Arg	Tyr	Gly	Gly	Trp	Thr	Leu
	65				70					75					80
Asn	Leu	Leu	Gly	Glu	Lys	Thr	Phe	Pro	Leu	Lys	Ala	Ser	Asp	Ser	Arg
				85					90				95		
Trp	Met	Ile	Arg	Thr	Gly	His	Glu	Leu	Asp	Phe	Ala	Leu	Met	Asp	Asn
			100					105					110		
Pro	Ala	Asn	Asn	Ala	His	Phe	Tyr	Ser	Leu	Leu	Tyr	Asn	Gly	Ser	Ala
		115					120					125			
Ala	Ala	Leu	Tyr	Arg	Leu	Gly	Ala	Lys	His	Leu	Arg	Ala	Ala	Trp	Met
	130					135				140					
Asp	Asn	Leu	Arg	Leu	Ala	Phe	Gly	Pro	Gly	Leu	Glu	Ile	Gly	Leu	Gly
	145				150					155				160	
Gly	Ile	Tyr	Ser	Thr	Arg	Asn	Gly	Asn	Asn	Pro	Ala	Thr	Leu	Lys	Leu
				165				170					175		
Tyr	Thr	Asn	Ala	Ile	Ala	Gln	Ala	Ser	Ile	Gly	Tyr	Tyr	Val	Pro	Ser
		180						185					190		
Glu	Thr	Phe	Pro	Leu	Tyr	Phe	Arg	Leu	Leu	Ser	Gln	Ile	Asn	Leu	Phe
	195						200					205			
Gly	Ile	Ala	Tyr	Gly	Asn	Gly	Phe	Gly	Glu	Ser	Tyr	Tyr	Glu	Asn	Phe
	210				215						220				
Leu	Leu	Asn	Asn	Gly	Ile	Ala	Gly	Ser	Leu	His	Phe	Thr	Tyr	Pro	Gly
	225			230						235				240	
Lys	Phe	Thr	Arg	Phe	Thr	Thr	Leu	Ile	Thr	Ala	Asp	Ile	Pro	Ile	Arg
			245						250				255		
Asn	Phe	Cys	Thr	Leu	Arg	Val	Gly	Tyr	Arg	Tyr	Ser	His	Leu	Gly	Ser
		260					265						270		
Ser	Leu	Asn	Ala	Leu	Asp	Thr	Arg	Ile	His	Ser	His	Thr	Ala	Phe	Ile
		275					280					285			
Gly	Phe	Val	Thr	Glu	Phe	Tyr	Arg	Phe	Arg	Gly	Arg	Lys	Ala	Met	Asn
	290					295					300				
Thr	Gly	Arg	Arg	Thr	Ser	Leu	Tyr	Tyr	His	Asp					
	305				310					315					

(2) INFORMATION FOR SEQ ID NO:497

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 285 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

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(A) NAME/KEY: misc\_feature  
(B) LOCATION 1...285

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:497

5 Met Val Val Thr Leu Leu Val Ile Val Gly Ile Val Val Val Val Arg  
1 5 10 15  
Tyr Ser Leu Arg Val His Val His Lys Thr Gly Thr Val Val Ser Ala  
20 25 30  
10 Ala Ile Phe Gly Phe Ile Leu Leu Gly Lys Thr Val Pro Cys Asp Thr  
35 40 45  
Arg Asn Phe Phe Ser Ser Glu Ser Asp Glu Pro Glu Ser Arg Val Ala  
50 55 60  
15 Thr Glu Ile Ala His Leu Cys Glu Ile Gly Phe Gln Ile His Ala Ser  
65 70 75 80  
Ser Ile His Val Ala Val Arg Thr Asp Phe Gly Gln Ala Gly Ile His  
85 90 95  
Cys Pro Met Ala Thr Asp Ala Ser Ala Thr Glu Phe Asp Arg Ser Ala  
100 105 110  
20 Glu Cys Ala Glu Arg Thr Ser Ala Gln Ile Asp Thr Ala Ile Arg Ser  
115 120 125  
Gln Ser Gln Ile Ile Arg Thr His Ile Asp Thr Cys Pro Lys Ser Ser  
130 135 140  
25 Gly Thr Ile Gly Gly Ser Thr His Thr Ser Leu His Leu Lys Val Phe  
145 150 155 160  
Asp Gly Arg Gly Glu Val Gly His Ile His Pro Lys Asp Gly Leu Arg  
165 170 175  
Phe Gly Val Val Glu Gly Tyr Ser Ile Gly Ser Tyr Val Asp Ala Ile  
180 185 190  
30 Gly Ile Gly Ala Thr His Ala Lys Ala Gly Ile Ser Asp Thr Arg Thr  
195 200 205  
Gly Ile Ala Gly Gly Tyr His Gly Gly Ser Gln His Gln Gln Ile Gly  
210 215 220  
35 Asp Val Thr Thr Ile Ile Gly Leu Gly Lys Phe Gly Leu Ala Asn Val  
225 230 235 240  
Gly Val Ser Asp Arg Gly Phe Arg Arg Gly Ala Ser Ser Tyr Asp Leu  
245 250 255  
Tyr Gly Leu Glu Leu His Ile Ala Lys Thr Ile Tyr Leu Ala Val Gly  
260 265 270  
40 Asp Gly Cys Leu Cys Arg Gln Ala Glu Arg Gln Asp Gly  
275 280 285

(2) INFORMATION FOR SEQ ID NO:498

45 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 599 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear  
50 (ii) MOLECULE TYPE: protein  
(iii) HYPOTHETICAL: YES  
55 (vi) ORIGINAL SOURCE:  
(A) ORGANISM: Porphyromonas gingivalis  
(ix) FEATURE:  
(A) NAME/KEY: misc\_feature  
(B) LOCATION 1...599

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:498

65 Met Glu Asn Leu Lys Asn Ile Gln Pro Arg Glu Asp Phe Asn Trp Glu  
1 5 10 15  
Glu Phe Glu Ala Gly Gly Val His Ala Ala Val Ser Arg Gln Glu Gln  
20 25 30  
Glu Ala Ala Tyr Asp Lys Thr Leu Asn Thr Ile Lys Glu Lys Glu Val  
35 40 45  
70 Val Met Gly Arg Val Thr Ala Ile Asn Lys Arg Glu Val Val Ile Asn  
50 55 60  
Val Gly Tyr Lys Ser Glu Gly Val Val Pro Ala Thr Glu Phe Arg Tyr  
65 70 75 80  
Asn Pro Glu Leu Lys Val Gly Asp Glu Val Glu Val Tyr Ile Glu Asn  
85 90 95  
75 Gln Glu Asp Lys Lys Gly Gln Leu Val Leu Ser His Arg Lys Gly Arg

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100 105 110  
 Ala Ala Arg Ser Trp Glu Arg Val Asn Glu Ala Leu Glu Lys Asp Glu  
 115 120 125  
 Ile Val Lys Gly Tyr Val Lys Cys Arg Thr Lys Gly Gly Met Ile Val  
 130 135 140  
 Asp Val Phe Gly Ile Glu Ala Phe Leu Pro Gly Ser Gln Ile Asp Val  
 145 150 155 160  
 Arg Pro Ile Arg Asp Tyr Asp Ala Phe Val Glu Lys Thr Met Glu Phe  
 165 170 175  
 10 Lys Ile Val Lys Ile Asn Gln Glu Tyr Lys Asn Val Val Val Ser His  
 180 185 190  
 Lys Val Leu Ile Glu Ala Glu Leu Glu Gln Gln Lys Lys Glu Ile Ile  
 195 200 205  
 15 Gly Lys Leu Glu Lys Gly Gln Val Leu Glu Gly Ile Val Lys Asn Ile  
 210 215 220  
 Thr Ser Tyr Gly Val Phe Ile Asp Leu Gly Gly Val Asp Gly Leu Ile  
 225 230 235 240  
 His Ile Thr Asp Leu Ser Trp Gly Arg Val Ala His Pro Glu Glu Ile  
 245 250 255  
 20 Val Gln Leu Asp Gln Lys Ile Asn Val Val Ile Leu Asp Phe Asp Glu  
 260 265 270  
 Asp Arg Lys Arg Ile Ala Leu Gly Leu Lys Gln Leu Met Pro His Pro  
 275 280 285  
 25 Trp Asp Ala Leu Asp Ser Glu Leu Lys Val Gly Asp Lys Val Lys Gly  
 290 295 300  
 Lys Val Val Val Met Ala Asp Tyr Gly Ala Phe Val Glu Ile Ala Gln  
 305 310 315 320  
 Gly Val Glu Gly Leu Ile His Val Ser Glu Met Ser Trp Thr Gln His  
 325 330 335  
 30 Leu Arg Ser Ala Gln Asp Phe Leu His Val Gly Asp Glu Val Glu Ala  
 340 345 350  
 Val Ile Leu Thr Leu Asp Arg Glu Glu Arg Lys Met Ser Leu Gly Leu  
 355 360 365  
 35 Lys Gln Leu Lys Pro Asp Pro Trp Ala Asp Ile Glu Thr Arg Phe Pro  
 370 375 380  
 Val Gly Ser Arg His His Ala Arg Val Arg Asn Phe Thr Asn Phe Gly  
 385 390 395 400  
 Val Phe Val Glu Ile Glu Glu Gly Val Asp Gly Leu Ile His Ile Ser  
 405 410 415  
 40 Asp Leu Ser Trp Thr Lys Lys Ile Lys His Pro Ser Glu Phe Thr Glu  
 420 425 430  
 Val Gly Ala Asp Ile Glu Val Gln Val Ile Glu Ile Asp Lys Glu Asn  
 435 440 445  
 45 Arg Arg Leu Ser Leu Gly His Lys Gln Leu Glu Glu Asn Pro Trp Asp  
 450 455 460  
 Val Phe Glu Thr Val Phe Thr Val Gly Ser Ile Glu Gly Thr Val  
 465 470 475 480  
 Ile Glu Val Met Asp Lys Gly Ala Val Val Ser Leu Pro Tyr Gly Val  
 485 490 495  
 50 Glu Gly Phe Ala Thr Pro Lys His Met Val Lys Glu Asp Gly Ser Gln  
 500 505 510  
 Ala Val Leu Glu Glu Lys Leu Pro Phe Lys Val Ile Glu Phe Asn Lys  
 515 520 525  
 55 Asp Ala Lys Arg Ile Ile Val Ser His Ser Arg Val Phe Glu Asp Glu  
 530 535 540  
 Gln Lys Met Ala Gln Arg Glu Ala Asn Ala Glu Arg Lys Ala Glu Ala  
 545 550 555 560  
 Lys Ala Ala Gln Lys Glu Ala Ala Ala Glu Ala Ala Asn Pro Ala Gln  
 565 570 575  
 60 Ala Val Glu Lys Ala Thr Leu Gly Asp Leu Gly Glu Leu Ala Ala Leu  
 580 585 590  
 Lys Glu Lys Leu Ser Glu Asn  
 595

65 (2) INFORMATION FOR SEQ ID NO:499

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 550 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

70

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

75

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(vi) ORIGINAL SOURCE:

(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

(A) NAME/KEY: misc feature

(B) LOCATION 1...550

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:499

10 Met Gly Arg Val Thr Ala Ile Asn Lys Arg Glu Val Val Ile Asn Val  
 1 5 10 15  
 Gly Tyr Lys Ser Glu Gly Val Val Pro Ala Thr Glu Phe Arg Tyr Asn  
 20 25 30  
 15 Pro Glu Leu Lys Val Gly Asp Glu Val Glu Val Tyr Ile Glu Asn Gln  
 35 40 45  
 Glu Asp Lys Lys Gly Gln Leu Val Leu Ser His Arg Lys Gly Arg Ala  
 50 55 60  
 Ala Arg Ser Trp Glu Arg Val Asn Glu Ala Leu Glu Lys Asp Glu Ile  
 65 70 75 80  
 20 Val Lys Gly Tyr Val Lys Cys Arg Thr Lys Gly Gly Met Ile Val Asp  
 85 90 95  
 Val Phe Gly Ile Glu Ala Phe Leu Pro Gly Ser Gln Ile Asp Val Arg  
 100 105 110  
 25 Pro Ile Arg Asp Tyr Asp Ala Phe Val Glu Lys Thr Met Glu Phe Lys  
 115 120 125  
 Ile Val Lys Ile Asn Gln Glu Tyr Lys Asn Val Val Val Ser His Lys  
 130 135 140  
 Val Leu Ile Glu Ala Glu Leu Glu Gln Gln Lys Lys Glu Ile Ile Gly  
 145 150 155 160  
 30 Lys Leu Glu Lys Gly Gln Val Leu Glu Gly Ile Val Lys Asn Ile Thr  
 165 170 175  
 Ser Tyr Gly Val Phe Ile Asp Leu Gly Gly Val Asp Gly Leu Ile His  
 180 185 190  
 35 Ile Thr Asp Leu Ser Trp Gly Arg Val Ala His Pro Glu Ile Val  
 195 200 205  
 Gln Leu Asp Gln Lys Ile Asn Val Val Ile Leu Asp Phe Asp Glu Asp  
 210 215 220  
 Arg Lys Arg Ile Ala Leu Gly Leu Lys Gln Leu Met Pro His Pro Trp  
 225 230 235 240  
 40 Asp Ala Leu Asp Ser Glu Leu Lys Val Gly Asp Lys Val Lys Gly Lys  
 245 250 255  
 Val Val Val Met Ala Asp Tyr Gly Ala Phe Val Glu Ile Ala Gln Gly  
 260 265 270  
 45 Val Glu Gly Leu Ile His Val Ser Glu Met Ser Trp Thr Gln His Leu  
 275 280 285  
 Arg Ser Ala Gln Asp Phe Leu His Val Gly Asp Glu Val Glu Ala Val  
 290 295 300  
 Ile Leu Thr Leu Asp Arg Glu Glu Arg Lys Met Ser Leu Gly Leu Lys  
 305 310 315 320  
 50 Gln Leu Lys Pro Asp Pro Trp Ala Asp Ile Glu Thr Arg Phe Pro Val  
 325 330 335  
 Gly Ser Arg His His Ala Arg Val Arg Asn Phe Thr Asn Phe Gly Val  
 340 345 350  
 55 Phe Val Glu Ile Glu Glu Gly Val Asp Gly Leu Ile His Ile Ser Asp  
 355 360 365  
 Leu Ser Trp Thr Lys Lys Ile Lys His Pro Ser Glu Phe Thr Glu Val  
 370 375 380  
 Gly Ala Asp Ile Glu Val Gln Val Ile Glu Ile Asp Lys Glu Asn Arg  
 385 390 395 400  
 60 Arg Leu Ser Leu Gly His Lys Gln Leu Glu Glu Asn Pro Trp Asp Val  
 405 410 415  
 Phe Glu Thr Val Phe Thr Val Gly Ser Ile His Glu Gly Thr Val Ile  
 420 425 430  
 65 Glu Val Met Asp Lys Gly Ala Val Val Ser Leu Pro Tyr Gly Val Glu  
 435 440 445  
 Gly Phe Ala Thr Pro Lys His Met Val Lys Glu Asp Gly Ser Gln Ala  
 450 455 460  
 Val Leu Glu Glu Lys Leu Pro Phe Lys Val Ile Glu Phe Asn Lys Asp  
 465 470 475 480  
 70 Ala Lys Arg Ile Ile Val Ser His Ser Arg Val Phe Glu Asp Glu Gln  
 485 490 495  
 Lys Met Ala Gln Arg Glu Ala Asn Ala Glu Arg Lys Ala Glu Ala Lys  
 500 505 510  
 75 Ala Ala Gln Lys Glu Ala Ala Ala Glu Ala Ala Asn Pro Ala Gln Ala  
 515 520 525

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Val Glu Lys Ala Thr Leu Gly Asp Leu Gly Glu Leu Ala Ala Leu Lys  
 530 535 540  
 Glu Lys Leu Ser Glu Asn  
 545 550

5

(2) INFORMATION FOR SEQ ID NO:500

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 458 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

10

(ii) MOLECULE TYPE: protein

15

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Porphyromonas gingivalis

20

(ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...458

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:500

Met Ile Val Asp Val Phe Gly Ile Glu Ala Phe Leu Pro Gly Ser Gln  
 1 5 10 15  
 Ile Asp Val Arg Pro Ile Arg Asp Tyr Asp Ala Phe Val Glu Lys Thr  
 20 25 30  
 Met Glu Phe Lys Ile Val Lys Ile Asn Gln Glu Tyr Lys Asn Val Val  
 35 40 45  
 Val Ser His Lys Val Leu Ile Glu Ala Glu Leu Glu Gln Gln Lys Lys  
 50 55 60  
 Glu Ile Ile Gly Lys Leu Glu Lys Gly Gln Val Leu Glu Gly Ile Val  
 65 70 75 80  
 Lys Asn Ile Thr Ser Tyr Gly Val Phe Ile Asp Leu Gly Gly Val Asp  
 85 90 95  
 Gly Leu Ile His Ile Thr Asp Leu Ser Trp Gly Arg Val Ala His Pro  
 100 105 110  
 Glu Glu Ile Val Gln Leu Asp Gln Lys Ile Asn Val Val Ile Leu Asp  
 115 120 125  
 Phe Asp Glu Asp Arg Lys Arg Ile Ala Leu Gly Leu Lys Gln Leu Met  
 130 135 140  
 Pro His Pro Trp Asp Ala Leu Asp Ser Glu Leu Lys Val Gly Asp Lys  
 145 150 155 160  
 Val Lys Gly Lys Val Val Val Met Ala Asp Tyr Gly Ala Phe Val Glu  
 165 170 175  
 Ile Ala Gln Gly Val Glu Gly Leu Ile His Val Ser Glu Met Ser Trp  
 180 185 190  
 Thr Gln His Leu Arg Ser Ala Gln Asp Phe Leu His Val Gly Asp Glu  
 195 200 205  
 Val Glu Ala Val Ile Leu Thr Leu Asp Arg Glu Glu Arg Lys Met Ser  
 210 215 220  
 Leu Gly Leu Lys Gln Leu Lys Pro Asp Pro Trp Ala Asp Ile Glu Thr  
 225 230 235 240  
 Arg Phe Pro Val Gly Ser Arg His His Ala Arg Val Arg Asn Phe Thr  
 245 250 255  
 Asn Phe Gly Val Phe Val Glu Ile Glu Glu Gly Val Asp Gly Leu Ile  
 260 265 270  
 His Ile Ser Asp Leu Ser Trp Thr Lys Lys Ile Lys His Pro Ser Glu  
 275 280 285  
 Phe Thr Glu Val Gly Ala Asp Ile Glu Val Gln Val Ile Glu Ile Asp  
 290 295 300  
 Lys Glu Asn Arg Arg Leu Ser Leu Gly His Lys Gln Leu Glu Glu Asn  
 305 310 315 320  
 Pro Trp Asp Val Phe Glu Thr Val Phe Thr Val Gly Ser Ile His Glu  
 325 330 335  
 Gly Thr Val Ile Glu Val Met Asp Lys Gly Ala Val Val Ser Leu Pro  
 340 345 350  
 Tyr Gly Val Glu Gly Phe Ala Thr Pro Lys His Met Val Lys Glu Asp  
 355 360 365  
 Gly Ser Gln Ala Val Leu Glu Lys Leu Pro Phe Lys Val Ile Glu  
 370 375 380  
 Phe Asn Lys Asp Ala Lys Arg Ile Ile Val Ser His Ser Arg Val Phe  
 385 390 395 400

75

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	Glu Asp Glu Gln Lys Met Ala Gln Arg Glu Ala Asn Ala Glu Arg Lys	405	410	415	
	Ala Glu Ala Lys Ala Ala Gln Lys Glu Ala Ala Ala Glu Ala Ala Asn	420	425	430	
5	Pro Ala Gln Ala Val Glu Lys Ala Thr Leu Gly Asp Leu Gly Glu Leu	435	440	445	
	Ala Ala Leu Lys Glu Lys Leu Ser Glu Asn	450	455		
10	(2) INFORMATION FOR SEQ ID NO:501				
	(i) SEQUENCE CHARACTERISTICS:				
	(A) LENGTH: 426 amino acids				
15	(B) TYPE: amino acid				
	(D) TOPOLOGY: linear				
	(ii) MOLECULE TYPE: protein				
	(iii) HYPOTHETICAL: YES				
20	(vi) ORIGINAL SOURCE:				
	(A) ORGANISM: Porphyromonas gingivalis				
	(ix) FEATURE:				
25	(A) NAME/KEY: misc_feature				
	(B) LOCATION 1...426				
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:501				
30	Met Glu Phe Lys Ile Val Lys Ile Asn Gln Glu Tyr Lys Asn Val Val	5	10	15	
	Val Ser His Lys Val Leu Ile Glu Ala Glu Leu Glu Gln Gln Lys Lys	20	25	30	
35	Glu Ile Ile Gly Lys Leu Glu Lys Gly Gln Val Leu Glu Gly Ile Val	35	40	45	
	Lys Asn Ile Thr Ser Tyr Gly Val Phe Ile Asp Leu Gly Gly Val Asp	50	55	60	
	Gly Leu Ile His Ile Thr Asp Leu Ser Trp Gly Arg Val Ala His Pro	65	70	75	
40	Glu Glu Ile Val Gln Leu Asp Gln Lys Ile Asn Val Val Ile Leu Asp	80	85	90	
	Phe Asp Glu Asp Arg Lys Arg Ile Ala Leu Gly Leu Lys Gln Leu Met	100	105	110	
45	Pro His Pro Trp Asp Ala Leu Asp Ser Glu Leu Lys Val Gly Asp Lys	115	120	125	
	Val Lys Gly Lys Val Val Val Met Ala Asp Tyr Gly Ala Phe Val Glu	130	135	140	
	Ile Ala Gln Gly Val Glu Gly Leu Ile His Val Ser Glu Met Ser Trp	145	150	155	
50	Thr Gln His Leu Arg Ser Ala Gln Asp Phe Leu His Val Gly Asp Glu	160	165	170	
	Val Glu Ala Val Ile Leu Thr Leu Asp Arg Glu Glu Arg Lys Met Ser	175	180	185	
55	Leu Gly Leu Lys Gln Leu Lys Pro Asp Pro Trp Ala Asp Ile Glu Thr	190	195	200	
	Arg Phe Pro Val Gly Ser Arg His His Ala Arg Val Arg Asn Phe Thr	205	210	215	
	Asn Phe Gly Val Phe Val Glu Ile Glu Glu Gly Val Asp Gly Leu Ile	220	225	230	
60	His Ile Ser Asp Leu Ser Trp Thr Lys Lys Ile Lys His Pro Ser Glu	235	240	245	
	Phe Thr Glu Val Gly Ala Asp Ile Glu Val Gln Val Ile Glu Ile Asp	250	255	260	
65	Lys Glu Asn Arg Arg Leu Ser Leu Gly His Lys Gln Leu Glu Glu Asn	265	270	275	
	Pro Trp Asp Val Phe Glu Thr Val Phe Thr Val Gly Ser Ile His Glu	280	285	290	
	Gly Thr Val Ile Glu Val Met Asp Lys Gly Ala Val Val Ser Leu Pro	295	300	305	
70	Tyr Gly Val Glu Gly Phe Ala Thr Pro Lys His Met Val Lys Glu Asp	310	315	320	
	Gly Ser Gln Ala Val Leu Glu Glu Lys Leu Pro Phe Lys Val Ile Glu	325	330	335	
	Phe Asn Lys Asp Ala Lys Arg Ile Ile Val Ser His Ser Arg Val Phe	340	345	350	
75		355	360	365	

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- Glu Asp Glu Gln Lys Met Ala Gln Arg Glu Ala Asn Ala Glu Arg Lys  
 370 375 380  
 Ala Glu Ala Lys Ala Ala Gln Lys Glu Ala Ala Ala Glu Ala Ala Asn  
 385 390 395 400  
 5 Pro Ala Gln Ala Val Glu Lys Ala Thr Leu Gly Asp Leu Gly Glu Leu  
 405 410 415  
 Ala Ala Leu Lys Glu Lys Leu Ser Glu Asn  
 420 425
- 10 (2) INFORMATION FOR SEQ ID NO:502  
 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 240 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
 15  
 (ii) MOLECULE TYPE: protein  
 (iii) HYPOTHETICAL: YES  
 20  
 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Porphyromonas gingivalis  
 (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...240  
 25  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:502
- 30 Met Lys Lys Ala Ile Leu Ser Gly Ala Ala Leu Leu Leu Gly Leu Cys  
 1 5 10 15  
 Ala Asn Ala Gln Asn Val Gln Leu His Tyr Asp Phe Gly His Ser Ile  
 20 25 30  
 35 Tyr Asp Glu Leu Asp Gly Arg Pro Lys Leu Thr Thr Thr Val Glu Asn  
 35 40 45  
 Phe Thr Pro Asp Lys Trp Gly Ser Thr Phe Phe Phe Ile Asp Met Asp  
 50 55 60  
 Tyr Thr Gly Lys Gly Ile Gln Ser Ala Tyr Trp Glu Ile Ser Arg Glu  
 65 70 75 80  
 40 Leu Lys Phe Trp Gln Ala Pro Val Ser Ile His Leu Glu Tyr Asn Gly  
 85 90 95  
 Gly Leu Ser Thr Ser Phe Thr Phe Gly His Asp Ala Leu Ile Gly Ala  
 100 105 110  
 Thr Tyr Thr Tyr Asn Asn Pro Ser Phe Thr Arg Gly Phe Thr Ile Thr  
 115 120 125  
 45 Pro Met Tyr Lys His Leu Gly Ala His Asp Phe His Thr Tyr Gln Ile  
 130 135 140  
 Thr Gly Thr Trp Tyr Met His Phe Leu Asp Gly Leu Leu Thr Phe Asn  
 145 150 155 160  
 50 Gly Phe Leu Asp Leu Trp Gly Phe Pro Gln Glu Asn Pro Ile Gly Gly  
 165 170 175  
 Pro Val Leu Lys Glu Gly Asp Lys Phe Val Phe Leu Ser Glu Pro Gln  
 180 185 190  
 Phe Trp Ile Asn Leu Asn Arg Ile Lys Gly Ile Asp Lys Asp Phe Asn  
 195 200 205  
 55 Leu Ser Ile Gly Thr Glu Met Glu Ile Ser Arg Asn Phe Ala Arg Met  
 210 215 220  
 Asp Lys Phe Ser Cys Ile Pro Thr Leu Ala Val Lys Trp Thr Phe Asn  
 225 230 235 240
- 60 (2) INFORMATION FOR SEQ ID NO:503  
 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 434 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
 65  
 (ii) MOLECULE TYPE: protein  
 (iii) HYPOTHETICAL: YES  
 70  
 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Porphyromonas gingivalis  
 (ix) FEATURE:
- 75

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(A) NAME/KEY: misc\_feature  
(B) LOCATION 1...434

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:503

5 Met Tyr Lys Asp Tyr Lys Gly Leu Tyr Ala Ser Leu Arg Trp Tyr Ala  
1 5 10 15  
Leu Ile Ile Gly Leu Leu Phe Ala Ala Asp Gly Ile Gln Ala Gln Asn  
20 25 30  
10 Asn Asn Phe Thr Glu Ser Pro Tyr Thr Arg Phe Gly Leu Gly Arg Leu  
35 40 45  
Gly Glu Arg Thr Thr Ile Ser Gly His Ser Met Gly Gly Leu Gly Val  
50 55 60  
15 Gly Leu Arg Gln Gly Thr Tyr Val Asn Ala Val Asn Pro Ala Ser Tyr  
65 70 75 80  
Ser Ala Val Asp Ser Met Thr Phe Ile Phe Asp Phe Gly Ala Ser Thr  
85 90 95  
Gly Ile Thr Trp Tyr Ala Glu Asn Gly Lys Lys Asp Asn Arg Lys Met  
100 105 110  
20 Gly Asn Ile Glu Tyr Phe Ala Met Leu Phe Pro Ile Ser Lys Ser Ile  
115 120 125  
Ala Met Ser Ala Gly Val Leu Pro Tyr Ser Ala Ser Gly Tyr Gln Phe  
130 135 140  
25 Gly Ser Val Asp Gln Val Glu Gly Gly Ser Val Gln Tyr Thr Arg Lys  
145 150 155 160  
Tyr Leu Gly Thr Gly Asn Leu Asn Asp Leu Tyr Val Gly Ile Gly Ala  
165 170 175  
Thr Pro Phe Lys Asn Phe Ser Ile Gly Ala Asn Ala Ser Ser Leu Phe  
180 185 190  
30 Gly Arg Phe Thr His Ser Arg Gln Val Ile Phe Ser Thr Glu Ala Pro  
195 200 205  
Tyr Asn Pro Val His Leu Ser Thr Leu Tyr Leu Lys Ala Ala Lys Phe  
210 215 220  
35 Asp Phe Gly Met Gln Tyr His Leu Leu Leu Lys Ser Asp Arg Ser Leu  
225 230 235 240  
Val Ile Gly Ala Val Tyr Ser Pro Arg Val Lys Met His Ser Glu Leu  
245 250 255  
Thr Gln Ile Lys Asn Gln Val Gln Asn Gly Val Val Val Glu Ser Glu  
260 265 270  
40 Thr Gln Glu Tyr Ile Lys Gly Met Asp Tyr Tyr Thr Leu Pro His Thr  
275 280 285  
Leu Gly Ile Gly Phe Ser Tyr Glu Lys Lys Asp Lys Leu Leu Leu Gly  
290 295 300  
45 Ala Asp Val Gln Tyr Ser Lys Trp Lys Gly Glu Lys Phe Tyr Lys Ser  
305 310 315 320  
Asp Cys Lys Phe Gln Asp Arg Ile Arg Val Ser Leu Gly Gly Glu Ile  
325 330 335  
Ile Pro Asp Ile Asn Ala Val Gly Met Trp Pro Lys Val Arg Tyr Arg  
340 345 350  
50 Phe Gly Leu His Gly Glu Asn Ser Tyr Leu Lys Val Pro Thr Lys Gly  
355 360 365  
Gly Val Tyr Gln Gly Tyr His Ile Val Gly Ala Val Phe Gly Ile Gly  
370 375 380  
55 Ile Pro Leu Asn Asp Arg Arg Ser Phe Val Asn Val Ser Leu Glu Tyr  
385 390 395 400  
Asp Arg Leu Ile Pro Lys Glu Gly Met Ile Lys Glu Asn Ala Leu Lys  
405 410 415  
Leu Thr Phe Gly Leu Thr Phe Asn Glu Ser Trp Phe Lys Lys Leu Lys  
420 425 430  
60 Leu Asn

(2) INFORMATION FOR SEQ ID NO:504

- 65 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 926 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear
- 70 (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- 75 (vi) ORIGINAL SOURCE:  
(A) ORGANISM: Porphyromonas gingivalis

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(ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...926

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:504

	Met	Arg	Ser	Ile	Tyr	Gln	Leu	Leu	Leu	Ser	Ile	Leu	Leu	Ala	Ser	Leu
	1			5						10					15	
10	Gly	Phe	Val	Gly	Leu	Glu	Ala	Gln	Gln	Ala	Gly	Val	Ala	Gly	Arg	Val
			20					25					30			
	Leu	Asp	Glu	Gly	Asn	Pro	Met	Ile	Gln	Ala	Asn	Val	Gln	Leu	Val	
		35				40					45					
15	Gln	Ser	Thr	Gly	Gln	Val	Ala	Val	Ala	Ala	Gly	Ala	Thr	Asn	Glu	Lys
		50			55						60					
	Gly	Leu	Phe	Ser	Leu	Lys	Thr	Ser	Gln	Glu	Gly	Asp	Tyr	Ile	Leu	Arg
	65				70					75					80	
	Val	Ser	Tyr	Val	Gly	Tyr	Thr	Thr	His	Asp	Glu	Lys	Ile	Ser	Leu	Arg
				85					90					95		
20	Asn	Gly	Gln	Thr	Ile	Thr	Leu	Lys	Asp	Ile	Ser	Met	Asn	Glu	Asp	Ala
			100						105					110		
	Arg	Leu	Leu	Gln	Ser	Val	Thr	Val	Gln	Ala	Lys	Ala	Ala	Glu	Val	Val
		115					120						125			
25	Val	Arg	Asn	Asp	Thr	Leu	Glu	Phe	Asn	Ala	Gly	Ser	Tyr	Thr	Val	Ala
		130				135					140					
	Gln	Gly	Ala	Ser	Ile	Glu	Glu	Leu	Ile	Lys	Lys	Leu	Pro	Gly	Ala	Glu
	145				150					155					160	
	Ile	Gly	Ser	Asp	Gly	Lys	Ile	Thr	Ile	Asn	Gly	Lys	Asp	Ile	Ser	Lys
				165					170					175		
30	Ile	Leu	Val	Asp	Gly	Lys	Glu	Phe	Phe	Ser	Lys	Asp	Pro	Gln	Val	Ala
			180						185					190		
	Ile	Lys	Asn	Leu	Pro	Ala	Asp	Met	Val	Asn	Lys	Val	Gln	Val	Leu	Asn
		195				200						205				
35	Lys	Leu	Ser	Glu	Leu	Ser	Arg	Met	Ser	Gly	Phe	Asp	Asp	Gly	Glu	Glu
		210				215					220					
	Glu	Thr	Val	Ile	Asn	Leu	Thr	Val	Lys	Pro	Glu	Lys	Lys	Lys	Gly	Leu
	225				230						235				240	
	Phe	Gly	Thr	Leu	Gln	Ala	Gly	Tyr	Gly	Thr	Asp	Gln	Arg	Tyr	Met	Ala
				245					250					255		
40	Gly	Gly	Asn	Val	Asn	Arg	Phe	Asp	Gly	Asn	Lys	Gln	Trp	Thr	Leu	Ile
			260					265						270		
	Gly	Ser	Ala	Asn	Asn	Thr	Asn	Asn	Met	Gly	Phe	Ser	Glu	Met	Asp	Ser
		275					280						285			
45	Glu	Met	Gly	Ser	Met	Thr	Phe	Phe	Ser	Pro	Gln	Gly	Gly	Gly	Arg	Arg
		290				295						300				
	Gly	Phe	Gly	Asn	Ser	Gly	Gly	Val	Thr	Ser	Ser	Ser	Met	Leu	Gly	Gly
	305				310					315					320	
	Asn	Phe	Ser	Val	Glu	Phe	Ser	Ser	Ala	Leu	Asn	Thr	Gly	Gly	Asp	Ala
				325					330					335		
50	Arg	Tyr	Gly	Tyr	Asn	Asp	Lys	Ala	Ile	Glu	Thr	Thr	Lys	Arg	Val	Glu
			340					345						350		
	Asn	Ile	Leu	Ala	Glu	Gly	Asn	Thr	Tyr	Met	Asp	Glu	Asn	Ile	Leu	Glu
		355					360						365			
55	Arg	Ser	Phe	Ser	His	Asn	Gly	Gln	Ala	Arg	Phe	Arg	Met	Gln	Trp	Lys
		370				375						380				
	Pro	Ser	Glu	Arg	Thr	Glu	Val	Val	Phe	Glu	Pro	Asp	Leu	Ser	Ile	Ser
	385				390					395					400	
	Lys	Ile	Asp	Gly	Phe	Phe	Asn	Asp	Thr	Tyr	Glu	Thr	Lys	Asp	Ala	Thr
				405					410					415		
60	Gly	Ile	Ser	Ile	Asn	Lys	Gly	Ser	Ile	His	Gln	Thr	Thr	Gln	Gly	Asn
			420					425						430		
	Asn	Phe	Arg	Leu	Asn	Gly	Glu	Leu	Asp	Ile	Ser	His	Lys	Leu	Asn	Asp
		435					440					445				
65	Glu	Gly	Arg	Thr	Ile	Ser	Ala	Ser	Val	Ser	Gly	Gly	Leu	Thr	Asp	Glu
		450					455					460				
	Asp	Gly	Asp	Gly	Ile	Tyr	Gln	Ala	Val	Leu	Gln	Ser	Val	Glu	Thr	Asn
	465				470					475				480		
	Gln	Lys	Gln	Phe	Asn	Asp	Asn	Ser	Asn	Leu	Gln	Tyr	Arg	Leu	Arg	Leu
				485					490					495		
70	Ser	Tyr	Val	Glu	Pro	Leu	Gly	Lys	Asn	Tyr	Phe	Ala	Gln	Ala	Ile	Leu
			500						505					510		
	Asn	Arg	Arg	Phe	Ser	Arg	Arg	Asn	Ser	Asp	Arg	Glu	Val	Tyr	Arg	Leu
		515						520					525			
75	Gly	Asp	Asp	Gly	Gln	Tyr	Ser	Ile	Leu	Asp	Ser	Gln	Tyr	Gly	Leu	Ser
		530					535					540				

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Tyr Ser Asn Glu Phe Thr Gln Tyr Arg Ile Gly Leu Asn Leu Lys Lys  
 545 550 555 560  
 Ile Ala Lys Thr Trp Asp Tyr Thr Val Gly Phe Asn Val Asp Pro Asn  
 565 570 575  
 5 Arg Thr Val Ser Tyr Arg Ser Val Ala Gly Val Glu Gln Asp Lys Leu  
 580 585 590  
 Ala Phe Asn Arg Val Asn Leu Ser Pro Met Leu Arg Ile Asn Tyr Lys  
 595 600 605  
 10 Pro Ser Arg Thr Thr Asn Leu Arg Val Asp Tyr Arg Gly Arg Thr Thr  
 610 615 620  
 Gln Pro Ser Ile Asn Gln Ile Ala Pro Val Gln Asp Ile Thr Asn Pro  
 625 630 635 640  
 Leu Phe Val Thr Glu Gly Asn Pro Gly Leu Lys Pro Ser Tyr Ser Asn  
 645 650 655  
 15 Asn Val Met Ala Met Phe Ser Asp Phe Asp Ala Lys Ser Gln Arg Ala  
 660 665 670  
 Phe Asn Ile Val Phe Phe Gly Asn Tyr Thr Phe Asp Asp Ile Val Pro  
 675 680 685  
 20 Asn Thr His Tyr Asp Pro Ser Thr Gly Ile Arg Thr Arg Tyr Glu  
 690 695 700  
 Asn Ala Ser Gly Thr Trp Gln Ala Asn Leu His Gly Thr Leu Ser Leu  
 705 710 715 720  
 Pro Leu Lys Asn Arg Ala Phe Ser Phe Arg Met Ser Leu Phe Asn Arg  
 725 730 735  
 25 Leu Ala Glu Gly Gln Ser Phe Ile Asn Asp Asp Lys Asn Lys Ala Leu  
 740 745 750  
 Ser Phe Arg Thr Arg Glu Arg Leu Thr Leu Thr Tyr Arg Asn Asn Trp  
 755 760 765  
 30 Ile Asp Thr Ser Ile Gly Gly Asn Ile Gly Phe Tyr Met Ala Asn Asn  
 770 775 780  
 Ser Leu Ser Gly Gln Lys Asp Ser Arg Thr Tyr Asp Phe Gly Gly Asn  
 785 790 795 800  
 Tyr Gln Val Ala Leu Thr Leu Pro Tyr Gly Phe Arg Ile Asp Ser Asp  
 805 810 815  
 35 Val Glu Tyr Asn Thr Asn Ser Gly Tyr Ser Gly Gly Phe Ser Leu Asp  
 820 825 830  
 Glu Trp Leu Trp Asn Ala Ser Leu Ser Tyr Ser Phe Leu Arg Asp Lys  
 835 840 845  
 40 Ala Gly Thr Leu Arg Val Asn Gly Tyr Asp Ile Leu Gly Gln Arg Ser  
 850 855 860  
 Ser Ile Ser Arg Ser Ala Ser Ala Ile Asn Ile Glu Glu Ser Met Ser  
 865 870 875 880  
 Asn Thr Ile Gly Arg Tyr Val Met Val Asp Phe Ile Tyr Arg Phe Asn  
 885 890 895  
 45 Ala Phe Ser Gly Gly Gly Ser Arg Ser Asp His Gln Arg Gly Asn Met  
 900 905 910  
 Asn Arg Pro Gly Pro Pro Phe Gly Gly Gly Arg Arg Pro Ser  
 915 920 925

50 (2) INFORMATION FOR SEQ ID NO:505

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
 55  
 (ii) MOLECULE TYPE: protein  
 (iii) HYPOTHETICAL: YES  
 60  
 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Porphyromonas gingivalis  
 (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...400  
 65  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:505

70 Met Val Met Lys Leu Ile Lys Arg Ser Leu Leu Leu Leu Gly Ala Val  
 1 5 10 15  
 Leu Leu Ile Thr Leu Pro Ala Tyr Ser Gln Asn Asp Asp Ile Phe Glu  
 20 25 30  
 75 Asp Asp Ile Tyr Thr Ser Arg Lys Glu Ile Arg Lys Gln Asn Gln Val  
 35 40 45

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Lys Asp Trp Gln Asn Gln Glu Asp Gly Tyr Gly Asp Asp Thr Glu Tyr  
 50 55 60  
 Thr Val Ala Ser Asp Arg Asp Ile Asp Ala Tyr Asn Arg Arg Asp Gly  
 65 70 75 80  
 5 Gln Ser Tyr Asp Gly Lys Lys Leu Ser Lys Asp Lys Lys Arg Asp Ser  
 85 90 95  
 Thr Arg Ser Ser Val Pro Gly Arg Tyr Ser Arg Arg Leu Ala Arg Phe  
 100 105 110  
 10 Tyr Lys Pro Asn Thr Ile Val Ile Ser Gly Ala Asp Asn Val Tyr Val  
 115 120 125  
 Thr Asp Asp Gly Glu Tyr Phe Val Tyr Gly Asp Glu Tyr Tyr Asp Asp  
 130 135 140  
 Ala Ser Ser Val Asn Ile Tyr Ile Asn Ser Pro Trp Cys Asp Pro Phe  
 145 150 155 160  
 15 Pro Tyr Thr Ser Trp Tyr Pro Ser Phe Ser Gly Trp Tyr Asn Tyr Thr  
 165 170 175  
 Trp Asn Tyr Pro Trp Phe Tyr Tyr Gly Ser His Ile Gly Trp Gly Gly  
 180 185 190  
 20 Tyr Tyr Pro Gly Tyr Asn Trp Tyr Trp Ser Tyr Tyr Tyr Asp Pro Phe  
 195 200 205  
 Tyr Asn Pro Tyr Gly Ile Gly Met Gly Trp Gly Tyr Pro Tyr Gly Trp  
 210 215 220  
 Gly Ser Tyr Tyr Gly Trp Gly Gly Tyr Pro Gly Val Ile His His Tyr  
 225 230 235 240  
 25 His His Tyr Pro Lys Lys Thr Tyr Ser Asn Gly Gln His Ser Gly Ala  
 245 250 255  
 Tyr Tyr Ser Tyr Gly Arg Pro Asn Arg Ile Lys Gly Gly Thr Ser Gly  
 260 265 270  
 30 Ala Lys Leu Gly Thr Gly Arg Tyr Asp Arg Ile Gln Asn Ser Ser Ser  
 275 280 285  
 Gln Lys Asn Lys Phe Gly Leu Gln Ser Asn Lys Pro Asn Asn Asn Leu  
 290 295 300  
 Gln Asn Val Lys Ser Gly Arg Thr Gly Arg Ala Asn Arg Asp Arg Asn  
 305 310 315 320  
 35 Ile Glu Thr Val Thr Pro Asn Asn Gly Gln Lys Gln Asn Arg Pro Val  
 325 330 335  
 Phe Gln Gln Asn Gln Ser Gly Asn Asp Arg Pro Thr Gly Arg Asn Ile  
 340 345 350  
 40 Arg Ser Glu Arg Gln Gly Glu Asn Asn Asp Arg Thr Phe Ser Thr Pro  
 355 360 365  
 Ser Arg Ser Asn Ser Asn Gly Gly Phe Ser Thr Pro Ser Arg Ser Ser  
 370 375 380  
 Ser Gly Ser Met Ser Gly Gly Gly Arg Ser Gly Arg Gly Arg Asn  
 385 390 395 400

(2) INFORMATION FOR SEQ ID NO:506

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 398 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

(A) NAME/KEY: misc\_feature

(B) LOCATION 1...398

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:506

Met Lys Leu Ile Lys Arg Ser Leu Leu Leu Leu Gly Ala Val Leu Leu  
 1 5 10 15  
 Ile Thr Leu Pro Ala Tyr Ser Gln Asn Asp Asp Ile Phe Glu Asp Asp  
 20 25 30  
 70 Ile Tyr Thr Ser Arg Lys Glu Ile Arg Lys Gln Asn Gln Val Lys Asp  
 35 40 45  
 Trp Gln Asn Gln Glu Asp Gly Tyr Gly Asp Asp Thr Glu Tyr Thr Val  
 50 55 60  
 Ala Ser Asp Arg Asp Ile Asp Ala Tyr Asn Arg Arg Asp Gly Gln Ser  
 65 70 75 80

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Tyr Asp Gly Lys Lys Leu Ser Lys Asp Lys Lys Arg Asp Ser Thr Arg  
 85 90 95  
 Ser Ser Val Pro Gly Arg Tyr Ser Arg Arg Leu Ala Arg Phe Tyr Lys  
 100 105 110  
 5 Pro Asn Thr Ile Val Ile Ser Gly Ala Asp Asn Val Tyr Val Thr Asp  
 115 120 125  
 Asp Gly Glu Tyr Phe Val Tyr Gly Asp Glu Tyr Tyr Asp Asp Ala Ser  
 130 135 140  
 10 Ser Val Asn Ile Tyr Ile Asn Ser Pro Trp Cys Asp Pro Phe Pro Tyr  
 145 150 155 160  
 Thr Ser Trp Tyr Pro Ser Phe Ser Gly Trp Tyr Asn Tyr Thr Trp Asn  
 165 170 175  
 Tyr Pro Trp Phe Tyr Tyr Gly Ser His Ile Gly Trp Gly Gly Tyr Tyr  
 180 185 190  
 15 Pro Gly Tyr Asn Trp Tyr Trp Ser Tyr Tyr Tyr Asp Pro Phe Tyr Asn  
 195 200 205  
 Pro Tyr Gly Ile Gly Met Gly Trp Gly Tyr Pro Tyr Gly Trp Gly Ser  
 210 215 220  
 20 Tyr Tyr Gly Trp Gly Gly Tyr Pro Gly Val Ile His His Tyr His His  
 225 230 235 240  
 Tyr Pro Lys Lys Thr Tyr Ser Asn Gly Gln His Ser Gly Ala Tyr Tyr  
 245 250 255  
 Ser Tyr Gly Arg Pro Asn Arg Ile Lys Gly Gly Thr Ser Gly Ala Lys  
 260 265 270  
 25 Leu Gly Thr Gly Arg Tyr Asp Arg Ile Gln Asn Ser Ser Ser Gln Lys  
 275 280 285  
 Asn Lys Phe Gly Leu Gln Ser Asn Lys Pro Asn Asn Asn Leu Gln Asn  
 290 295 300  
 30 Val Lys Ser Gly Arg Thr Gly Arg Ala Asn Arg Asp Arg Asn Ile Glu  
 305 310 315 320  
 Thr Val Thr Pro Asn Asn Gly Gln Lys Gln Asn Arg Pro Val Phe Gln  
 325 330 335  
 Gln Asn Gln Ser Gly Asn Asp Arg Pro Thr Gly Arg Asn Ile Arg Ser  
 340 345 350  
 35 Glu Arg Gln Gly Glu Asn Asn Asp Arg Thr Phe Ser Thr Pro Ser Arg  
 355 360 365  
 Ser Asn Ser Asn Gly Gly Phe Ser Thr Pro Ser Arg Ser Ser Ser Gly  
 370 375 380  
 40 Ser Met Ser Gly Gly Gly Gly Arg Ser Gly Arg Gly Arg Asn  
 385 390 395

(2) INFORMATION FOR SEQ ID NO:507

45 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 581 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
 50 (ii) MOLECULE TYPE: protein  
 (iii) HYPOTHETICAL: YES  
 (vi) ORIGINAL SOURCE:  
 55 (A) ORGANISM: Porphyromonas gingivalis  
 (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION: 1...581  
 60 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:507

Met Ile Arg Lys Leu Ile Leu Leu Leu Ala Leu Met Pro Val Ala Ser  
 1 5 10 15  
 65 Val Ala Phe Ala Val Pro Thr Asp Ser Thr Glu Ser Lys Asp Asn Arg  
 20 25 30  
 Ile Leu Thr Ser Met Gln Ser Ser Ser Leu Asn Arg Asp Asp Ala Pro  
 35 40 45  
 Asp Lys Trp Gln Pro Met His Ala Asn Phe Ser Ile Gln Ser Asp Met  
 50 55 60  
 70 Leu Leu Ser Thr Ala Gln Lys Ser Lys Asn Thr Trp Phe Gly Asn Ser  
 65 70 75 80  
 Tyr Ile Met Gly Ile Ile Lys Asn Asn Tyr Leu Glu Phe Gly Ala Arg  
 85 90 95  
 75 Phe Glu Asp Leu Tyr Lys Pro Leu Pro Gly His Glu Pro Glu Met Gly  
 100 105 110

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5 Arg Gly Val Pro His Met Tyr Val Lys Gly Ser Tyr His Trp Ala Glu  
 115 120 125  
 Leu Thr Met Gly Asp Phe Tyr Asp Gln Phe Gly Ser Gly Met Val Phe  
 130 135 140  
 10 Arg Thr Tyr Glu Glu Arg Asn Leu Gly Ile Asp Asn Ala Val Arg Gly  
 145 150 155 160  
 Gly Arg Ile Val Leu Thr Pro Phe Asp Gly Val Arg Val Lys Gly Ile  
 165 170 175  
 15 Ala Gly Gln Gln Arg Asn Tyr Phe Asp Arg Thr Gly Lys Val Phe Asn  
 180 185 190  
 Ser Gly Arg Gly Tyr Leu Leu Gly Ser Asp Leu Glu Leu Asn Val Glu  
 195 200 205  
 Arg Trp Ser Ser Ala Met Arg Asp Asn Asp Tyr His Leu Ala Ile Gly  
 210 215 220  
 20 Gly Ser Phe Val Ser Lys His Glu Ala Asp Glu Asp Ile Phe Val Gly  
 225 230 235 240  
 Val Gly Glu Asp Arg Lys Arg Leu Asn Leu Pro Leu Asn Val Pro Ile  
 245 250 255  
 25 Met Gly Leu Arg Thr Asn Phe Gln Lys Gly Gly Leu Ala Leu Tyr Ala  
 260 265 270  
 Glu Tyr Gly Tyr Lys Tyr Asn Asp Pro Ser Ala Asp Asn Asp Tyr Ile  
 275 280 285  
 Tyr His Asp Gly Gln Ala Ala Leu Leu Ser Ala Ser Tyr Ser Lys Lys  
 290 295 300  
 30 Gly Met Ser Ile Leu Leu Gln Ala Lys Arg Cys Glu Asn Phe Ala Phe  
 305 310 315 320  
 Arg Ser Lys Arg Ser Ala Gln Leu Thr Pro Leu Met Ile Asn Tyr Met  
 325 330 335  
 35 Pro Ala Phe Thr Gln Ala His Thr Tyr Thr Leu Ala Ala Ile Tyr Pro  
 340 345 350  
 Tyr Ala Thr Gln Pro Gln Gly Glu Trp Ala Phe Gln Gly Glu Leu Arg  
 355 360 365  
 Tyr Asn Phe Ala Arg Arg Thr Ala Leu Gly Gly Arg Tyr Gly Thr Gly  
 370 375 380  
 40 Leu Arg Ile Asn Val Ser His Val Arg Gly Leu Asp Lys Lys Met Leu  
 385 390 395 400  
 Lys Glu Asn Pro Asp Glu Leu Ile Gly Thr Asp Gly Tyr Thr Val Ser  
 405 410 415  
 Phe Phe Gly Met Gly Asp Leu Tyr Tyr Ser Asp Ile Asp Val Glu Ile  
 420 425 430  
 Thr Lys Lys Val Ser Pro Gly Phe Asn Phe Thr Leu Thr Tyr Leu Asn  
 435 440 445  
 Gln Ile Tyr Asn Asn Lys Val Leu His Gly Ala Ala Gly Glu Lys Pro  
 450 455 460  
 45 Glu Lys Ile Tyr Ala Asn Ile Phe Val Tyr Asp Gly Lys Tyr Lys Leu  
 465 470 475 480  
 Ser Asn Lys Val Ala Leu Arg Thr Glu Leu Gln Tyr Leu His Thr Lys  
 485 490 495  
 50 Gln Asp Gln Gly Asp Trp Ile Tyr Gly Met Ala Glu Leu Ser Ile Leu  
 500 505 510  
 Pro Ser Leu Met Leu Ser Leu Ser Glu Gln Tyr Asn Ile Gly Glu Thr  
 515 520 525  
 Lys Lys His Tyr Val Met Gly Ser Val Thr Tyr Thr His Gly Ala His  
 530 535 540  
 55 Arg Val Ala Phe Ser Ala Gly Lys Thr Arg Ala Gly Met Asn Cys Ser  
 545 550 555 560  
 Gly Gly Val Cys Arg Val Val Pro Glu Thr Gln Gly Phe Tyr Leu Ser  
 565 570 575  
 60 Tyr Ser Thr Asn Leu  
 580

(2) INFORMATION FOR SEQ ID NO:508

- 65 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 239 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
 70 (ii) MOLECULE TYPE: protein  
 (iii) HYPOTHETICAL: YES  
 (vi) ORIGINAL SOURCE:  
 75 (A) ORGANISM: Porphyromonas gingivalis

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## (ix) FEATURE:

(A) NAME/KEY: misc feature  
(B) LOCATION 1...239

## 5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:508

```

Met Arg Ser Leu Phe Leu Ser Ala Leu Arg Ser Ser Ser Leu His Gly
1      5      10      15
Ser Glu Arg Arg Ser Arg Ile Ser Ser Val Val Met Ser Ile Arg
10     20     25     30
Gln Lys Ile Arg Leu Phe His Leu Ser Val Cys Ala Gln Thr His Asp
35     40     45
His Leu Ile Glu Ile His Leu Val Cys Ile Glu Phe Gly Ala Ile Asp
50     55     60
Thr Asp Glu Phe Arg Leu Ser Ser His Ala Tyr Thr Thr Ser Pro Thr
15     65     70     75     80
His Thr Gly Ala Ile His His Asn Cys Ile Glu Arg Ser Tyr Gly Arg
85     90     95
Tyr Leu Val Thr Phe Gly Gln Glu Arg Asn Glu Leu His His His Ser
20     100    105    110
Arg Pro Asp Arg Asn Ala Glu Val Tyr Arg Phe Pro Phe Asp Asn Ala
115    120    125
Phe His Ser Ile Arg Tyr Glu Ala Phe Arg Pro Ile Arg Pro Ile Val
130    135    140
25 Cys His Asp Asp His Phe Ile Ala Ile Gly Ser His Leu Phe Phe Lys
145    150    155    160
Asp Asn Gln Ile Phe Ser Ser Gly Ser Tyr Asp Asn Tyr Thr Val
165    170    175
30 Ala Cys Phe Val Glu Ser Leu His Asp Arg Glu Gln Arg Ser His Thr
180    185    190
His Thr Ala Ser Gly Thr Asn His Cys Ala Asp Leu Phe Asp Met Arg
195    200    205
Thr Leu Ser Gln Arg Thr Tyr His Ile Arg Asp Ile Val Ala Asp Phe
210    215    220
35 Glu Phe Gly Gln Phe Leu Gly Arg Phe Ala His Gly Leu Asn His
225    230    235

```

## (2) INFORMATION FOR SEQ ID NO:509

40 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 211 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

45 (ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

50 (vi) ORIGINAL SOURCE:  
(A) ORGANISM: Porphyromonas gingivalis

55 (ix) FEATURE:  
(A) NAME/KEY: misc feature  
(B) LOCATION 1...211

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:509

```

Met Ser Ile Arg Gln Lys Ile Arg Leu Phe His Leu Ser Val Cys Ala
1      5      10      15
Gln Thr His Asp His Leu Ile Glu Ile His Leu Val Cys Ile Glu Phe
60     20     25     30
Gly Ala Ile Asp Thr Asp Glu Phe Arg Leu Ser Ser His Ala Tyr Thr
35     40     45
Thr Ser Pro Thr His Thr Gly Ala Ile His His Asn Cys Ile Glu Arg
65     50     55     60
Ser Tyr Gly Arg Tyr Leu Val Thr Phe Gly Gln Glu Arg Asn Glu Leu
65     70     75     80
His His His Ser Arg Pro Asp Arg Asn Ala Glu Val Tyr Arg Phe Pro
85     90     95
70 Phe Asp Asn Ala Phe His Ser Ile Arg Tyr Glu Ala Phe Arg Pro Ile
100    105    110
Arg Pro Ile Val Cys His Asp Asp His Phe Ile Ala Ile Gly Ser His
115    120    125
75 Leu Phe Phe Lys Asp Asn Gln Ile Phe Ser Ser Gly Ser Gln Tyr Asp
130    135    140

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Asn Tyr Thr Val Ala Cys Phe Val Glu Ser Leu His Asp Arg Glu Gln  
 145 150 155 160  
 Arg Ser His Thr His Thr Ala Ser Gly Thr Asn His Cys Ala Asp Leu  
 165 170 175  
 5 Phe Asp Met Arg Thr Leu Ser Gln Arg Thr Tyr His Ile Arg Asp Ile  
 180 185 190  
 Val Ala Asp Phe Glu Phe Gly Gln Phe Leu Gly Arg Phe Ala His Gly  
 195 200 205  
 10 Leu Asn His  
 210

(2) INFORMATION FOR SEQ ID NO:510

15 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 781 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
 (ii) MOLECULE TYPE: protein  
 20 (iii) HYPOTHETICAL: YES  
 (iv) ORIGINAL SOURCE:  
 (A) ORGANISM: Porphyromonas gingivalis  
 25 (ix) FEATURE:  
 (A) NAME/KEY: misc feature  
 (B) LOCATION 1...781  
 30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:510

Met Asp Arg Pro Lys Pro Ser Tyr Ile Val Arg Ile Ala Ala Ile Leu  
 1 5 10 15  
 35 Cys Leu Phe Val Gly Arg Pro Leu Phe Ala Gln Ser Tyr Val Asp Tyr  
 20 25 30  
 Val Asp Pro Leu Ile Gly Thr Leu Ser Ser Phe Glu Leu Ser Ala Gly  
 35 40 45  
 Asn Thr Tyr Pro Val Ile Gly Leu Pro Trp Gly Met Asn Ser Trp Thr  
 50 55 60  
 40 Pro Met Thr Gly Val Pro Gly Asp Gly Trp Gln Tyr Thr Tyr Ser Ala  
 65 70 75 80  
 His Lys Ile Arg Gly Phe Lys Gln Thr His Gln Pro Ser Pro Trp Ile  
 85 90 95  
 45 Asn Asp Tyr Gly Gln Phe Ser Leu Leu Pro Leu Thr Ala Pro Gln Lys  
 100 105 110  
 Pro Ser Ser Asn Asp Ser Ile Ala Leu Thr Lys Trp Cys Lys Gln Leu  
 115 120 125  
 Phe Ser Asp Glu Gln Thr Ser Trp Phe Ser His Lys Ala Glu Thr Ala  
 130 135 140  
 50 Thr Pro Tyr Tyr Tyr Ser Val Tyr Leu Ala Asp Tyr Asp Thr Arg Val  
 145 150 155 160  
 Glu Met Ala Pro Thr Glu Arg Ala Ala Ile Phe Arg Ile Arg Tyr Ser  
 165 170 175  
 55 Gly Asn Thr Glu Ser Gly Ser Gly Arg Trp Leu Arg Leu Asp Ala Phe  
 180 185 190  
 Thr Gly Gly Ser Glu Ile Ser Ile Val Asp Pro His Thr Val Val Gly  
 195 200 205  
 Ile Ser Arg Lys Asn Ser Gly Gly Val Pro Ala Asn Phe Ala Cys Tyr  
 210 215 220  
 60 Phe Ile Leu Gln Ser Asp Thr Pro Met Ala Asp Val Leu Leu Glu Thr  
 225 230 235 240  
 Asp Thr Gly Lys Ser Asp Glu Gly Thr Arg Ala Trp Ala Ala Cys Arg  
 245 250 255  
 65 Phe Asp Ser Gln Glu Val Thr Val Arg Val Ala Ser Ser Phe Ile Ser  
 260 265 270  
 Val Glu Gln Ala Glu Arg Asn Leu Ala Glu Val Lys Gly Gln Ser Phe  
 275 280 285  
 Asp Arg Ile Arg Leu Ala Gly Arg Glu Ala Trp Asn Lys Val Leu Gly  
 290 295 300  
 70 Arg Ile His Val Glu Gly Gly Thr Lys Asp Glu Arg Thr Thr Phe Tyr  
 305 310 315 320  
 Ser Ala Leu Tyr Arg Cys Leu Leu Phe Pro Arg Arg Phe Tyr Glu Glu  
 325 330 335  
 75 Asp Ala Ser Gly Asn Phe Val His Tyr Ser Pro Tyr Asn Gly Glu Val  
 340 345 350

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Leu Pro Gly Tyr Leu Tyr Thr Asp Thr Gly Phe Trp Asp Thr Phe Arg  
 355 360 365  
 Ala Leu Phe Pro Leu Leu Asn Leu Leu Tyr Pro Asp Glu Asn Ile Lys  
 370 375 380  
 5 Ile Gln Glu Gly Leu Leu Asn Val Tyr Arg Glu Ser Gly Phe Phe Pro  
 385 390 395 400  
 Glu Trp Ala Ser Pro Gly His Arg Asp Cys Met Ile Gly Asn Asn Ser  
 405 410 415  
 10 Ala Ser Val Leu Ala Asp Ala Tyr Leu Lys Gly Val Arg Val Glu Asp  
 420 425 430  
 Thr Arg Thr Leu Met Asn Gly Leu Leu His Ala Thr Lys Ala Val His  
 435 440 445  
 Pro Lys Ile Ser Ser Thr Gly Arg Lys Gly Trp Glu Trp Tyr Asn Ser  
 450 455 460  
 15 Leu Gly Tyr Val Pro Ala Asp Ala Gly Ile Asp Glu Ser Ala Ala Arg  
 465 470 475 480  
 Thr Leu Glu Tyr Ala Tyr Asn Asp Trp Cys Ile Leu Arg Leu Gly Arg  
 485 490 495  
 20 Thr Leu Gly Trp Asp Arg Ala Ala Leu Asp Thr Leu Ala His Arg Ser  
 500 505 510  
 Met Asn Tyr Arg His Leu Phe Asp Pro Glu Thr Lys Leu Met Arg Gly  
 515 520 525  
 Arg Asn Gln Asp Gly Ser Phe Arg Thr Pro Phe Ser Pro Phe Lys Trp  
 530 535 540  
 25 Gly Asp Val Phe Thr Glu Gly Asn Ala Trp His Tyr Thr Trp Ser Val  
 545 550 555 560  
 Phe His Asp Val Gln Gly Leu Ile Asp Leu Met Gly Gly Asp Arg Pro  
 565 570 575  
 30 Phe Val Ser Met Leu Asp Ser Val Phe Asn Thr Pro Pro Met Phe Asp  
 580 585 590  
 Glu Ser Tyr Tyr Gly Phe Val Ile His Glu Ile Arg Glu Met Gln Ile  
 595 600 605  
 Ala Asp Met Gly Asn Tyr Ala His Gly Asn Gln Pro Ile Gln His Met  
 610 615 620  
 35 Ile Tyr Leu Tyr Asn His Ala Gly His Pro Trp Lys Ala Gln Glu Arg  
 625 630 635 640  
 Leu Arg Glu Val Met Gly Arg Leu Tyr Arg Pro Thr Pro Asp Gly Tyr  
 645 650 655  
 40 Cys Gly Asp Glu Asp Asn Gly Gln Thr Ser Ala Trp Tyr Val Phe Ser  
 660 665 670  
 Ala Leu Gly Phe Tyr Pro Val Thr Pro Ala Thr Asp Gln Tyr Val Leu  
 675 680 685  
 Gly Ser Pro Ile Phe Ser Lys Val Ile Leu Ser Phe Pro Asp Gly His  
 690 695 700  
 45 Lys Thr Val Leu His Ala Pro Ala Asn Ser Ala Asp Thr Pro Tyr Ile  
 705 710 715 720  
 Arg Ser Ile Ser Val Glu Gly Lys Glu Trp Ser Cys Asn Tyr Leu Thr  
 725 730 735  
 50 His Glu Gln Leu Arg Ser Ser Ala Ser Ile Gln Trp Met Met Asp Thr  
 740 745 750  
 Lys Pro Asn Tyr Asn Arg Gly Met Lys Glu Ser Asp Arg Pro Tyr Ser  
 755 760 765  
 Phe Ser Thr Glu Gln Gln Arg Arg Ala Asn His Ser Asn  
 770 775 780

(2) INFORMATION FOR SEQ ID NO:511

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 271 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
 (ii) MOLECULE TYPE: protein  
 (iii) HYPOTHETICAL: YES  
 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Porphyromonas gingivalis  
 (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...271  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:511

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Met Met Lys Ser Met Arg Ser Val Leu Leu Leu Leu Phe Pro Leu Ser  
 1 5 10 15  
 Leu Ile Thr Ala Leu Gly Cys Ser Asn Asn Lys Ala Ala Glu Ser Lys  
 20 25 30  
 5 Ser Val Ser Phe Asp Ser Ala Tyr Leu Glu Arg Tyr Ile Pro Leu Arg  
 35 40 45  
 Ala Asp Ile Asp Thr Pro Ser Leu His Val Met Ile Ser Tyr Val Tyr  
 50 55 60  
 10 Pro Ser Gly Asp Asp Met Leu Thr Glu Ile Phe Asn Gly Leu Leu Phe  
 65 70 75 80  
 Gly Asp Ser Leu Met Asp Ser Ser Ser Pro Glu Asn Ala Met Glu Gly  
 85 90 95  
 Tyr Ala Gln Met Leu Gly Glu Asp Tyr Arg Ser Asn Asn Ala Glu Ala  
 100 105 110  
 15 Asn Leu Gln Gly Leu Pro Ser Asp Leu Leu Asp Tyr Ile Tyr Lys Gln  
 115 120 125  
 Glu Asn Thr Ile Ala Tyr Cys Asp Thr Gly Leu Ile Ser Thr Arg Ile  
 130 135 140  
 20 Asn Thr Tyr Thr Tyr Glu Gly Gly Ala His Thr Glu Asn Thr Val Arg  
 145 150 155 160  
 Phe Ala Asn Ile Leu Arg Thr Thr Gly Lys Val Leu Glu Glu Arg Asp  
 165 170 175  
 Ile Phe Lys Ile Asp Tyr Ala Glu Arg Leu Ser Ala Leu Ile Ile Gly  
 180 185 190  
 25 Gln Leu Val His Asp Phe Gly Lys Thr Thr Pro Ala Glu Leu Asp Ala  
 195 200 205  
 Ile Gly Phe Phe Asn Ala Glu Ile Gln Pro Asn Gly Asn Phe Met  
 210 215 220  
 30 Ile Asp Asp Lys Gly Leu Thr Tyr Cys Phe Asn Glu Tyr Gln Ile Ala  
 225 230 235 240  
 Ala Tyr Ala Arg Gly Ala Val Tyr Val Arg Leu Gly Tyr Asp Val Leu  
 245 250 255  
 Ala Pro Leu Leu Arg Asp Asp Ser Pro Leu Lys Arg Tyr Leu Pro  
 260 265 270

(2) INFORMATION FOR SEQ ID NO:512

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 270 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

(A) NAME/KEY: misc feature

(B) LOCATION 1...270

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:512

Met Lys Ser Met Arg Ser Val Leu Leu Leu Leu Phe Pro Leu Ser Leu  
 1 5 10 15  
 Ile Thr Ala Leu Gly Cys Ser Asn Asn Lys Ala Ala Glu Ser Lys Ser  
 20 25 30  
 60 Val Ser Phe Asp Ser Ala Tyr Leu Glu Arg Tyr Ile Pro Leu Arg Ala  
 35 40 45  
 Asp Ile Asp Thr Pro Ser Leu His Val Met Ile Ser Tyr Val Tyr Pro  
 50 55 60  
 65 Ser Gly Asp Asp Met Leu Thr Glu Ile Phe Asn Gly Leu Leu Phe Gly  
 65 70 75 80  
 Asp Ser Leu Met Asp Ser Ser Ser Pro Glu Asn Ala Met Glu Gly Tyr  
 85 90 95  
 Ala Gln Met Leu Gly Glu Asp Tyr Arg Ser Asn Asn Ala Glu Ala Asn  
 100 105 110  
 70 Leu Gln Gly Leu Pro Ser Asp Leu Leu Asp Tyr Ile Tyr Lys Gln Glu  
 115 120 125  
 Asn Thr Ile Ala Tyr Cys Asp Thr Gly Leu Ile Ser Thr Arg Ile Asn  
 130 135 140  
 75 Thr Tyr Thr Tyr Glu Gly Gly Ala His Thr Glu Asn Thr Val Arg Phe  
 145 150 155 160

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Ala Asn Ile Leu Arg Thr Thr Gly Lys Val Leu Glu Glu Arg Asp Ile  
 165 170 175  
 Phe Lys Ile Asp Tyr Ala Glu Arg Leu Ser Ala Leu Ile Ile Gly Gln  
 180 185 190  
 5 Leu Val His Asp Phe Gly Lys Thr Thr Pro Ala Glu Leu Asp Ala Ile  
 195 200 205  
 Gly Phe Phe Asn Ala Glu Glu Ile Gln Pro Asn Gly Asn Phe Met Ile  
 210 215 220  
 10 Asp Asp Lys Gly Leu Thr Tyr Cys Phe Asn Glu Tyr Gln Ile Ala Ala  
 225 230 235 240  
 Tyr Ala Arg Gly Ala Val Tyr Val Arg Leu Gly Tyr Asp Val Leu Ala  
 245 250 255  
 Pro Leu Leu Arg Asp Asp Ser Pro Leu Lys Arg Tyr Leu Pro  
 260 265 270

(2) INFORMATION FOR SEQ ID NO:513

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 267 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

(A) NAME/KEY: misc\_feature

(B) LOCATION 1...267

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:513

Met Arg Ser Val Leu Leu Leu Leu Phe Pro Leu Ser Leu Ile Thr Ala  
 1 5 10 15  
 Leu Gly Cys Ser Asn Asn Lys Ala Ala Glu Ser Lys Ser Val Ser Phe  
 20 25 30  
 40 Asp Ser Ala Tyr Leu Glu Arg Tyr Ile Pro Leu Arg Ala Asp Ile Asp  
 35 40 45  
 Thr Pro Ser Leu His Val Met Ile Ser Tyr Val Tyr Pro Ser Gly Asp  
 50 55 60  
 45 Asp Met Leu Thr Glu Ile Phe Asn Gly Leu Leu Phe Gly Asp Ser Leu  
 65 70 75 80  
 Met Asp Ser Ser Ser Pro Glu Asn Ala Met Glu Gly Tyr Ala Gln Met  
 85 90 95  
 Leu Gly Glu Asp Tyr Arg Ser Asn Asn Ala Glu Ala Asn Leu Gln Gly  
 100 105 110  
 50 Leu Pro Ser Asp Leu Leu Asp Tyr Ile Tyr Lys Gln Glu Asn Thr Ile  
 115 120 125  
 Ala Tyr Cys Asp Thr Gly Leu Ile Ser Thr Arg Ile Asn Thr Tyr Thr  
 130 135 140  
 55 Tyr Glu Gly Gly Ala His Thr Glu Asn Thr Val Arg Phe Ala Asn Ile  
 145 150 155 160  
 Leu Arg Thr Thr Gly Lys Val Leu Glu Glu Arg Asp Ile Phe Lys Ile  
 165 170 175  
 Asp Tyr Ala Glu Arg Leu Ser Ala Leu Ile Ile Gly Gln Leu Val His  
 180 185 190  
 60 Asp Phe Gly Lys Thr Thr Pro Ala Glu Leu Asp Ala Ile Gly Phe Phe  
 195 200 205  
 Asn Ala Glu Glu Ile Gln Pro Asn Gly Asn Phe Met Ile Asp Asp Lys  
 210 215 220  
 65 Gly Leu Thr Tyr Cys Phe Asn Glu Tyr Gln Ile Ala Ala Tyr Ala Arg  
 225 230 235 240  
 Gly Ala Val Tyr Val Arg Leu Gly Tyr Asp Val Leu Ala Pro Leu Leu  
 245 250 255  
 Arg Asp Asp Ser Pro Leu Lys Arg Tyr Leu Pro  
 260 265

(2) INFORMATION FOR SEQ ID NO:514

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 259 amino acids

(B) TYPE: amino acid

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(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

5 (iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Porphyromonas gingivalis

10 (ix) FEATURE:

(A) NAME/KEY: misc\_feature

(B) LOCATION 1...259

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:514

15 Met Lys Lys Thr Thr Leu Thr Gly Ser Ile Cys Ala Leu Leu Leu Phe  
1 5 10 15  
Leu Gly Leu Ser Ala Asn Ala Gln Ser Lys Leu Lys Ile Lys Ser Ile  
20 20 25 30  
Glu Ala Ala Thr Thr Phe Ser Ser Ala Thr Ala Gly Asn Gly Phe Gly  
35 40 45  
Gly Asn Ile Phe Gly Met Asp Met Ser Ile Arg Met Arg Val His His  
50 55 60  
Ser Ile Leu Pro Glu Gly Leu Asp Phe Ser Val Gly Ile His Glu Arg  
25 65 70 75 80  
Arg Ala His Trp Glu Glu Ala Gly Ser Pro Lys Leu Met Tyr Thr Asn  
85 90 95  
Val Pro Ser Ile Ile Gly Ile Val Glu Lys Val Ile Val Phe Glu Asp  
100 105 110  
30 Ala Glu Asp Phe Phe Asp Lys Lys Ala Leu Gly Arg Phe Leu Ile Ser  
115 120 125  
Leu Gly Ile Ser Tyr Thr Lys His Leu Gly Ala Tyr Trp Gly Trp Thr  
130 135 140  
Asn Asp Ala His Ile Leu Phe Ser Pro Ile Pro Lys Ser Lys Val His  
35 145 150 155 160  
Tyr Asp Thr Tyr Thr Arg Ala Gly Ser Asp Leu Val Leu Gln Ser Glu  
165 170 175  
Asp Val Ala Thr Val Ser Asn Gly Phe Ser Pro Gly Ile Gly Leu Lys  
180 185 190  
40 Ser Ser Ile Trp Trp Lys Met Pro Ile Lys Ser Lys Tyr Asp Phe Arg  
195 200 205  
Leu Gly Phe Ser Leu Gly Tyr Glu Tyr Leu Asn Leu Leu Tyr Pro Tyr  
210 215 220  
45 Arg Asn Phe Lys Leu Asp Gly Asn Lys Pro Leu Ser Ala Leu Ser Pro  
225 230 235 240  
Arg Met Asn His Ile Gly His Val Gly Phe Asn Phe Thr Val Gly Leu  
245 250 255  
Trp Thr Asn

50 (2) INFORMATION FOR SEQ ID NO:515

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1266 amino acids

55 (B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

60 (iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Porphyromonas gingivalis

65 (ix) FEATURE:

(A) NAME/KEY: misc\_feature

(B) LOCATION 1...1266

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:515

70 Met Gly Lys Tyr Lys Arg Ala Lys Tyr Arg Tyr Trp Leu Phe Pro Phe  
1 5 10 15  
Cys Ser Asp Tyr Tyr Thr Phe Glu Gly Val Thr Phe Leu Cys Ala Ser  
20 25 30  
75 Asp Asp Met Thr Thr Lys Lys Pro Gln Ala Ile Leu Asp Leu Glu Lys

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				35					40					45		
	Ala	Tyr	Asn	Ile	Glu	Ile	Pro	Asp	Leu	Ser	Ser	Gln	Glu	Gly	Ile	Ser
	50						55					60				
5	Trp	Ser	Val	Asn	Arg	Tyr	Phe	Lys	Gln	Asp	Ser	Ser	Gly	Ala	Val	Val
	65					70					75					80
	Glu	Leu	Cys	Leu	Arg	Glu	Cys	Gln	Ile	Glu	Ser	Met	Thr	Trp	Leu	Ile
					85					90					95	
10	Asp	Phe	Pro	Ala	Leu	Lys	Lys	Leu	Asp	Leu	Ser	Tyr	Asn	Gln	Ile	Ser
				100					105					110		
	Lys	Leu	Glu	Gly	Leu	Glu	Arg	Leu	Thr	Ser	Leu	Thr	Lys	Leu	Arg	Leu
			115					120					125			
15	Arg	Ser	Asn	Gln	Ile	Arg	Lys	Leu	Glu	Gly	Leu	Asp	Ser	Leu	Thr	Ser
							135					140				
	Leu	Thr	Lys	Leu	Ser	Leu	Ser	Asp	Asn	Gln	Ile	Ser	Lys	Leu	Glu	Gly
					150						155				160	
20	Leu	Glu	Arg	Leu	Thr	Ser	Leu	Ala	Glu	Leu	Tyr	Leu	Leu	Asp	Asn	Gln
					165					170					175	
	Ile	Ser	Lys	Leu	Glu	Gly	Leu	Glu	Arg	Leu	Thr	Ser	Leu	Ala	Thr	Leu
				180					185					190		
25	Glu	Leu	Ser	Gly	Asn	Gln	Ile	Arg	Lys	Leu	Glu	Gly	Leu	Glu	Arg	Leu
					195			200					205			
	Thr	Ser	Leu	Ala	Thr	Leu	Glu	Leu	Ser	Gly	Asn	Gln	Ile	Arg	Lys	Leu
							215					220				
30	Glu	Gly	Leu	Glu	Arg	Leu	Thr	Ser	Leu	Thr	Lys	Leu	Arg	Leu	Arg	Ser
						230					235				240	
	Asn	Gln	Ile	Ser	Lys	Leu	Glu	Gly	Leu	Glu	Arg	Leu	Thr	Ser	Leu	Ala
					245					250					255	
35	Thr	Leu	Glu	Leu	Ser	Gly	Asn	Gln	Ile	Arg	Lys	Leu	Glu	Gly	Leu	Glu
				260					265					270		
	Arg	Leu	Thr	Ser	Leu	Ala	Thr	Leu	Glu	Leu	Ser	Gly	Asn	Gln	Ile	Ser
							280					285				
40	Lys	Leu	Glu	Gly	Leu	Glu	Arg	Leu	Ser	Ser	Leu	Thr	Lys	Leu	Arg	Leu
							295					300				
	Arg	Ser	Asn	Gln	Ile	Ser	Lys	Leu	Glu	Gly	Leu	Glu	Arg	Leu	Thr	Ser
						310					315				320	
45	Leu	Thr	Lys	Leu	Ser	Leu	Ser	Asp	Asn	Gln	Ile	Ser	Lys	Leu	Glu	Gly
										330					335	
	Leu	Glu	Arg	Leu	Thr	Ser	Leu	Ala	Glu	Leu	Tyr	Leu	Leu	Asp	Asn	Gln
									345					350		
50	Ile	Arg	Lys	Leu	Glu	Gly	Leu	Glu	Arg	Leu	Thr	Ser	Leu	Thr	Lys	Leu
								360					365			
	Arg	Leu	Arg	Ser	Asn	Gln	Ile	Ser	Lys	Leu	Glu	Gly	Leu	Asp	Ser	Leu
							375					380				
55	Thr	Ser	Leu	Thr	Lys	Leu	Ser	Leu	Ser	Asp	Asn	Gln	Ile	Ser	Lys	Leu
											395				400	
	Glu	Gly	Leu	Glu	Arg	Leu	Thr	Ser	Leu	Ala	Glu	Leu	Tyr	Leu	Leu	Asp
										410				415		
60	Asn	Gln	Ile	Arg	Lys	Leu	Glu	Gly	Leu	Asp	Gly	Leu	Ala	Ser	Leu	Thr
										425				430		
	Arg	Leu	Ser	Leu	Arg	Arg	Asn	Gln	Ile	Ser	Lys	Leu	Glu	Gly	Leu	Asp
												445				
65	Arg	Leu	Lys	Val	Leu	Arg	Lys	Leu	Asp	Val	Ser	Gly	Asn	Asp	Ile	Gln
								455				460				
	Ser	Ile	Asp	Asp	Ile	Lys	Leu	Leu	Ala	Pro	Ile	Leu	Glu	Gln	Thr	Leu
							470				475				480	
70	Glu	Lys	Leu	Arg	Ile	His	Asp	Asn	Pro	Phe	Val	Ala	Ser	Ser	Gly	Leu
										490					495	
	Ile	Leu	Ser	Pro	Tyr	Asp	Asn	His	Leu	Pro	Glu	Ile	Lys	Ala	Leu	Leu
										505				510		
75	Glu	Lys	Glu	Lys	Glu	Lys	Gln	Lys	Lys	Thr	Ser	Val	Glu	Tyr	His	Pro
									520				525			
	Phe	Cys	Lys	Val	Met	Leu	Leu	Gly	Asn	His	Ser	Ser	Gly	Lys	Thr	Thr
									535				540			
80	Phe	Leu	Ser	Gln	Tyr	Asp	Thr	Asn	Tyr	Thr	Tyr	Gln	Lys	Asn	Thr	His
											555				560	
	Val	Leu	Ser	Ile	His	Arg	Ser	Asn	Asn	Pro	Asn	Ala	Ile	Phe	Tyr	Asp
										570					575	
85	Phe	Gly	Gly	Gln	Asp	Tyr	Tyr	His	Gly	Ile	Tyr	Gln	Ala	Phe	Phe	Thr
										585				590		
	Thr	Gln	Ser	Leu	Tyr	Leu	Leu	Phe	Trp	Asp	Ala	Lys	Lys	Asp	Arg	Asn
										600			605			
90	Phe	Val	Ser	Val	Asp	Asp	Lys	Glu	Tyr	Gln	Thr	Leu	Asn	Phe	Asn	Arg
								615				620				
	Pro	Tyr	Trp	Leu	Gly	Gln	Ile	Ala	Tyr	Ala	Cys	Asn	Arg	Cys	Met	Ser
											635				640	

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	Val	Gly	Gly	Asn	Pro	Asp	Gly	Lys	Asp	Thr	Pro	Gln	Thr	Thr	Asp	Asp
				645						650					655	
	Thr	Ile	Ile	Ile	Gln	Thr	His	Ala	Asp	Glu	Thr	Gly	Ala	Lys	Gln	Gln
				660					665					670		
5	Thr	Leu	Gly	Cys	Ala	Ala	Glu	Asn	Gly	Val	Leu	Glu	Glu	Ile	Tyr	Val
			675					680						685		
	Ser	Leu	Glu	Pro	Lys	Ala	Asn	Ser	Ala	Val	His	Ala	Leu	Asn	Tyr	Leu
			690				695					700				
10	Asn	Glu	Arg	Val	Arg	Glu	Val	Val	Ala	Ser	Arg	Ser	Lys	Ser	Ile	Gln
						710					715					720
	Ile	Thr	Glu	Lys	Asp	Lys	Gly	Leu	Tyr	Glu	Ala	Leu	Pro	Thr	Ile	Ala
						725					730				735	
	Gly	Asp	Asn	Lys	His	Ile	Pro	Ile	Ser	Leu	Glu	Ala	Leu	Ala	Ala	Gln
				740					745					750		
15	Leu	Asn	Lys	Gly	Arg	Ala	Glu	Asn	Asp	Leu	Tyr	Thr	Ile	Glu	Tyr	Leu
				755				760						765		
	Gln	Thr	Glu	Leu	Asn	Gln	Leu	Ser	Leu	Arg	Gly	Glu	Val	Leu	Tyr	Tyr
							775					780				
20	Arg	Glu	Asn	Glu	Lys	Leu	Asn	Asn	Tyr	Val	Trp	Leu	Asp	Pro	Ala	Ala
							790				795					800
	Phe	Val	Gln	Met	Ile	His	Gly	Glu	Ile	Leu	Gln	Lys	Asp	Asn	Ile	Asn
							805				810				815	
	Arg	Gly	Thr	Val	Pro	Lys	Asp	Ile	Phe	Glu	Cys	Lys	Leu	His	Asn	Leu
							820			825					830	
25	Ser	Ser	Gly	Ser	Ile	Phe	Glu	Glu	Asp	Gly	Gln	Asn	Gly	Asn	Met	Ile
				835				840					845			
	Leu	Gln	Leu	Leu	Leu	Glu	Glu	Leu	Ile	Val	Tyr	Glu	Asp	Lys	Asp	Cys
							855					860				
30	Tyr	Val	Ile	Pro	Gly	Tyr	Leu	Pro	Leu	His	Ser	Asp	Asp	Glu	Ala	Tyr
							870				875					880
	Lys	Trp	Leu	Thr	Leu	Gly	Phe	Glu	Arg	Pro	Asn	Phe	Val	Leu	Lys	Phe
							885			890					895	
	Glu	Arg	Phe	Ile	Pro	Phe	Gly	Leu	Ile	Asn	Gln	Ile	Ile	Ala	Tyr	Tyr
							900				905				910	
35	Gly	Arg	Glu	Glu	Gly	Ala	Leu	Lys	Arg	Tyr	Trp	Arg	Asp	Gln	Val	Ile
								920					925			
	Phe	Thr	Ala	Gly	Arg	Glu	Met	Asp	Arg	Gln	Thr	Leu	Glu	Gln	Glu	Glu
							935					940				
40	Glu	Lys	Glu	Gly	Leu	Pro	Lys	Thr	Asn	Ala	Glu	Asp	Tyr	Gln	Ile	Trp
							950				955					960
	Ile	Lys	Leu	Asp	Phe	Thr	Asp	Leu	Ala	Ile	Ser	Val	Phe	Ile	Lys	Glu
							965				970				975	
	Gln	Arg	Lys	Thr	Ser	Ala	Lys	Asp	Met	Gln	Arg	Lys	Glu	Ala	Thr	Ile
							980			985					990	
45	Leu	Ser	Asp	Met	Leu	Asp	Met	Tyr	Trp	Asn	Asn	Ile	Pro	Pro	Arg	Glu
								1000					1005			
	Gln	Ile	Gly	Asp	Lys	Asp	Thr	Glu	Gln	Thr	Arg	Ser	Thr	Ile	Arg	Glu
							1010					1020				
50	Thr	Asn	Arg	Lys	Lys	Arg	Pro	Ile	Gln	Asp	Leu	Tyr	Leu	Ser	Cys	Ala
							1030				1035					1040
	Gln	Ala	Asp	Lys	Asp	Leu	Thr	Glu	Ser	His	Tyr	Ile	His	Leu	Gly	Thr
							1045				1050				1055	
	Leu	Asp	Asp	Glu	Ser	Lys	Thr	Thr	Ala	Arg	Ile	Ala	Ala	Tyr	Pro	Leu
							1060			1065				1070		
55	Lys	Asn	Gly	Val	Ile	Asp	Lys	Glu	Arg	Val	Arg	Glu	Val	Ser	Thr	Arg
							1075			1080				1085		
	Pro	Tyr	Lys	His	Leu	Ser	Val	Asn	Lys	Asn	Leu	Ala	Thr	Ala	Lys	Gln
							1090			1095			1100			
	Ile	Phe	Ile	Ser	Tyr	Ser	Lys	Glu	Asp	Gln	Thr	Glu	Leu	Glu	Thr	Cys
							1110				1115					1120
60	Leu	Gln	Phe	Phe	Lys	Pro	Leu	Glu	Lys	Asn	Gly	Gln	Ile	Glu	Ile	Tyr
							1125				1130				1135	
	Tyr	Asp	Lys	Leu	Thr	Lys	Phe	Glu	Thr	Pro	Ile	His	Pro	Glu	Ile	Arg
							1140				1145				1150	
65	Lys	Arg	Ile	Val	Glu	Ala	Asp	Cys	Ile	Ile	Ala	Leu	Ile	Ser	Gln	Arg
							1155			1160				1165		
	Tyr	Leu	Ala	Thr	Asp	Tyr	Ile	Leu	Asp	His	Glu	Leu	Pro	Val	Phe	Arg
							1170			1175			1180			
70	Glu	Tyr	Asn	Lys	Thr	Ile	Val	Pro	Ile	Leu	Ile	Lys	Pro	Cys	Thr	Phe
							1185				1190					1200
	Glu	Asp	Asp	Glu	Phe	Leu	Arg	Glu	Lys	Tyr	Phe	Ala	Gln	Lys	Ala	Gln
							1205				1210				1215	
	Ile	Ile	Asn	Leu	Gly	Lys	Glu	Gly	Lys	Thr	Ile	Lys	Ala	Tyr	Asp	Ser
							1220				1225				1230	
75	Ile	Thr	Ala	Ser	Ala	His	Arg	Asp	Glu	Asn	Trp	Val	Ala	Val	Val	Arg

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1235 1240 1245  
 Glu Phe Lys Glu Lys Ile Leu Arg Ile Thr Lys Gln Glu Val Asn Thr  
 1250 1255 1260  
 Asp Glu  
 1265

5

(2) INFORMATION FOR SEQ ID NO:516

10

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1232 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

15

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

20

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...1232

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:516

Met Thr Thr Lys Lys Pro Gln Ala Ile Leu Asp Leu Glu Lys Ala Tyr  
 1 5 10 15  
 Asn Ile Glu Ile Pro Asp Leu Ser Ser Gln Glu Gly Ile Ser Trp Ser  
 20 25 30  
 Val Asn Arg Tyr Phe Lys Gln Asp Ser Ser Gly Ala Val Val Glu Leu  
 35 40 45  
 Cys Leu Arg Glu Cys Gln Ile Glu Ser Met Thr Trp Leu Ile Asp Phe  
 50 55 60  
 Pro Ala Leu Lys Lys Leu Asp Leu Ser Tyr Asn Gln Ile Ser Lys Leu  
 65 70 75 80  
 Glu Gly Leu Glu Arg Leu Thr Ser Leu Thr Lys Leu Arg Leu Arg Ser  
 85 90 95  
 Asn Gln Ile Arg Lys Leu Glu Gly Leu Asp Ser Leu Thr Ser Leu Thr  
 100 105 110  
 Lys Leu Ser Leu Ser Asp Asn Gln Ile Ser Lys Leu Glu Gly Leu Glu  
 115 120 125  
 Arg Leu Thr Ser Leu Ala Glu Leu Tyr Leu Leu Asp Asn Gln Ile Ser  
 130 135 140  
 Lys Leu Glu Gly Leu Glu Arg Leu Thr Ser Leu Ala Thr Leu Glu Leu  
 145 150 155 160  
 Ser Gly Asn Gln Ile Arg Lys Leu Glu Gly Leu Glu Arg Leu Thr Ser  
 165 170 175  
 Leu Ala Thr Leu Glu Leu Ser Gly Asn Gln Ile Arg Lys Leu Glu Gly  
 180 185 190  
 Leu Glu Arg Leu Thr Ser Leu Thr Lys Leu Arg Leu Arg Ser Asn Gln  
 195 200 205  
 Ile Ser Lys Leu Glu Gly Leu Glu Arg Leu Thr Ser Leu Ala Thr Leu  
 210 215 220  
 Glu Leu Ser Gly Asn Gln Ile Arg Lys Leu Glu Gly Leu Glu Arg Leu  
 225 230 235 240  
 Thr Ser Leu Ala Thr Leu Glu Leu Ser Gly Asn Gln Ile Ser Lys Leu  
 245 250 255  
 Glu Gly Leu Glu Arg Leu Ser Ser Leu Thr Lys Leu Arg Leu Arg Ser  
 260 265 270  
 Asn Gln Ile Ser Lys Leu Glu Gly Leu Glu Arg Leu Thr Ser Leu Thr  
 275 280 285  
 Lys Leu Ser Leu Ser Asp Asn Gln Ile Ser Lys Leu Glu Gly Leu Glu  
 290 295 300  
 Arg Leu Thr Ser Leu Ala Glu Leu Tyr Leu Leu Asp Asn Gln Ile Arg  
 305 310 315 320  
 Lys Leu Glu Gly Leu Glu Arg Leu Thr Ser Leu Thr Lys Leu Arg Leu  
 325 330 335  
 Arg Ser Asn Gln Ile Ser Lys Leu Glu Gly Leu Asp Ser Leu Thr Ser  
 340 345 350  
 Leu Thr Lys Leu Ser Leu Ser Asp Asn Gln Ile Ser Lys Leu Glu Gly  
 355 360 365  
 Leu Glu Arg Leu Thr Ser Leu Ala Glu Leu Tyr Leu Leu Asp Asn Gln  
 370 375 380  
 Ile Arg Lys Leu Glu Gly Leu Asp Gly Leu Ala Ser Leu Thr Arg Leu

75



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		385				390				395						400	
		Ser	Leu	Arg	Arg	Asn	Gln	Ile	Ser	Lys	Leu	Glu	Gly	Leu	Asp	Arg	Leu
						405					410					415	
5		Lys	Val	Leu	Arg	Lys	Leu	Asp	Val	Ser	Gly	Asn	Asp	Ile	Gln	Ser	Ile
					420					425					430		
		Asp	Asp	Ile	Lys	Leu	Leu	Ala	Pro	Ile	Leu	Glu	Gln	Thr	Leu	Glu	Lys
				435					440					445			
		Leu	Arg	Ile	His	Asp	Asn	Pro	Phe	Val	Ala	Ser	Ser	Gly	Leu	Ile	Leu
				450				455					460				
10		Ser	Pro	Tyr	Asp	Asn	His	Leu	Pro	Glu	Ile	Lys	Ala	Leu	Leu	Glu	Lys
						470						475					480
		Glu	Lys	Glu	Lys	Gln	Lys	Lys	Thr	Ser	Val	Glu	Tyr	His	Pro	Phe	Cys
					485						490					495	
15		Lys	Val	Met	Leu	Leu	Gly	Asn	His	Ser	Ser	Gly	Lys	Thr	Thr	Phe	Leu
					500					505					510		
		Ser	Gln	Tyr	Asp	Thr	Asn	Tyr	Thr	Tyr	Gln	Lys	Asn	Thr	His	Val	Leu
				515					520					525			
		Ser	Ile	His	Arg	Ser	Asn	Asn	Pro	Asn	Ala	Ile	Phe	Tyr	Asp	Phe	Gly
				530				535					540				
20		Gly	Gln	Asp	Tyr	Tyr	His	Gly	Ile	Tyr	Gln	Ala	Phe	Phe	Thr	Thr	Gln
						550						555					560
		Ser	Leu	Tyr	Leu	Leu	Phe	Trp	Asp	Ala	Lys	Lys	Asp	Arg	Asn	Phe	Val
					565						570					575	
25		Ser	Val	Asp	Asp	Lys	Glu	Tyr	Gln	Thr	Leu	Asn	Phe	Asn	Arg	Pro	Tyr
				580						585					590		
		Trp	Leu	Gly	Gln	Ile	Ala	Tyr	Ala	Cys	Asn	Arg	Cys	Met	Ser	Val	Gly
				595					600					605			
		Gly	Asn	Pro	Asp	Gly	Lys	Asp	Thr	Pro	Gln	Thr	Thr	Asp	Asp	Thr	Ile
				610				615					620				
30		Ile	Ile	Gln	Thr	His	Ala	Asp	Glu	Thr	Gly	Ala	Lys	Gln	Gln	Thr	Leu
						630						635					640
		Gly	Cys	Ala	Ala	Glu	Asn	Gly	Val	Leu	Glu	Glu	Ile	Tyr	Val	Ser	Leu
					645						650					655	
35		Glu	Pro	Lys	Ala	Asn	Ser	Ala	Val	His	Ala	Leu	Asn	Tyr	Leu	Asn	Glu
				660						665					670		
		Arg	Val	Arg	Glu	Val	Val	Ala	Ser	Arg	Ser	Lys	Ser	Ile	Gln	Ile	Thr
				675					680					685			
		Glu	Lys	Asp	Lys	Gly	Leu	Tyr	Glu	Ala	Leu	Pro	Thr	Ile	Ala	Gly	Asp
				690				695					700				
40		Asn	Lys	His	Ile	Pro	Ile	Ser	Leu	Glu	Ala	Leu	Ala	Ala	Gln	Leu	Asn
						710						715					720
		Lys	Gly	Arg	Ala	Glu	Asn	Asp	Leu	Tyr	Thr	Ile	Glu	Tyr	Leu	Gln	Thr
						725					730					735	
45		Glu	Leu	Asn	Gln	Leu	Ser	Leu	Arg	Gly	Glu	Val	Leu	Tyr	Tyr	Arg	Glu
					740					745					750		
		Asn	Glu	Lys	Leu	Asn	Asn	Tyr	Val	Trp	Leu	Asp	Pro	Ala	Ala	Phe	Val
				755					760					765			
		Gln	Met	Ile	His	Gly	Glu	Ile	Leu	Gln	Lys	Asp	Asn	Ile	Asn	Arg	Gly
				770				775					780				
50		Thr	Val	Pro	Lys	Asp	Ile	Phe	Glu	Cys	Lys	Leu	His	Asn	Leu	Ser	Ser
						790						795					800
		Gly	Ser	Ile	Phe	Glu	Glu	Asp	Gly	Gln	Asn	Gly	Asn	Met	Ile	Leu	Gln
						805					810					815	
55		Leu	Leu	Leu	Glu	Glu	Leu	Ile	Val	Tyr	Glu	Asp	Lys	Asp	Cys	Tyr	Val
					820					825					830		
		Ile	Pro	Gly	Tyr	Leu	Pro	Leu	His	Ser	Asp	Asp	Glu	Ala	Tyr	Lys	Trp
				835					840					845			
		Leu	Thr	Leu	Gly	Phe	Glu	Arg	Pro	Asn	Phe	Val	Leu	Lys	Phe	Glu	Arg
				850				855					860				
60		Phe	Ile	Pro	Phe	Gly	Leu	Ile	Asn	Gln	Ile	Ile	Ala	Tyr	Tyr	Gly	Arg
						870						875					880
		Glu	Glu	Gly	Ala	Leu	Lys	Arg	Tyr	Trp	Arg	Asp	Gln	Val	Ile	Phe	Thr
						885					890					895	
65		Ala	Gly	Arg	Glu	Met	Asp	Arg	Gln	Thr	Leu	Glu	Gln	Glu	Glu	Glu	Lys
					900					905						910	
		Glu	Gly	Leu	Pro	Lys	Thr	Asn	Ala	Glu	Asp	Tyr	Gln	Ile	Trp	Ile	Lys
				915					920					925			
		Leu	Asp	Phe	Thr	Asp	Leu	Ala	Ile	Ser	Val	Phe	Ile	Lys	Glu	Gln	Arg
				930				935					940				
70		Lys	Thr	Ser	Ala	Lys	Asp	Met	Gln	Arg	Lys	Glu	Ala	Thr	Ile	Leu	Ser
						950						955					960
		Asp	Met	Leu	Asp	Met	Tyr	Trp	Asn	Asn	Ile	Pro	Pro	Arg	Glu	Gln	Ile
						965					970					975	
75		Gly	Asp	Lys	Asp	Thr	Glu	Gln	Thr	Arg	Ser	Thr	Ile	Arg	Glu	Thr	Asn
					980					985					990		

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Arg Lys Lys Arg Pro Ile Gln Asp Leu Tyr Leu Ser Cys Ala Gln Ala  
 995 1000 1005  
 Asp Lys Asp Leu Thr Glu Ser His Tyr Ile His Leu Gly Thr Leu Asp  
 1010 1015 1020  
 5 Asp Glu Ser Lys Thr Thr Ala Arg Ile Ala Ala Tyr Pro Leu Lys Asn  
 1025 1030 1035 1040  
 Gly Val Ile Asp Lys Glu Arg Val Arg Glu Val Ser Thr Arg Pro Tyr  
 1045 1050 1055  
 10 Lys His Leu Ser Val Asn Lys Asn Leu Ala Thr Ala Lys Gln Ile Phe  
 1060 1065 1070  
 Ile Ser Tyr Ser Lys Glu Asp Gln Thr Glu Leu Glu Thr Cys Leu Gln  
 1075 1080 1085  
 Phe Phe Lys Pro Leu Glu Lys Asn Gly Gln Ile Glu Ile Tyr Tyr Asp  
 1090 1095 1100  
 15 Lys Leu Thr Lys Phe Glu Thr Pro Ile His Pro Glu Ile Arg Lys Arg  
 1105 1110 1115 1120  
 Ile Val Glu Ala Asp Cys Ile Ile Ala Leu Ile Ser Gln Arg Tyr Leu  
 1125 1130 1135  
 20 Ala Thr Asp Tyr Ile Leu Asp His Glu Leu Pro Val Phe Arg Glu Tyr  
 1140 1145 1150  
 Asn Lys Thr Ile Val Pro Ile Leu Ile Lys Pro Cys Thr Phe Glu Asp  
 1155 1160 1165  
 Asp Glu Phe Leu Arg Glu Lys Tyr Phe Ala Gln Lys Ala Gln Ile Ile  
 1170 1175 1180  
 25 Asn Leu Gly Lys Glu Gly Lys Thr Ile Lys Ala Tyr Asp Ser Ile Thr  
 1185 1190 1195 1200  
 Ala Ser Ala His Arg Asp Glu Asn Trp Val Ala Val Val Arg Glu Phe  
 1205 1210 1215  
 30 Lys Glu Lys Ile Leu Arg Ile Thr Lys Gln Glu Val Asn Thr Asp Glu  
 1220 1225 1230

## (2) INFORMATION FOR SEQ ID NO:517

- 35 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1175 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
 40 (ii) MOLECULE TYPE: protein  
 (iii) HYPOTHETICAL: YES  
 (vi) ORIGINAL SOURCE:  
 45 (A) ORGANISM: Porphyromonas gingivalis  
 (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...1175  
 50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:517

Met Thr Trp Leu Ile Asp Phe Pro Ala Leu Lys Lys Leu Asp Leu Ser  
 1 5 10 15  
 55 Tyr Asn Gln Ile Ser Lys Leu Glu Gly Leu Glu Arg Leu Thr Ser Leu  
 20 25 30  
 Thr Lys Leu Arg Leu Arg Ser Asn Gln Ile Arg Lys Leu Glu Gly Leu  
 35 40 45  
 Asp Ser Leu Thr Ser Leu Thr Lys Leu Ser Leu Ser Asp Asn Gln Ile  
 50 55 60  
 60 Ser Lys Leu Glu Gly Leu Glu Arg Leu Thr Ser Leu Ala Glu Leu Tyr  
 65 70 75 80  
 Leu Leu Asp Asn Gln Ile Ser Lys Leu Glu Gly Leu Glu Arg Leu Thr  
 85 90 95  
 65 Ser Leu Ala Thr Leu Glu Leu Ser Gly Asn Gln Ile Arg Lys Leu Glu  
 100 105 110  
 Gly Leu Glu Arg Leu Thr Ser Leu Ala Thr Leu Glu Leu Ser Gly Asn  
 115 120 125  
 Gln Ile Arg Lys Leu Glu Gly Leu Glu Arg Leu Thr Ser Leu Thr Lys  
 130 135 140  
 70 Leu Arg Leu Arg Ser Asn Gln Ile Ser Lys Leu Glu Gly Leu Glu Arg  
 145 150 155 160  
 Leu Thr Ser Leu Ala Thr Leu Glu Leu Ser Gly Asn Gln Ile Arg Lys  
 165 170 175  
 75 Leu Glu Gly Leu Glu Arg Leu Thr Ser Leu Ala Thr Leu Glu Leu Ser  
 180 185 190

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	Gly	Asn	Gln	Ile	Ser	Lys	Leu	Glu	Gly	Leu	Glu	Arg	Leu	Ser	Ser	Leu	
	Thr	Lys	195	Arg	Leu	Arg	Ser	200	Asn	Gln	Ile	Ser	Lys	205	Leu	Gly	Leu
	210	Arg	Leu	Thr	Ser	Leu	Thr	215	Lys	Leu	Ser	Leu	Ser	Asp	Asn	Gln	Ile
5	225	Ser	Lys	Leu	Glu	Gly	Leu	Glu	Arg	Leu	Thr	Ser	Leu	Ala	Glu	Leu	Tyr
						245					250				255		
10	Leu	Leu	Asp	Asn	Gln	Ile	Arg	Lys	Leu	Gly	Leu	Glu	Arg	Leu	Thr		
	Ser	Leu	Thr	Lys	Leu	Arg	Leu	Arg	Ser	Asn	Gln	Ile	Ser	Lys	Leu	Glu	
			275					280					285				
	Gly	Leu	Asp	Ser	Leu	Thr	Ser	Leu	Thr	Lys	Leu	Ser	Leu	Ser	Asp	Asn	
			290				295					300					
15	Gln	Ile	Ser	Lys	Leu	Glu	Gly	Leu	Glu	Arg	Leu	Thr	Ser	Leu	Ala	Glu	
	305	Leu	Tyr	Leu	Leu	Asp	Asn	Gln	Ile	Arg	Lys	Leu	Glu	Gly	Leu	Asp	Gly
						325					330				335		
20	Leu	Ala	Ser	Leu	Thr	Arg	Leu	Ser	Leu	Arg	Arg	Asn	Gln	Ile	Ser	Lys	
				340					345					350			
	Leu	Glu	Gly	Leu	Asp	Arg	Leu	Lys	Val	Leu	Arg	Lys	Leu	Asp	Val	Ser	
				355				360					365				
	Gly	Asn	Asp	Ile	Gln	Ser	Ile	Asp	Asp	Ile	Lys	Leu	Leu	Ala	Pro	Ile	
			370				375					380					
25	Leu	Glu	Gln	Thr	Leu	Glu	Lys	Leu	Arg	Ile	His	Asp	Asn	Pro	Phe	Val	
	385	Ala	Ser	Ser	Gly	Leu	Ile	Leu	Ser	Pro	Tyr	Asp	Asn	His	Leu	Pro	Glu
					405					410					415		
30	Ile	Lys	Ala	Leu	Leu	Glu	Lys	Glu	Lys	Glu	Lys	Gln	Lys	Lys	Thr	Ser	
				420				425						430			
	Val	Glu	Tyr	His	Pro	Phe	Cys	Lys	Val	Met	Leu	Leu	Gly	Asn	His	Ser	
			435					440					445				
	Ser	Gly	Lys	Thr	Thr	Phe	Leu	Ser	Gln	Tyr	Asp	Thr	Asn	Tyr	Thr	Tyr	
			450				455					460					
35	Gln	Lys	Asn	Thr	His	Val	Leu	Ser	Ile	His	Arg	Ser	Asn	Asn	Pro	Asn	
	465	Ala	Ile	Phe	Tyr	Asp	Phe	Gly	Gly	Gln	Asp	Tyr	Tyr	His	Gly	Ile	Tyr
					485					490					495		
40	Gln	Ala	Phe	Phe	Thr	Thr	Gln	Ser	Leu	Tyr	Leu	Leu	Phe	Trp	Asp	Ala	
				500					505					510			
	Lys	Lys	Asp	Arg	Asn	Phe	Val	Ser	Val	Asp	Asp	Lys	Glu	Tyr	Gln	Thr	
			515				520						525				
	Leu	Asn	Phe	Asn	Arg	Pro	Tyr	Trp	Leu	Gly	Gln	Ile	Ala	Tyr	Ala	Cys	
		530					535					540					
45	Asn	Arg	Cys	Met	Ser	Val	Gly	Gly	Asn	Pro	Asp	Gly	Lys	Asp	Thr	Pro	
	545	Gln	Thr	Thr	Asp	Asp	Thr	Ile	Ile	Ile	Gln	Thr	His	Ala	Asp	Glu	Thr
					565					570					575		
50	Gly	Ala	Lys	Gln	Thr	Leu	Gly	Cys	Ala	Ala	Glu	Asn	Gly	Val	Leu		
				580				585					590				
	Glu	Glu	Ile	Tyr	Val	Ser	Leu	Glu	Pro	Lys	Ala	Asn	Ser	Ala	Val	His	
		595					600						605				
	Ala	Leu	Asn	Tyr	Leu	Asn	Glu	Arg	Val	Arg	Glu	Val	Val	Ala	Ser	Arg	
		610					615					620					
55	Ser	Lys	Ser	Ile	Gln	Ile	Thr	Glu	Lys	Asp	Lys	Gly	Leu	Tyr	Glu	Ala	
	625	Leu	Pro	Thr	Ile	Ala	Gly	Asp	Asn	Lys	His	Ile	Pro	Ile	Ser	Leu	Glu
					645					650					655		
60	Ala	Leu	Ala	Ala	Gln	Leu	Asn	Lys	Gly	Arg	Ala	Glu	Asn	Asp	Leu	Tyr	
				660					665					670			
	Thr	Ile	Glu	Tyr	Leu	Gln	Thr	Glu	Leu	Asn	Gln	Leu	Ser	Leu	Arg	Gly	
			675					680					685				
	Glu	Val	Leu	Tyr	Tyr	Arg	Glu	Asn	Glu	Lys	Leu	Asn	Asn	Tyr	Val	Trp	
		690					695					700					
65	Leu	Asp	Pro	Ala	Ala	Phe	Val	Gln	Met	Ile	His	Gly	Glu	Ile	Leu	Gln	
	705	Lys	Asp	Asn	Ile	Asn	Arg	Gly	Thr	Val	Pro	Lys	Asp	Ile	Phe	Glu	Cys
					725					730					735		
70	Lys	Leu	His	Asn	Leu	Ser	Ser	Gly	Ser	Ile	Phe	Glu	Glu	Asp	Gly	Gln	
				740				745					750				
	Asn	Gly	Asn	Met	Ile	Leu	Gln	Leu	Leu	Glu	Glu	Leu	Ile	Val	Tyr		
			755				760					765					
	Glu	Asp	Lys	Asp	Cys	Tyr	Val	Ile	Pro	Gly	Tyr	Leu	Pro	Leu	His	Ser	
		770					775					780					
75	Asp	Asp	Glu	Ala	Tyr	Lys	Trp	Leu	Thr	Leu	Gly	Phe	Glu	Arg	Pro	Asn	

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785                      790                      795                      800  
 Phe Val Leu Lys Phe Glu Arg Phe Ile Pro Phe Gly Leu Ile Asn Gln  
                                  805                      810                      815  
 5    Ile Ile Ala Tyr Tyr Gly Arg Glu Glu Gly Ala Leu Lys Arg Tyr Trp  
                                  820                      825                      830  
 Arg Asp Gln Val Ile Phe Thr Ala Gly Arg Glu Met Asp Arg Gln Thr  
                                  835                      840                      845  
 Leu Glu Gln Glu Glu Glu Lys Glu Gly Leu Pro Lys Thr Asn Ala Glu  
                                  850                      855                      860  
 10    Asp Tyr Gln Ile Trp Ile Lys Leu Asp Phe Thr Asp Leu Ala Ile Ser  
                                  865                      870                      875                      880  
 Val Phe Ile Lys Glu Gln Arg Lys Thr Ser Ala Lys Asp Met Gln Arg  
                                  885                      890                      895  
 15    Lys Glu Ala Thr Ile Leu Ser Asp Met Leu Asp Met Tyr Trp Asn Asn  
                                  900                      905                      910  
 Ile Pro Pro Arg Glu Gln Ile Gly Asp Lys Asp Thr Glu Gln Thr Arg  
                                  915                      920                      925  
 Ser Thr Ile Arg Glu Thr Asn Arg Lys Lys Arg Pro Ile Gln Asp Leu  
                                  930                      935                      940  
 20    Tyr Leu Ser Cys Ala Gln Ala Asp Lys Asp Leu Thr Glu Ser His Tyr  
                                  945                      950                      955                      960  
 Ile His Leu Gly Thr Leu Asp Asp Glu Ser Lys Thr Thr Ala Arg Ile  
                                  965                      970                      975  
 25    Ala Ala Tyr Pro Leu Lys Asn Gly Val Ile Asp Lys Glu Arg Val Arg  
                                  980                      985                      990  
 Glu Val Ser Thr Arg Pro Tyr Lys His Leu Ser Val Asn Lys Asn Leu  
                                  995                      1000                      1005  
 Ala Thr Ala Lys Gln Ile Phe Ile Ser Tyr Ser Lys Glu Asp Gln Thr  
                                  1010                      1015                      1020  
 30    Glu Leu Glu Thr Cys Leu Gln Phe Phe Lys Pro Leu Glu Lys Asn Gly  
                                  1025                      1030                      1035                      1040  
 Gln Ile Glu Ile Tyr Tyr Asp Lys Leu Thr Lys Phe Glu Thr Pro Ile  
                                  1045                      1050                      1055  
 35    His Pro Glu Ile Arg Lys Arg Ile Val Glu Ala Asp Cys Ile Ile Ala  
                                  1060                      1065                      1070  
 Leu Ile Ser Gln Arg Tyr Leu Ala Thr Asp Tyr Ile Leu Asp His Glu  
                                  1075                      1080                      1085  
 Leu Pro Val Phe Arg Glu Tyr Asn Lys Thr Ile Val Pro Ile Leu Ile  
                                  1090                      1095                      1100  
 40    Lys Pro Cys Thr Phe Glu Asp Asp Glu Phe Leu Arg Glu Lys Tyr Phe  
                                  1105                      1110                      1115                      1120  
 Ala Gln Lys Ala Gln Ile Ile Asn Leu Gly Lys Glu Gly Lys Thr Ile  
                                  1125                      1130                      1135  
 45    Lys Ala Tyr Asp Ser Ile Thr Ala Ser Ala His Arg Asp Glu Asn Trp  
                                  1140                      1145                      1150  
 Val Ala Val Val Arg Glu Phe Lys Glu Lys Ile Leu Arg Ile Thr Lys  
                                  1155                      1160                      1165  
 Gln Glu Val Asn Thr Asp Glu  
                                  1170                      1175  
 50

(2) INFORMATION FOR SEQ ID NO:518

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 229 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
 (ii) MOLECULE TYPE: protein  
 (iii) HYPOTHETICAL: YES  
 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Porphyromonas gingivalis  
 (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...229

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:518

Met Met Lys Lys Ala Phe Val Phe Val Leu Leu Val Cys Leu Phe Ser  
 1                      5                      10                      15  
 Ser Phe Ser Ser Ser Ala Gln Thr Thr Thr Asn Ser Ser Arg Ser Tyr  
                                  20                      25                      30  
 75    Phe Thr Gly Arg Ile Glu Lys Val Ser Leu Asn Leu Gly Val Pro Pro

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35 40 45  
 Val Ser Thr Glu Val Trp Gly Met Thr His Asp Ala Asn Gly Leu Pro  
 50 55 60  
 5 Phe Glu Ile Pro Ile Ser Phe Ser Arg Phe Asn Ser Gln Gly Asp Ile  
 65 70 75 80  
 Ala Thr Thr Tyr Tyr Ile Ala Asn Ser Glu Ala Thr Leu Asn Glu Trp  
 85 90 95  
 Cys Asp Tyr Ala His Pro Gly Gly Ile Val Arg Val Glu Gly Arg Phe  
 100 105 110  
 10 Trp Lys Met Thr Tyr Asn Ile Pro Thr Tyr Asn Ala Val Cys Thr Arg  
 115 120 125  
 Ile Thr Phe Glu Asn Gln Glu Ile Glu Gly Thr Ile Val Leu Ile Pro  
 130 135 140  
 15 Lys Pro Lys Val Ser Leu Pro His Val Ser Glu Ser Val Pro Cys Ile  
 145 150 155 160  
 Arg Thr Glu Ala Gly Arg Glu Phe Ile Leu Cys Glu Glu Asp Asp Thr  
 165 170 175  
 Phe Val Ser His Asp Gly Asn Glu Val Thr Ile Gly Gly Lys Pro Phe  
 180 185 190  
 20 Leu Leu Asn Thr Asn Val Lys Ile Val Gly Asp Val Ser Gln Lys Tyr  
 195 200 205  
 Ala Val Gly Val Gly Glu Ile Arg Phe Leu Gln Ile Cys Ala Gln Thr  
 210 215 220  
 25 Val Ser Gln Gln Lys  
 225

(2) INFORMATION FOR SEQ ID NO:519

- 30 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 228 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
 35 (ii) MOLECULE TYPE: protein  
 (iii) HYPOTHETICAL: YES  
 (vi) ORIGINAL SOURCE:  
 40 (A) ORGANISM: Porphyromonas gingivalis  
 (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...228  
 45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:519

Met Lys Lys Ala Phe Val Phe Val Leu Leu Val Cys Leu Phe Ser Ser  
 1 5 10 15  
 50 Phe Ser Ser Ser Ala Gln Thr Thr Thr Asn Ser Ser Arg Ser Tyr Phe  
 20 25 30  
 Thr Gly Arg Ile Glu Lys Val Ser Leu Asn Leu Gly Val Pro Pro Val  
 35 40 45  
 Ser Thr Glu Val Trp Gly Met Thr His Asp Ala Asn Gly Leu Pro Phe  
 50 55 60  
 55 Glu Ile Pro Ile Ser Phe Ser Arg Phe Asn Ser Gln Gly Asp Ile Ala  
 65 70 75 80  
 Thr Thr Tyr Tyr Ile Ala Asn Ser Glu Ala Thr Leu Asn Glu Trp Cys  
 85 90 95  
 60 Asp Tyr Ala His Pro Gly Gly Ile Val Arg Val Glu Gly Arg Phe Trp  
 100 105 110  
 Lys Met Thr Tyr Asn Ile Pro Thr Tyr Asn Ala Val Cys Thr Arg Ile  
 115 120 125  
 Thr Phe Glu Asn Gln Glu Ile Glu Gly Thr Ile Val Leu Ile Pro Lys  
 130 135 140  
 65 Pro Lys Val Ser Leu Pro His Val Ser Glu Ser Val Pro Cys Ile Arg  
 145 150 155 160  
 Thr Glu Ala Gly Arg Glu Phe Ile Leu Cys Glu Glu Asp Asp Thr Phe  
 165 170 175  
 70 Val Ser His Asp Gly Asn Glu Val Thr Ile Gly Gly Lys Pro Phe Leu  
 180 185 190  
 Leu Asn Thr Asn Val Lys Ile Val Gly Asp Val Ser Gln Lys Tyr Ala  
 195 200 205  
 Val Gly Val Gly Glu Ile Arg Phe Leu Gln Ile Cys Ala Gln Thr Val  
 210 215 220  
 75 Ser Gln Gln Lys

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(2) INFORMATION FOR SEQ ID NO:520

5

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 540 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

10

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

15

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...540

20

(iii) SEQUENCE DESCRIPTION: SEQ ID NO:520

	Met	Lys	Thr	Lys	Val	Leu	Arg	Lys	Phe	Val	Val	Ala	Ala	Phe	Ala	Val
	1			5						10				15		
25	Ala	Thr	Leu	Cys	Pro	Leu	Ala	Gln	Ala	Gln	Thr	Met	Gly	Gly	Asp	Asp
			20						25					30		
	Val	Lys	Val	Val	Gln	Tyr	Asn	Gln	Glu	Lys	Leu	Val	Gln	Thr	Arg	Met
		35						40					45			
30	Ser	Val	Ala	Asp	Asn	Gly	Trp	Ile	Tyr	Val	Met	Thr	His	Ser	Gly	Tyr
	50				55					60						
	Asp	Thr	Gly	Asn	Ser	Asn	Val	Lys	Ile	Phe	Arg	Ser	Lys	Asp	Gln	Gly
	65				70					75					80	
	Ala	Thr	Tyr	Gln	Lys	Leu	Arg	Asp	Trp	Asp	Pro	Ser	Asp	Asp	Tyr	Gln
			85							90				95		
35	Phe	Gln	Asp	Phe	Asp	Ile	Val	Val	Thr	Gly	Lys	Asn	Glu	Ser	Asp	Ile
			100						105				110			
	Lys	Ile	Trp	Ser	Val	Glu	Leu	Met	Asn	Lys	Pro	Gly	Gly	Tyr	Lys	Ser
		115						120				125				
40	Arg	Val	Ala	Val	Phe	Ser	Arg	Asp	Ala	Asn	Ala	Gln	Asn	Ala	Lys	Leu
	130						135					140				
	Val	Tyr	Lys	Glu	Asp	Phe	Ser	Asn	Val	Gln	Leu	Tyr	Asp	Val	Asp	Ile
	145				150					155					160	
	Ala	Ser	Asn	Tyr	Arg	Ser	Pro	Ser	Ser	Leu	Asn	Asn	Gly	Gly	Asn	Pro
			165						170					175		
45	Phe	Ala	Leu	Ala	Phe	Ala	Tyr	Thr	Gly	Phe	Asn	Asn	Thr	His	Lys	Ile
		180							185					190		
	Ser	Phe	Val	Asp	Tyr	Val	Phe	Ser	Leu	Asn	Gly	Gly	Gln	Asn	Phe	Asn
		195					200					205				
50	Lys	Asn	Leu	Leu	Phe	Ser	Gln	Asp	Gly	Glu	Lys	Lys	Ile	Asp	Lys	Val
	210					215						220				
	Asp	Leu	Ser	Leu	Gly	Ser	Thr	Ser	Glu	Ser	Met	Gly	His	Asn	Ala	Trp
	225				230					235					240	
	Pro	Leu	Met	Gly	Val	Val	Phe	Glu	Met	Asn	Lys	Gln	Gly	Gly	Lys	Ser
			245							250					255	
55	Asp	Ile	Gly	Phe	Leu	Ser	Asn	Phe	Val	Asp	Asn	Asp	Pro	Glu	Phe	Gln
			260						265					270		
	Trp	Ser	Gly	Pro	Ile	Lys	Val	Ser	Glu	Ser	Asp	Met	Ser	Phe	Ser	Pro
		275						280				285				
60	Lys	Ile	Gln	Met	Leu	Leu	Asp	Glu	Asp	Asn	Asn	Thr	Ile	Asn	Gly	Glu
	290					295						300				
	Ser	Cys	His	Asn	Phe	Met	Ile	Thr	Tyr	Ser	Asp	Tyr	Asp	Ser	Glu	Tyr
	305				310					315					320	
	Ser	Asp	Trp	Asp	Ile	Arg	Tyr	Val	Tyr	Pro	Lys	Lys	Ser	Phe	Lys	Tyr
			325						330					335		
65	Glu	Lys	Gly	Lys	Thr	Pro	Thr	Met	Asp	Asp	Leu	Val	Glu	Ala	Phe	Leu
			340					345					350			
	Thr	Ala	Ser	Tyr	Gln	Ser	Glu	Thr	Asn	Ser	Gly	Leu	Gly	Tyr	Asp	Lys
		355					360					365				
70	Asn	Ala	Asn	His	Tyr	Leu	Ile	Thr	Tyr	Ala	Lys	Lys	Glu	Glu	Asn	Gly
	370					375						380				
	Thr	Asn	Thr	Leu	Lys	Tyr	Arg	Trp	Ala	Asn	Tyr	Asp	Lys	Ile	His	Asn
	385				390					395					400	
	Lys	Asp	Leu	Trp	Ser	Asp	Thr	Phe	Thr	Tyr	Thr	Ser	Ser	Ala	Asn	Ala
			405						410					415		
75	Leu	Tyr	Thr	Pro	Gln	Val	Asp	Ile	Asn	Pro	Thr	Lys	Gly	Leu	Val	Cys

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5 Trp Ser Trp Val Glu Tyr Leu Pro Gly Lys Arg Ile Val Trp Ser Asp  
 435 440 445  
 Thr Gln Trp Thr His Ala Asn Gly Val Glu Asp Ile Val Met Gln Glu  
 450 455 460  
 Gly Ser Met Lys Leu Tyr Pro Asn Pro Ala Gln Glu Tyr Ala Val Ile  
 465 470 475 480  
 Ser Leu Pro Thr Ala Ala Asn Cys Lys Ala Val Val Tyr Asp Met Gln  
 485 490 495  
 10 Gly Arg Val Val Ala Glu Ala Ser Phe Ser Gly Asn Glu Tyr Arg Leu  
 500 505 510  
 Asn Val Gln His Leu Ala Lys Gly Thr Tyr Ile Leu Lys Val Val Ser  
 515 520 525  
 15 Asp Thr Glu Arg Phe Val Glu Lys Leu Ile Val Glu  
 530 535 540

(2) INFORMATION FOR SEQ ID NO:521

20 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 771 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
  
 25 (ii) MOLECULE TYPE: protein  
 (iii) HYPOTHETICAL: YES  
  
 30 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Porphyromonas gingivalis  
  
 (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...771  
  
 35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:521

Met Leu Thr Ile Arg Asn Phe Leu Leu Phe Cys Cys Leu Ser Leu Ile  
 1 5 10 15  
 40 Ala Phe Ala Ala Asp Ala Gln Ser Ser Val Ser Ser Gly Arg Arg Leu  
 20 25 30  
 Thr Glu Tyr Val Asn Pro Phe Ile Gly Thr Ala Asn Tyr Gly Thr Thr  
 35 40 45  
 Asn Pro Gly Ala Val Leu Pro Asn Gly Leu Met Ser Val Thr Pro Phe  
 50 55 60  
 45 Asn Val Ser Gly Ser Thr Glu Asn Arg Phe Asp Lys Asp Ser Arg Trp  
 65 70 75 80  
 Trp Ser Ala Pro Tyr Ser Ala Asp Asn Ser Tyr Cys Ile Gly Phe Ser  
 85 90 95  
 50 His Val Asn Leu Ser Gly Val Gly Cys Pro Glu Leu Ser Gly Ile Leu  
 100 105 110  
 Leu Met Ala Thr Ser Gly Thr Phe Asp Pro Asp Tyr Cys Cys Tyr Gly  
 115 120 125  
 Ser Ser Leu Ser Arg Glu Tyr Ala Arg Pro Gly Glu Tyr Lys Ala Val  
 130 135 140  
 55 Leu Asp Lys Tyr Gly Ile Asp Ala Ala Val Thr Val Thr Glu Arg Thr  
 145 150 155 160  
 Ala Leu Thr Glu Phe Ala Phe Pro Glu Gly Glu Gly His Ile Leu Leu  
 165 170 175  
 60 Asn Leu Gly Gln Ala Leu Ser Asn Glu Ser Gly Ala Ser Val Arg Phe  
 180 185 190  
 Leu Asn Asp Ser Thr Val Val Gly Ser Arg Leu Met Gly Thr Phe Cys  
 195 200 205  
 Tyr Asn Pro Gln Ala Val Phe Arg Gln Tyr Phe Val Leu Gln Val Ser  
 210 215 220  
 65 Arg Arg Pro Ile Ser Ala Gly Tyr Trp Lys Lys Gln Pro Pro Met Thr  
 225 230 235 240  
 Val Glu Ala Gln Trp Asp Ser Thr Ala Gly Lys Tyr Lys Gln Tyr Asp  
 245 250 255  
 70 Gly Tyr Lys Arg Glu Met Ser Gly Asp Asp Ile Gly Val Arg Phe Ser  
 260 265 270  
 Phe Asn Cys Asp Gln Gly Glu Lys Ile Tyr Val Arg Ser Ala Val Ser  
 275 280 285  
 Phe Val Ser Glu Ala Asn Ala Leu Tyr Asn Leu Glu Ala Glu Gln Glu  
 290 295 300  
 75 Glu Val Phe Lys Ser Val Gly Asn Pro Ala Lys Ala Phe Ser Ala

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305          310          315          320
Ile Arg Ser Arg Ala Ile Glu Arg Trp Glu Glu Ala Leu Gly Thr Val
325
5  Glu Val Glu Gly Gly Thr Pro Asp Glu Lys Thr Ile Phe Tyr Thr Ala
340
Leu Tyr His Leu Leu Ile His Pro Asn Ile Leu Gln Asp Ala Asn Gly
355
Glu Tyr Pro Met Met Gly Ser Gly Lys Thr Gly Asn Thr Ala His Asp
370
10 Arg Tyr Thr Val Phe Ser Leu Trp Asp Thr Tyr Arg Asn Val His Pro
385
Leu Leu Cys Leu Leu Tyr Pro Glu Lys Gln Leu Asp Met Val Arg Thr
405
15 Leu Ile Asp Met Tyr Arg Glu Ser Gly Trp Leu Pro Arg Trp Glu Leu
420
Tyr Gly Gln Glu Thr Leu Thr Met Glu Gly Asp Pro Ser Leu Ile Val
435
Ile Asn Asp Thr Trp Gln Arg Gly Leu Arg Ala Phe Asp Thr Ala Thr
450
20 Ala Tyr Glu Ala Met Lys Lys Asn Ala Ser Ser Ala Gly Ala Thr His
465
Pro Ile Arg Pro Asp Asn Asp Asp Tyr Leu Thr Leu Gly Phe Val Pro
485
25 Leu Arg Glu Gln Tyr Asp Asn Ser Val Ser His Ala Leu Glu Tyr Tyr
500
Leu Ala Asp Trp Asn Leu Ser Arg Phe Ala His Ala Leu Gly His Lys
515
Glu Asp Ala Ala Leu Phe Gly Lys Arg Ser Leu Gly Tyr Arg His Tyr
530
30 Tyr Asn Lys Glu Tyr Gly Met Leu Cys Pro Leu Leu Pro Asp Gly Ser
545
Phe Leu Thr Pro Phe Asp Pro Lys Gln Gly Glu Asn Phe Glu Pro Asn
565
35 Pro Gly Phe His Glu Gly Ser Ala Tyr Asn Tyr Ala Phe Phe Val Pro
580
His Asp Ile Gln Gly Leu Ala Arg Leu Met Gly Gly Ala Lys Val Phe
595
Ser Glu Arg Leu Gln Lys Val Phe Asp Glu Gly Tyr Tyr Asp Pro Thr
610
40 Asn Glu Pro Asp Ile Ala Tyr Pro Tyr Leu Phe Ser Tyr Phe Pro Lys
625
Glu Ala Trp Arg Thr Gln Lys Leu Thr Arg Glu Leu Ile Asp Lys His
645
45 Phe Cys Asn Ala Pro Asn Gly Leu Pro Gly Asn Asp Asp Ala Gly Thr
660
Met Ser Ala Trp Leu Val Tyr Ser Met Leu Gly Phe Tyr Pro Asp Cys
675
Pro Gly Ser Pro Thr Tyr Thr Leu Thr Ser Pro Val Phe Pro Arg Val
690
50 Arg Ile Arg Leu Asn Pro Gln Tyr Tyr Pro Gln Gly Glu Leu Ile Ile
705
Thr Thr Asn Thr Glu Asn Gln Pro Thr Asp Ser Ile Tyr Ile His Thr
725
55 Val Ser Leu Gly Asn Lys Thr Leu Pro His Gly Thr Arg His Ile Ser
740
His Ala Asp Leu Val Arg Cys Gly His Leu Arg Tyr Glu Leu Ser Asn
755
Arg Pro Arg
770

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(2) INFORMATION FOR SEQ ID NO:522

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 776 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: Porphyromonas gingivalis
- (ix) FEATURE:



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(A) NAME/KEY: misc\_feature  
(B) LOCATION 1...776

(iii) SEQUENCE DESCRIPTION: SEQ ID NO:522

5 Met Cys Lys Ile Arg Phe Ser Leu Leu Gln Ala Leu Val Val Cys Leu  
1 5 10 15  
Leu Phe Thr Ser Phe Ser Leu Gln Ala Gln Glu Glu Gly Ile Trp Asn  
20 25 30  
10 Thr Leu Leu Ala Ile His Lys Thr Glu Lys Ala Val Glu Thr Pro Lys  
35 40 45  
Lys Val Phe Ala Val Ala Asn Gly Val Leu Tyr Ser Val Gly Lys Glu  
50 55 60  
15 Ala Pro His Glu Ala Lys Ile Phe Asp Arg Ile Ser Gly Leu Ser Asp  
65 70 75 80  
Thr Ser Val Ser Ser Ile Ala Tyr Ser Glu Gln Leu Lys Ser Leu Val  
85 90 95  
Ile Tyr Tyr Ala Ser Gly Asn Ile Asp Ile Leu Asp Glu Ala Gly Arg  
100 105 110  
20 Val Thr Asn Val Pro Ala Leu Lys Asp Asn Ile Asp Leu Ile Asp Lys  
115 120 125  
Thr Leu Asn Arg Leu Leu Ile Val Gly Asn Arg Ala Tyr Leu Ala Gly  
130 135 140  
25 Gly Phe Gly Leu Ser Val Leu Asp Val Ala Glu Ala Arg Ile Pro Ala  
145 150 155 160  
Thr Tyr Ala Lys Gly Thr Lys Val Thr Asp Val Ala Lys Leu Asp Asn  
165 170 175  
Asp Arg Leu Leu Met Leu Lys Glu Gly Gln Leu Phe Ile Gly Lys Glu  
180 185 190  
30 Thr Asp Asn Leu Gln Asp Pro Ala Ala Trp Thr Ala Leu Ser Leu Asn  
195 200 205  
Leu Pro Met Gly Ser Val Thr Gly Leu Gly Ile Val Gly Glu Asp Ile  
210 215 220  
35 Cys Phe Leu Leu Ala Asp Gly Arg Val Tyr Val Ala Ala Asn Gln Ser  
225 230 235 240  
Phe Glu Pro Glu Leu Leu Leu Ser Ser Ser Ala Asp Ser Arg Leu Tyr  
245 250 255  
Val Thr Asp Arg Gly Leu Phe Ile Cys Ala Glu Asn Arg Ile Tyr Phe  
260 265 270  
40 Ile Glu Lys Gly Arg Lys Thr Thr Gln Phe Pro Ile Ala Asp Val Leu  
275 280 285  
Gly Val Gly Ala Met Asn Glu Ser Asn Thr Ala Tyr Ile Ala Leu Gly  
290 295 300  
45 Glu Glu Gly Leu Ala Ser Leu Leu Ala Glu Gly Ser Thr Ala Glu  
305 310 315 320  
Ala Met Pro Val Ala Phe Asp Gly Pro Gly Asp Asn Asp Phe Tyr Glu  
325 330 335  
Met Arg Phe Ser His Gly Arg Leu Tyr Ala Ala Ser Gly Leu Trp Gly  
340 345 350  
50 Thr Asn Leu Met Gly His Ala Gly Met Val Lys Leu Tyr Asp Gly Asn  
355 360 365  
Arg Trp Thr Asn Phe Asp Lys Lys Thr Val Gln Glu Gln Leu Gly Gly  
370 375 380  
55 Gly Phe Ser Phe Asn Asp Ala Ile Asp Ile Ala Val Ser Asn Gly Asp  
385 390 395 400  
Pro Asp His Phe Phe Val Gly Thr Trp Gly Asn Gly Leu Phe Glu Phe  
405 410 415  
Lys Asp Gly Lys Ala Ile Ala Arg Tyr Ser Gly Asn Glu Thr Ala Ile  
420 425 430  
60 Ala Glu Cys Asn Pro Gly Asp Ala Arg Val Lys Ala Ile Ala Phe Asp  
435 440 445  
Asn Lys Gly Asn Leu Trp Gly Thr Leu Gly Ala Val Gly Lys Asn Ile  
450 455 460  
65 Phe Met Tyr Asp Pro Gln Ser Ser Thr Trp His Ser Phe Ser Tyr Pro  
465 470 475 480  
Asp Val Ala Asn Leu Ala Ser Phe Gly Asn Met Ile Ile Leu Pro Asn  
485 490 495  
Gly Asp Lys Trp Val Asn Ile Leu His Arg Ser Gly Gly Ser Thr Arg  
500 505 510  
70 Lys Gly Val Leu Ile Phe Asn Asp Arg Gly Thr Pro Glu Thr Thr Ser  
515 520 525  
Asp Asp Ser His Leu Tyr Val Glu Gln Phe Val Asn Arg Leu Gly Ala  
530 535 540  
75 Ala Ile Gly His Lys Thr Ile Tyr Ala Met Ala Val Asp His Asn Gly  
545 550 555 560

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Ser Val Trp Met Gly Ser Asp Ile Gly Ile Phe Gly Val Tyr Asn Ala  
 565 570 575  
 Ala Gly Val Leu Ser Ser Thr Ser Thr Pro Ile Ala Val Arg Pro Val  
 580 585 590  
 5 Gly Gly Glu Glu Pro Asn Leu Tyr Tyr Val Leu Asp Lys Val Thr Val  
 595 600 605  
 Thr Asp Ile Val Val Asp Lys Leu Asn His Lys Trp Val Ala Thr Gln  
 610 615 620  
 10 Gly Thr Gly Leu Tyr Leu Leu Ser Glu Asp Cys Ser Lys Ile Leu Ala  
 625 630 635 640  
 Gln Phe Thr Val Glu Asn Ser Pro Leu Leu Ser Asn Asn Ile Leu Ser  
 645 650 655  
 Leu Ala Leu Asn Asp Asp Asn Gly Leu Leu Tyr Ile Gly Thr Ala Asp  
 660 665 670  
 15 Gly Leu Met Thr Phe Gln Thr Gly Thr Gly Ser Gly Ser Ala Ser Glu  
 675 680 685  
 Leu Asp Gly Val Tyr Val Tyr Pro Asn Pro Leu Arg Pro Glu Tyr Pro  
 690 695 700  
 20 Asp Gly Val Thr Ile Ala Gly Leu Gln Ala Gly Cys Ser Val Lys Ile  
 705 710 715 720  
 Thr Asp Thr Thr Gly Arg Leu Leu Tyr Gln Thr Glu Ser Val Thr Thr  
 725 730 735  
 Glu Val Lys Trp Asn Ala Arg Gly Ala Asp Gly Asn Arg Val Ala Ser  
 740 745 750  
 25 Gly Val Tyr Ala Val Ala Val Tyr Asp Pro Val Ser Lys Lys Ser Lys  
 755 760 765  
 Leu Ile Arg Phe Ala Val Ile Arg  
 770 775  
 30 (2) INFORMATION FOR SEQ ID NO:523  
 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1158 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
 35 (ii) MOLECULE TYPE: protein  
 (iii) HYPOTHETICAL: YES  
 40 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Porphyromonas gingivalis  
 (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...1158  
 45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:523  
 50 Met Lys Arg Ile Leu Pro Ile Val Ala Phe Leu Ser Leu Phe Leu Ala  
 1 5 10 15  
 Leu Ala Leu Pro Ala Lys Ala Gln Arg Ala Met Gly Lys Thr Ala Asp  
 20 25 30  
 55 Arg Ser Leu Met Ala Ser Gly His Trp Val Lys Ile Arg Val Asp Ala  
 35 40 45  
 Ser Gly Val Tyr Arg Leu Thr Asp Glu Gln Leu Arg Ala Asn Gly Phe  
 50 55 60  
 Ser Asp Pro Ser Lys Val Gly Val Phe Gly Tyr Gly Gly Gly Val Leu  
 65 70 75 80  
 60 Pro Glu Asp Leu Ser Arg Ile Thr Thr Asp Asp Leu Pro Pro Val Pro  
 85 90 95  
 Val Leu Arg Gln Gly Asn Ala Leu Tyr Phe Tyr Ala Val Gly Pro Val  
 100 105 110  
 65 Thr Trp Phe Tyr Asn Pro Ala Lys Thr Thr Met Glu His Thr Val Asn  
 115 120 125  
 Thr Tyr Ser Thr His Gly Tyr Tyr Phe Leu Ser Asp Ala Ala Gly Ala  
 130 135 140  
 Pro Leu Gln Met Ser Gln Tyr Thr Gly Gly Gly Ala Ser Ala Glu Ala  
 145 150 155 160  
 70 Leu Ile Asp Tyr Tyr Asp Glu Leu Met Leu His Glu Gln Glu Leu Tyr  
 165 170 175  
 Ser Pro Lys Glu Ser Gly Arg Asp Leu Tyr Gly Glu Ser Phe Ser Ala  
 180 185 190  
 75 Val Asn Thr Arg Thr Val Lys Phe Pro Leu Arg Gly Asn Thr Arg Ser  
 195 200 205

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	Ser	Gly	Glu	Leu	Gly	Thr	Val	Phe	Ser	Tyr	Ile	Ala	Lys	Ala	Arg	Ser
	210						215					220				
	Ala	Gly	Gly	Gly	Arg	Glu	Met	Ser	Leu	Ser	Ala	Asn	Gly	Ile	Leu	Ile
	225					230					235					240
5	Phe	Ser	Asp	Pro	Phe	Ser	Met	Thr	Ser	Asn	Glu	Val	Ser	Asn	Ser	Tyr
					245					250					255	
	Leu	Ala	Gly	Lys	Lys	Arg	Arg	Leu	Tyr	His	Ser	Thr	Pro	Met	Asn	Ser
				260					265					270		
10	Leu	Val	Asn	Glu	Leu	Arg	Leu	Asp	Ala	Asn	Tyr	Ser	Met	Thr	Gly	Asp
			275					280					285			
	Ala	Val	Asn	Leu	Asp	Phe	Ile	Glu	Val	Ala	Thr	Gln	Asn	Asp	Leu	Arg
		290					295					300				
	Tyr	Asp	Gly	Ala	Pro	Met	His	Ile	Arg	Arg	Phe	Ser	Asn	Leu	Pro	Val
	305					310					315					320
15	Leu	Gly	Gly	Glu	Ser	Cys	Arg	Phe	Val	Ile	Ser	Glu	Val	Pro	Glu	Ser
					325					330					335	
	Leu	Val	Val	Leu	Gln	Ala	Asn	Ser	Ser	Leu	Thr	Ala	Ser	Leu	Val	Pro
				340					345					350		
20	Val	Lys	Thr	Val	Gly	Asp	Lys	Thr	Ile	Glu	Phe	Val	Ala	Pro	Pro	Lys
		355						360					365			
	Gly	Gln	Asp	Arg	Arg	Thr	Ile	Asn	Thr	Phe	Tyr	Ala	Val	Asp	Leu	Ser
		370					375					380				
	Gln	Ala	Ser	Ala	Pro	Glu	Ile	Leu	Gly	Ala	Val	Pro	Asn	Gln	Asn	Leu
	385					390					395					400
25	His	Gly	Glu	Glu	Ile	Pro	Asp	Leu	Ile	Ile	Val	Ser	Thr	Gln	Ala	Leu
					405					410					415	
	Leu	Leu	Glu	Ala	Asp	Arg	Leu	Ala	Thr	Tyr	Arg	Arg	Glu	Lys	Asn	Gly
				420					425					430		
30	Leu	Lys	Val	Leu	Val	Val	Leu	Gln	Glu	Gln	Val	Phe	Asn	Glu	Phe	Ser
			435					440					445			
	Gly	Gly	Thr	Pro	Asp	Ala	Thr	Ala	Tyr	Arg	Leu	Phe	Ala	Lys	Met	Phe
		450					455					460				
	Tyr	Asp	Arg	Trp	Lys	Ala	Asn	Ala	Pro	Val	Gly	Glu	Thr	Phe	Pro	Met
	465					470					475					480
35	Gln	Met	Leu	Leu	Phe	Gly	Asp	Gly	Ala	His	Asp	Asn	Arg	Lys	Val	Ser
					485					490					495	
	Val	Ala	Trp	Gln	Lys	Pro	Tyr	Leu	Gln	Gln	Thr	Glu	Phe	Leu	Leu	Thr
				500					505					510		
40	Phe	Gln	Ala	Val	Asn	Ser	Thr	Asn	Val	Asn	Ser	Tyr	Val	Thr	Asp	Asp
			515					520					525			
	Tyr	Phe	Gly	Leu	Leu	Asp	Asp	Gln	Pro	Ala	Ser	Val	Asn	Ile	Gly	Trp
		530					535					540				
	Arg	Asn	Tyr	Asn	Met	Ala	Val	Gly	Arg	Phe	Pro	Val	Arg	Thr	Pro	Ala
	545					550					555					560
45	Glu	Ala	Arg	Ile	Ala	Val	Asp	Lys	Thr	Ile	Arg	Tyr	Glu	Glu	Asp	Arg
					565					570					575	
	Glu	Ser	Gly	Ala	Trp	Arg	Ile	Arg	Ala	Cys	Phe	Ala	Ala	Asp	Asn	Gly
				580					585					590		
50	Asp	Lys	His	Ala	Thr	Glu	Thr	Ser	Arg	Leu	Ile	Asp	Thr	Val	Lys	Arg
			595					600					605			
	Tyr	Ala	Pro	Ala	Ile	Met	Pro	Val	Arg	Ala	Phe	Gln	Asp	Val	Tyr	Pro
		610				615					620					
	His	Val	Ile	Glu	Asn	Gly	Leu	His	Ser	Ile	Pro	Gly	Ala	Lys	Lys	Lys
	625					630					635					640
55	Met	Leu	Glu	Thr	Leu	Gln	Ser	Gly	Ile	Ile	Leu	Leu	Asn	Tyr	Ala	Gly
					645					650					655	
	His	Gly	Gly	Pro	Ala	Gly	Trp	Ser	Asp	Glu	His	Leu	Leu	Thr	Leu	Asn
				660					665					670		
60	Asp	Ile	His	Lys	Phe	Asn	Tyr	Lys	His	Met	Pro	Ile	Trp	Ile	Thr	Ala
			675					680					685			
	Thr	Cys	Asp	Phe	Ala	Asn	Tyr	Asp	Ser	Gln	Thr	Thr	Ser	Ala	Gly	Glu
		690					695					700				
	Glu	Val	Phe	Leu	His	Glu	Lys	Ser	Gly	Thr	Pro	Ile	Met	Phe	Ser	Thr
	705					710					715					720
65	Thr	Arg	Val	Val	Tyr	Asn	Thr	Gln	Asn	Glu	Lys	Ile	Asn	Gly	Phe	Met
					725					730					735	
	Leu	Arg	Arg	Met	Phe	Glu	Lys	Ala	Lys	Asp	Gly	Arg	Tyr	Arg	Thr	Met
				740					745					750		
70	Gly	Glu	Ile	Ile	Arg	Ser	Ala	Lys	Gln	Gly	Met	Leu	Ser	Thr	Val	Phe
				755				760					765			
	Pro	Asp	Ser	Ile	Asn	Gln	Leu	Ser	Phe	Phe	Leu	Met	Gly	Asp	Pro	Ser
		770					775					780				
	Val	Arg	Met	Asn	Leu	Pro	Thr	His	Lys	Val	Gln	Leu	Thr	Ala	Ile	Asn
					785						795					800
75	Gly	Gln	Asp	Pro	Glu	Gly	Gln	Tyr	Gly	Thr	Ile	Met	Leu	Lys	Ser	Leu

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		65				70				75						80	
		Ser	Gln	Tyr	Thr	Asp 85	Ala	Met	Leu	Tyr	His 90	Gln	Lys	Gly	Leu	Asn 95	Ala
5		Ala	Leu	Asn	Leu	Arg	Asp	Thr	Ile	Val 105	Ala	Ala	Gln	Ala	Trp	Asn	His
		Leu	Gly	Thr	Asp	Ser	Arg	Arg	Ile	Gly	Ala	Leu	Ala	Glu	Ala	Ser	Asp
		Tyr	His	Tyr	Lys	Ala	Leu	Ser	Leu	Ile	Glu	Ser	Phe	Ser	Gly	Asn	Gln
		Asn	Arg	Pro	Ala	Ile	Lys	Ala	Arg	Ser	Ala	Ala	Leu	Asn	Gly	Ile	Gly
10		Asn	Ile	Asn	Leu	Glu 165	Leu	Gly	Tyr	His	Asp 170	Glu	Ala	Glu	Lys	Asn	Phe
		Leu	Lys	Ala	Leu	Gln	Gly	Glu	Lys	Glu	Leu	Asp	Ser	Pro	Leu	Gly	Gln
		Ala	Ile	Asn	Tyr	Ala	Asn	Leu	Gly	Arg	Ile	Tyr	Arg	Gln	Arg	Lys	Glu
		Tyr	Asp	Lys	Ala	Arg	Thr	Tyr	Phe	Leu	Leu	Ser	Leu	Glu	Gln	Asn	Asn
15		Met	Ala	Glu	Asn	Leu	Met	Gly	Ile	Gly	Leu	Cys	Ser	Ile	Asn	Leu	Gly
		Glu	Val	Asp	Glu	Glu	Lys	Gly	Asp	Tyr	Gln	Lys	Ala	Leu	Gln	Glu	Tyr
		Ala	Thr	Ala	Tyr	Lys	Leu	Met	Glu	Gln	Leu	Ser	Asp	Arg	Trp	His	Trp
		Leu	Asn	Ser	Cys	Ile	Pro	Met	Ala	Arg	Ile	Asn	Leu	Lys	Gln	Gly	Asn
20		Glu	Arg	Leu	Tyr	Gln	His	Phe	Ile	Ser	Leu	Ala	Glu	Gly	Thr	Ala	Lys
		Glu	Ile	Asn	Ser	Thr	Ser	His	Leu	Ile	Glu	Ile	Tyr	Asn	Leu	Gln	Tyr
		Glu	Asn	Leu	Glu	Arg	Lys	Lys	Glu	Tyr	Lys	Gln	Ala	Leu	Glu	Ala	Phe
		Cys	Leu	Ser	Lys	Thr	Leu	Ser	Asp	Ser	Met	Ser	Ile	Ala	His	Lys	Val
25		Ser	Ser	Ile	Gln	Glu	Thr	Arg	Phe	Asn	Tyr	Glu	Arg	Asn	Lys	Ser	Gln
		Lys	Glu	Leu	Glu	Glu	Ile	Gln	Gln	Val	Ser	Lys	Ala	Lys	Gln	Glu	Lys
		Ser	Lys	Phe	Ile	Leu	Leu	Ser	Thr	Leu	Phe	Ala	Leu	Phe	Ile	Ser	Ile
		Leu	Leu	Ile	Ser	Val	Leu	Thr	Tyr	Ala	Tyr	Arg	Gln	Gly	Lys	Lys	His
30		Asn	Lys	Leu	Ile	Lys	Glu	Thr	Asp	Lys	Leu	Arg	Ser	Gly	Phe	Phe	Thr
		Gly	Ile	Thr	His	Glu	Phe	Arg	Thr	Pro	Ile	Thr	Val	Ile	Gln	Gly	Leu
		Asn	Glu	Lys	Met	Ser	Ser	Ser	Pro	Asp	Leu	Gln	Ala	Ser	Asp	Arg	Thr
		Glu	Leu	His	Lys	Ile	Ile	Asp	Arg	Gln	Ser	Ser	His	Met	Leu	Asn	Leu
35		Val	Asn	Gln	Leu	Leu	Asp	Ile	Cys	Lys	Ile	Arg	Ser	Gly	Val	Ser	Thr
		Pro	Glu	Trp	Arg	Asn	Gly	Asp	Ile	Val	Ser	Phe	Val	Gln	Ile	Leu	Ile
		Asp	Ser	Phe	Ala	Pro	Tyr	Ala	Gln	Ala	Gln	Asp	Ile	Thr	Leu	Glu	Leu
		Gln	Pro	Glu	Ser	Lys	Pro	Ile	Val	Val	Asp	Phe	Val	Pro	Ser	Tyr	Leu
40		Gln	Lys	Ile	Ile	Ser	Asn	Leu	Leu	Ser	Asn	Ala	Ile	Lys	Tyr	Ser	Leu
		Ala	Gly	Gly	Arg	Val	Val	Ile	Ser	Leu	Ala	Lys	Thr	Lys	Asn	Glu	Lys
		Asn	Leu	Ile	Ile	Arg	Val	Ala	Asp	Asn	Gly	Ile	Gly	Ile	Asp	Lys	Thr
		Asp	Gln	Ala	His	Ile	Phe	Asp	Ile	Phe	Tyr	Arg	Gly	Gln	Ser	Ala	Thr
45		Glu	Lys	His	Gly	Ser	Gly	Val	Gly	Leu	Ser	Phe	Thr	Asn	Ile	Leu	Val
		Glu	Asn	Leu	Arg	Gly	Thr	Ile	Lys	Val	Glu	Ser	Gln	Pro	Gly	Lys	Gly
		Ser	Ala	Phe	Thr	Ile	Ser	Ile	Pro	Thr	Gln	Asn	Gln	Ser	Ser	Ser	Ala
		Glu	Ile	Leu	Pro	Trp	Leu	Pro	Ser	Ser	Asp	Asp	Ile	Val	Met	Pro	Val
50		Glu	Ile	Leu	Pro	Trp	Leu	Pro	Ser	Ser	Asp	Asp	Ile	Val	Met	Pro	Val
		Asp	Gln	Ala	His	Ile	Phe	Asp	Ile	Phe	Tyr	Arg	Gly	Gln	Ser	Ala	Thr
		Glu	Lys	His	Gly	Ser	Gly	Val	Gly	Leu	Ser	Phe	Thr	Asn	Ile	Leu	Val
		Glu	Asn	Leu	Arg	Gly	Thr	Ile	Lys	Val	Glu	Ser	Gln	Pro	Gly	Lys	Gly
55		Ser	Ala	Phe	Thr	Ile	Ser	Ile	Pro	Thr	Gln	Asn	Gln	Ser	Ser	Ser	Ala
		Glu	Ile	Leu	Pro	Trp	Leu	Pro	Ser	Ser	Asp	Asp	Ile	Val	Met	Pro	Val
		Asp	Gln	Ala	His	Ile	Phe	Asp	Ile	Phe	Tyr	Arg	Gly	Gln	Ser	Ala	Thr
		Glu	Lys	His	Gly	Ser	Gly	Val	Gly	Leu	Ser	Phe	Thr	Asn	Ile	Leu	Val
60		Glu	Asn	Leu	Arg	Gly	Thr	Ile	Lys	Val	Glu	Ser	Gln	Pro	Gly	Lys	Gly
		Ser	Ala	Phe	Thr	Ile	Ser	Ile	Pro	Thr	Gln	Asn	Gln	Ser	Ser	Ser	Ala
		Glu	Ile	Leu	Pro	Trp	Leu	Pro	Ser	Ser	Asp	Asp	Ile	Val	Met	Pro	Val
		Asp	Gln	Ala	His	Ile	Phe	Asp	Ile	Phe	Tyr	Arg	Gly	Gln	Ser	Ala	Thr
65		Glu	Lys	His	Gly	Ser	Gly	Val	Gly	Leu	Ser	Phe	Thr	Asn	Ile	Leu	Val
		Glu	Asn	Leu	Arg	Gly	Thr	Ile	Lys	Val	Glu	Ser	Gln	Pro	Gly	Lys	Gly
		Ser	Ala	Phe	Thr	Ile	Ser	Ile	Pro	Thr	Gln	Asn	Gln	Ser	Ser	Ser	Ala
		Glu	Ile	Leu	Pro	Trp	Leu	Pro	Ser	Ser	Asp	Asp	Ile	Val	Met	Pro	Val
70		Asp	Gln	Ala	His	Ile	Phe	Asp	Ile	Phe	Tyr	Arg	Gly	Gln	Ser	Ala	Thr
		Glu	Lys	His	Gly	Ser	Gly	Val	Gly	Leu	Ser	Phe	Thr	Asn	Ile	Leu	Val
		Glu	Asn	Leu	Arg	Gly	Thr	Ile	Lys	Val	Glu	Ser	Gln	Pro	Gly	Lys	Gly
		Ser	Ala	Phe	Thr	Ile	Ser	Ile	Pro	Thr	Gln	Asn	Gln	Ser	Ser	Ser	Ala
75		Glu	Ile	Leu	Pro	Trp	Leu	Pro	Ser	Ser	Asp	Asp	Ile	Val	Met	Pro	Val
		Asp	Gln	Ala	His	Ile	Phe	Asp	Ile	Phe	Tyr	Arg	Gly	Gln	Ser	Ala	Thr
		Glu	Lys	His	Gly	Ser	Gly	Val	Gly	Leu	Ser	Phe	Thr	Asn	Ile	Leu	Val
		Glu	Asn	Leu	Arg	Gly	Thr	Ile	Lys	Val	Glu	Ser	Gln	Pro	Gly	Lys	Gly
80		Ser	Ala	Phe	Thr	Ile	Ser	Ile	Pro	Thr	Gln	Asn	Gln	Ser	Ser	Ser	Ala
		Glu	Ile	Leu	Pro	Trp	Leu	Pro	Ser	Ser	Asp	Asp	Ile	Val	Met	Pro	Val
		Asp	Gln	Ala	His	Ile	Phe	Asp	Ile	Phe	Tyr	Arg	Gly	Gln	Ser	Ala	Thr
		Glu	Lys	His	Gly	Ser	Gly	Val	Gly	Leu	Ser	Phe	Thr	Asn	Ile	Leu	Val
85		Glu	Asn	Leu	Arg	Gly	Thr	Ile	Lys	Val	Glu	Ser	Gln	Pro	Gly	Lys	Gly
		Ser	Ala	Phe	Thr	Ile	Ser	Ile	Pro	Thr	Gln	Asn	Gln	Ser	Ser	Ser	Ala
		Glu	Ile	Leu	Pro	Trp	Leu	Pro	Ser	Ser	Asp	Asp	Ile	Val	Met	Pro	Val
		Asp	Gln	Ala	His	Ile	Phe	Asp	Ile	Phe	Tyr	Arg	Gly	Gln	Ser	Ala	Thr
90		Glu	Lys	His	Gly	Ser	Gly	Val	Gly	Leu	Ser	Phe	Thr	Asn	Ile	Leu	Val
		Glu	Asn	Leu	Arg	Gly	Thr	Ile	Lys	Val	Glu	Ser	Gln	Pro	Gly	Lys	Gly
		Ser	Ala	Phe	Thr	Ile	Ser	Ile	Pro	Thr	Gln	Asn	Gln	Ser	Ser	Ser	Ala
		Glu	Ile	Leu	Pro	Trp	Leu	Pro	Ser	Ser	Asp	Asp	Ile	Val	Met	Pro	Val
95		Asp	Gln	Ala	His	Ile	Phe	Asp	Ile	Phe	Tyr	Arg	Gly	Gln	Ser	Ala	Thr
		Glu	Lys	His	Gly	Ser	Gly	Val	Gly	Leu	Ser	Phe	Thr	Asn	Ile	Leu	Val
		Glu	Asn	Leu	Arg	Gly	Thr	Ile	Lys	Val	Glu	Ser	Gln	Pro	Gly	Lys	Gly
		Ser	Ala	Phe	Thr	Ile	Ser	Ile	Pro	Thr	Gln	Asn	Gln	Ser	Ser	Ser	Ala
100		Glu	Ile	Leu	Pro	Trp	Leu	Pro	Ser	Ser	Asp	Asp	Ile	Val	Met	Pro	Val
		Asp	Gln	Ala	His	Ile	Phe	Asp	Ile	Phe	Tyr	Arg	Gly	Gln	Ser	Ala	Thr
		Glu	Lys	His	Gly	Ser	Gly	Val	Gly	Leu	Ser	Phe	Thr	Asn	Ile	Leu	Val
		Glu	Asn	Leu	Arg	Gly	Thr	Ile	Lys	Val	Glu	Ser	Gln	Pro	Gly	Lys	Gly
105		Ser	Ala	Phe	Thr	Ile	Ser	Ile	Pro	Thr	Gln	Asn	Gln	Ser	Ser	Ser	Ala
		Glu	Ile	Leu	Pro	Trp	Leu	Pro	Ser	Ser	Asp	Asp	Ile	Val	Met	Pro	Val
		Asp	Gln	Ala	His	Ile	Phe	Asp	Ile	Phe	Tyr	Arg	Gly	Gln	Ser	Ala	Thr
		Glu	Lys	His	Gly	Ser	Gly	Val	Gly	Leu	Ser	Phe	Thr	Asn	Ile	Leu	Val
110		Glu	Asn	Leu	Arg	Gly	Thr	Ile	Lys	Val	Glu	Ser	Gln	Pro	Gly	Lys	Gly
		Ser	Ala	Phe	Thr	Ile	Ser	Ile	Pro	Thr	Gln	Asn	Gln	Ser	Ser	Ser	Ala
		Glu	Ile	Leu	Pro	Trp	Leu	Pro	Ser	Ser	Asp	Asp	Ile	Val	Met	Pro	Val
		Asp	Gln	Ala	His	Ile	Phe	Asp	Ile	Phe	Tyr	Arg	Gly	Gln	Ser	Ala	Thr
115		Glu	Lys	His	Gly	Ser	Gly	Val	Gly	Leu	Ser	Phe	Thr	Asn	Ile	Leu	Val
		Glu	Asn	Leu	Arg	Gly	Thr	Ile	Lys	Val	Glu	Ser	Gln	Pro	Gly	Lys	Gly
		Ser	Ala	Phe	Thr	Ile	Ser	Ile	Pro	Thr	Gln	Asn	Gln	Ser	Ser	Ser	Ala
		Glu	Ile	Leu	Pro	Trp	Leu	Pro	Ser	Ser	Asp	Asp	Ile	Val	Met	Pro	Val
120		Asp	Gln	Ala	His	Ile	Phe	Asp	Ile	Phe	Tyr	Arg	Gly	Gln	Ser	Ala	Thr
		Glu	Lys	His	Gly	Ser	Gly	Val	Gly	Leu	Ser	Phe	Thr	Asn	Ile	Leu	Val
		Glu	Asn	Leu	Arg	Gly	Thr	Ile	Lys	Val	Glu	Ser	Gln	Pro	Gly	Lys	Gly
		Ser	Ala	Phe	Thr	Ile	Ser	Ile	Pro	Thr	Gln	Asn	Gln	Ser	Ser	Ser	Ala
125		Glu	Ile	Leu	Pro	Trp	Leu	Pro	Ser	Ser	Asp	Asp	Ile	Val	Met	Pro	Val
		Asp	Gln	Ala	His	Ile	Phe	Asp	Ile	Phe	Tyr	Arg	Gly	Gln	Ser	Ala	Thr
		Glu	Lys	His	Gly	Ser	Gly	Val	Gly	Leu	Ser	Phe	Thr	Asn	Ile	Leu	Val
		Glu	Asn	Leu	Arg	Gly	Thr	Ile	Lys	Val	Glu	Ser	Gln	Pro	Gly	Lys	Gly
130		Ser	Ala	Phe	Thr	Ile	Ser	Ile	Pro	Thr	Gln	Asn	Gln	Ser	Ser	Ser	Ala
		Glu	Ile	Leu	Pro	Trp	Leu	Pro	Ser	Ser	Asp	Asp	Ile	Val	Met	Pro	Val
		Asp	Gln	Ala	His	Ile	Phe	Asp	Ile	Phe	Tyr	Arg	Gly	Gln	Ser	Ala	Thr
		Glu	Lys	His	Gly	Ser	Gly	Val	Gly	Leu	Ser	Phe	Thr	Asn	Ile	Leu	Val
135		Glu	Asn	Leu	Arg	Gly	Thr	Ile	Lys	Val	Glu	Ser	Gln	Pro	Gly	Lys	Gly
		Ser	Ala	Phe	Thr	Ile	Ser	Ile	Pro	Thr	Gln	Asn	Gln	Ser	Ser	Ser	Ala
		Glu	Ile	Leu	Pro	Trp	Leu	Pro	Ser	Ser	Asp	Asp	Ile	Val	Met	Pro	Val
		Asp	Gln	Ala	His	Ile	Phe	Asp	Ile	Phe	Tyr	Arg	Gly	Gln	Ser	Ala	Thr
140		Glu	Lys	His	Gly	Ser	Gly	Val	Gly	Leu	Ser	Phe	Thr	Asn	Ile	Leu	Val
		Glu	Asn	Leu	Arg	Gly	Thr	Ile	Lys	Val	Glu	Ser	Gln	Pro	Gly	Lys	Gly

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5 His Ile Ala Pro Asp Asp Ser Pro Thr Ser Pro Met Val Ala Ala Leu  
 675 680 685  
 Asn His Arg Phe Glu Asp Glu Arg Pro Thr Ile Leu Leu Val Glu Asp  
 690 695 700  
 10 Asn Lys Asp Ile Asn Leu Leu Val Lys Leu Leu Cys Asp Arg Tyr  
 705 710 715 720  
 Asn Val Leu Ser Ala Ala Asn Gly Lys Glu Gly Ile Ala Leu Ala Thr  
 725 730 735  
 15 Glu His Ile Pro Asp Ile Ile Ile Thr Asp Ile Met Met Pro Ile Met  
 740 745 750  
 Asp Gly Ile Glu Met Thr Ile Arg Met Lys Gln Ser Pro Leu Leu Cys  
 755 760 765  
 His Ile Pro Ile Val Ala Leu Thr Ala Lys Ser Thr Glu Gln Asp Arg  
 770 775 780  
 20 Leu Glu Gly Ile Lys Ser Gly Val Val Ser Tyr Leu Cys Lys Pro Phe  
 785 790 795 800  
 Ser Pro Glu Glu Leu Leu Met Arg Ile Glu Gln Leu Leu Lys Asp Arg  
 805 810 815  
 25 Glu Leu Leu Lys Lys Phe Tyr Met Gln Lys Leu Met Leu Asp Arg Lys  
 820 825 830  
 Pro Glu Glu Glu Pro Gln Pro Ile Asp Asp Ser Ser Met Gln Phe Leu  
 835 840 845  
 Leu Ala Ala Lys Asp Ala Val Ser Gly Gly Ile Lys Gln Asn Pro Asp  
 850 855 860  
 30 Phe Ser Ala Gln Asp Leu Ala Glu Lys Met Cys Met Ser Pro Ser Gln  
 865 870 875 880  
 Leu Asn Arg Lys Leu Thr Ser Val Val Gly Cys Ser Thr Ile Gly Tyr  
 885 890 895  
 35 Ile Gln Gln Ile Lys Ile Lys Leu Ala Cys Lys Leu Leu Ala Asp Glu  
 900 905 910  
 Ser Lys Asn Ile Ser Asp Ile Ser Ile Glu Ala Gly Phe Ser Asp Pro  
 915 920 925  
 Ala Tyr Phe Ser Arg Thr Phe Lys Arg Tyr Met Asn Cys Ser Pro Ser  
 930 935 940  
 40 Gln Tyr Arg Gln Lys Leu Leu Ala Met Pro Gly Ser Asp Lys Glu Thr  
 945 950 955 960  
 Val

40 (2) INFORMATION FOR SEQ ID NO:525

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 556 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
 (ii) MOLECULE TYPE: protein  
 (iii) HYPOTHETICAL: YES  
 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: *Porphyromonas gingivalis*  
 (ix) FEATURE:  
 (A) NAME/KEY: misc feature  
 (B) LOCATION 1...556  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:525

60 Met Lys Lys Leu Leu Gln Ala Lys Ala Leu Ile Leu Ala Leu Gly Leu  
 1 5 10 15  
 Phe Gln Leu Pro Ala Ile Ala Gln Thr Gln Met Gln Ala Asp Arg Thr  
 20 25 30  
 65 Asn Gly Gln Phe Ala Thr Glu Glu Met Gln Arg Ala Phe Gln Glu Thr  
 35 40 45  
 Asn Pro Pro Ala Gly Pro Val Arg Ala Ile Ala Glu Tyr Glu Arg Ser  
 50 55 60  
 Ala Ala Val Leu Val Arg Tyr Pro Phe Gly Ile Pro Met Glu Leu Ile  
 65 70 75 80  
 70 Lys Glu Leu Ala Lys Asn Asp Lys Val Ile Thr Ile Val Ala Ser Glu  
 85 90 95  
 Ser Gln Lys Asn Thr Val Ile Thr Gln Tyr Thr Gln Ser Gly Val Asn  
 100 105 110  
 75 Leu Ser Asn Cys Asp Phe Ile Ile Ala Lys Thr Asp Ser Tyr Trp Thr  
 115 120 125

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5 Arg Asp Tyr Thr Gly Trp Phe Ala Met Tyr Asp Thr Asn Lys Val Gly  
 130 135 140  
 Leu Val Asp Phe Ile Tyr Asn Arg Pro Arg Pro Asn Asp Asp Glu Phe  
 145 150 155 160  
 10 Pro Lys Tyr Glu Ala Gln Tyr Leu Gly Ile Glu Met Phe Gly Met Lys  
 165 170 175  
 Leu Lys Gln Thr Gly Gly Asn Tyr Met Thr Asp Gly Tyr Gly Ser Ala  
 180 185 190  
 Val Gln Ser His Ile Ala Tyr Thr Glu Asn Ser Ser Leu Ser Gln Ala  
 195 200 205  
 15 Gln Val Asn Gln Lys Met Lys Asp Tyr Leu Gly Ile Thr His His Asp  
 210 215 220  
 Val Val Gln Asp Pro Asn Gly Glu Tyr Ile Asn His Val Asp Cys Trp  
 225 230 235 240  
 Gly Lys Tyr Leu Ala Pro Asn Lys Ile Leu Ile Arg Lys Val Pro Asp  
 245 250 255  
 20 Asn His Pro Gln His Gln Ala Leu Glu Asp Met Ala Ala Tyr Phe Ala  
 260 265 270  
 Ala Gln Thr Cys Ala Trp Gly Thr Lys Tyr Glu Val Tyr Arg Ala Leu  
 275 280 285  
 Ala Thr Asn Glu Gln Pro Tyr Thr Asn Ser Leu Ile Leu Asn Asn Arg  
 290 295 300  
 Val Phe Val Pro Val Asn Gly Pro Ala Ser Val Asp Asn Asp Ala Leu  
 305 310 315 320  
 25 Asn Val Tyr Lys Thr Ala Met Pro Gly Tyr Glu Ile Ile Gly Val Lys  
 325 330 335  
 Gly Ala Ser Gly Thr Pro Trp Leu Gly Thr Asp Ala Leu His Cys Arg  
 340 345 350  
 30 Thr His Glu Val Ala Asp Lys Gly Tyr Leu Tyr Ile Lys His Tyr Pro  
 355 360 365  
 Ile Leu Gly Glu Gln Ala Gly Pro Asp Tyr Lys Ile Glu Ala Asp Val  
 370 375 380  
 Val Ser Cys Ala Asn Ala Thr Ile Ser Pro Val Gln Cys Tyr Tyr Arg  
 385 390 395 400  
 35 Ile Asn Gly Ser Gly Ser Phe Lys Ala Ala Asp Met Thr Met Glu Ser  
 405 410 415  
 Thr Gly His Tyr Thr Tyr Ser Phe Thr Gly Leu Asn Lys Asn Asp Lys  
 420 425 430  
 40 Val Glu Tyr Tyr Ile Ser Ala Ala Asp Asn Ser Gly Arg Lys Glu Thr  
 435 440 445  
 Tyr Pro Phe Ile Gly Glu Pro Asp Pro Phe Lys Phe Thr Cys Met Asn  
 450 455 460  
 Glu Thr Asn Thr Cys Thr Val Thr Gly Ala Ala Lys Ala Leu Arg Ala  
 465 470 475 480  
 45 Trp Phe Asn Ala Gly Arg Ser Glu Leu Ala Val Ser Val Ser Leu Asn  
 485 490 495  
 Ile Ala Gly Thr Tyr Arg Ile Lys Leu Tyr Asn Thr Ala Gly Glu Glu  
 500 505 510  
 50 Val Ala Ala Met Thr Lys Glu Leu Val Ala Gly Thr Ser Val Phe Ser  
 515 520 525  
 Met Asp Val Tyr Ser Gln Ala Pro Gly Thr Tyr Val Leu Val Val Glu  
 530 535 540  
 Gly Asn Gly Ile Arg Glu Thr Met Lys Ile Leu Lys  
 545 550 555

(2) INFORMATION FOR SEQ ID NO:526

- 60 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 428 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
  
 (ii) MOLECULE TYPE: protein  
  
 65 (iii) HYPOTHETICAL: YES  
  
 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Porphyromonas gingivalis  
  
 70 (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION: 1...428  
  
 75 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:526

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Met Lys Leu Ser Ser Lys Lys Ile Leu Ala Ile Ile Ala Leu Leu Thr  
 1 5 10 15  
 Met Gly His Ala Val Gln Ala Gln Phe Val Pro Ala Pro Thr Thr Gly  
 20 25 30  
 5 Ile Arg Met Ser Val Thr Thr Thr Lys Ala Val Gly Glu Lys Ile Glu  
 35 40 45  
 Leu Leu Val His Ser Ile Glu Lys Lys Gly Ile Trp Ile Asp Leu Asn  
 50 55 60  
 10 Gly Asp Ala Thr Tyr Gln Gln Gly Glu Glu Ile Thr Val Phe Asp Glu  
 65 70 75 80  
 Ala Tyr His Glu Tyr Thr Ile Gly Thr Gln Thr Leu Thr Ile Tyr Gly  
 85 90 95  
 Asn Thr Thr Arg Leu Gly Cys Arg Ser Thr Gly Ala Thr Ala Val Asp  
 100 105 110  
 15 Val Thr Lys Asn Pro Asn Leu Thr Tyr Leu Ala Cys Pro Lys Asn Asn  
 115 120 125  
 Leu Lys Ser Leu Asp Leu Thr Gln Asn Pro Lys Leu Leu Arg Val Trp  
 130 135 140  
 20 Cys Asp Ser Asn Glu Ile Glu Ser Leu Asp Leu Ser Gly Asn Pro Ala  
 145 150 155 160  
 Leu Ile Ile Leu Gly Cys Asp Arg Asn Lys Leu Thr Glu Leu Lys Thr  
 165 170 175  
 Asp Asn Asn Pro Lys Leu Ala Ser Leu Trp Cys Ser Asp Asn Asn Leu  
 180 185 190  
 25 Thr Glu Leu Glu Leu Ser Ala Asn Pro Arg Leu Asn Asp Leu Trp Cys  
 195 200 205  
 Phe Gly Asn Arg Ile Thr Lys Leu Asp Leu Ser Ala Asn Pro Leu Leu  
 210 215 220  
 30 Val Thr Leu Trp Cys Ser Asp Asn Glu Leu Ser Thr Leu Asp Leu Ser  
 225 230 235 240  
 Lys Asn Ser Asp Val Ala Tyr Leu Trp Cys Ser Ser Asn Lys Leu Thr  
 245 250 255  
 Ser Leu Asn Leu Ser Gly Val Lys Gly Leu Ser Val Leu Val Cys His  
 260 265 270  
 35 Ser Asn Gln Ile Ala Gly Glu Glu Met Thr Lys Val Val Asn Ala Leu  
 275 280 285  
 Pro Thr Leu Ser Pro Gly Ala Gly Ala Gln Ser Lys Phe Val Val Val  
 290 295 300  
 40 Asp Leu Lys Asp Thr Asp Glu Lys Asn Ile Cys Thr Val Lys Asp Val  
 305 310 315 320  
 Glu Lys Ala Lys Ser Lys Asn Trp Arg Val Phe Asp Phe Asn Gly Asp  
 325 330 335  
 Ser Asp Asn Met Leu Pro Tyr Glu Gly Ser Pro Thr Ser Asn Leu Ala  
 340 345 350  
 45 Val Asp Ala Pro Thr Val Arg Ile Tyr Pro Asn Pro Val Gly Arg Tyr  
 355 360 365  
 Ala Leu Val Glu Ile Pro Glu Ser Leu Leu Gly Gln Glu Ala Ala Leu  
 370 375 380  
 50 Tyr Asp Met Asn Gly Val Lys Val Tyr Ser Phe Ala Val Glu Ser Leu  
 385 390 395 400  
 Arg Gln Asn Ile Asp Leu Thr His Leu Pro Asp Gly Thr Tyr Phe Phe  
 405 410 415  
 Arg Leu Asp Asn Tyr Thr Thr Lys Leu Ile Lys Gln  
 420 425

(2) INFORMATION FOR SEQ ID NO:527

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 310 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
 (ii) MOLECULE TYPE: protein  
 (iii) HYPOTHETICAL: YES  
 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Porphyromonas gingivalis  
 (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION: 1...310  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:527



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```

      Met Arg Lys Thr Ile Ile Phe Cys Leu Leu Leu Ala Leu Phe Gly Cys
      1      5      10      15
5    Ser Trp Ala Gln Glu Arg Val Asp Glu Lys Val Phe Ser Ala Gly Thr
      20      25      30
      Ser Ile Phe Arg Gly Ile Leu Lys Val Lys Ala Pro Leu Met Tyr
      35      40      45
      Gly Asp Arg Glu Val Trp Gly Met Ala Arg Ala Ser Glu Asp Phe Phe
      50      55      60
10   Phe Ile Leu Pro Val Thr Asp Asp Leu Thr Pro Val Leu Phe Tyr Asn
      65      70      75      80
      Arg Leu Thr Asn Glu Pro Cys Phe Val Ser Asp Gln Gly Ile Thr Glu
      85      90      95
      Tyr Phe Lys Phe Ala Gln Glu Gly Asp Tyr Ile Glu Val Glu Gly Ser
      100      105      110
15   Ser Val Phe Met Ala Asn Leu Leu Tyr Tyr Arg Phe Phe Pro Thr Arg
      115      120      125
      Ile Thr Ser Tyr Asn Ala Pro Ile Glu Gly Val Val Ser Lys Thr Gly
      130      135      140
20   Asn Pro Ala Phe Thr Ile Pro Met Leu Pro Gly Val Ser Asp Cys Ile
      145      150      155      160
      Glu Ile Ser Asn Asn Arg Lys Val Phe Leu Thr Asn Gln Leu Gly Val
      165      170      175
      Val Asn Ile Thr Asp Gly Met Glu Pro Pro Ile Ile Ala Gly Val Ser
      180      185      190
25   Ala Ser Tyr Gly Ser Ser Val Arg Val Tyr Gly His Val Ser Gln Arg
      195      200      205
      Trp Asp Ile Ile Gly His Cys Tyr Leu Asp Ile Tyr Pro Thr Asn Cys
      210      215      220
30   Tyr Pro Leu Ser Thr Lys Pro Val Ala Gly Asp Asp Glu Val Phe Val
      225      230      235      240
      Lys Gln Gln Gly Arg Gln Ile Glu Ile Asp Ser Asn Ser Pro Ile Val
      245      250      255
      Gln Val Val Val Tyr Asp Leu Glu Gly Lys Ser Val Phe Arg Lys Arg
      260      265      270
35   Met Thr Glu Asn Ala Tyr Thr Leu Ser Phe Arg Ala Pro Met Leu Gly
      275      280      285
      Phe Met Thr Ile Met Ile Glu Thr Gln Asn Ser Ile Ile Asn Lys Lys
      290      295      300
40   Leu Asn Val Thr Gln Leu
      305      310

```

## (2) INFORMATION FOR SEQ ID NO:528

- 45 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 405 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear
- 50 (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:  
 55 (A) ORGANISM: Porphyromonas gingivalis
- (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...405
- 60 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:528

```

      Met Lys Lys Thr Thr Ile Ile Ser Leu Ile Val Phe Gly Ala Phe Phe
      1      5      10      15
65   Ala Ala Val Gly Gln Thr Lys Asp Asn Ser Ser Tyr Lys Pro Phe Ser
      20      25      30
      Lys Glu Asp Ile Ala Gly Gly Val Tyr Ser Leu Pro Thr Gln Asn Arg
      35      40      45
      Ala Gln Lys Asp Asn Ala Glu Trp Leu Leu Thr Ala Thr Val Ser Thr
      50      55      60
70   Asn Gln Ser Ala Asp Thr His Phe Ile Phe Asp Glu Asn Asn Arg Tyr
      65      70      75      80
      Ile Ala Arg Asp Ile Lys Ala Asn Gly Val Arg Lys Ser Thr Asp Ser
      85      90      95
      Ile Tyr Tyr Asp Ala Asn Gly Arg Ile Ser His Val Asp Leu Tyr Ile
      100      105      110

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Ser Phe Ser Gly Gly Glu Pro Ala Leu Asp Thr Arg Phe Lys Tyr Thr  
 115 120 125  
 Tyr Asp Asp Glu Gly Lys Met Thr Val Arg Glu Val Phe Met Leu Val  
 130 135 140  
 5 Met Asp Pro Asn Thr Pro Ile Ser Arg Leu Glu Tyr His Tyr Asp Ala  
 145 150 155 160  
 Gln Gly Arg Leu Thr His Trp Ile Ser Phe Ala Phe Gly Ala Glu Ser  
 165 170 175  
 10 Gln Lys Asn Thr Tyr His Tyr Asn Glu Lys Gly Leu Leu Val Ser Glu  
 180 185 190  
 Val Leu Ser Asn Ala Met Gly Thr Thr Tyr Ser Asp Thr Gly Lys Thr  
 195 200 205  
 Glu Tyr Ser Tyr Asp Asp Ala Asp Asn Met Val Lys Ala Glu Tyr Phe  
 210 215 220  
 15 Val Val Gln Gln Gly Lys Ala Trp Gln Val Leu Lys Arg Glu Glu Tyr  
 225 230 235 240  
 Thr Tyr Glu Asp Asn Ile Cys Ile Gln Tyr Leu Ala Ile Asn Gly Thr  
 245 250 255  
 20 Asp Thr Lys Val Tyr Lys Arg Asp Ile Glu Ser Asp Lys Ser Ile Ser  
 260 265 270  
 Ala Asn Val Ile Asp Ile Pro Ser Met Pro Glu Gln Thr Trp Pro Asn  
 275 280 285  
 Met Tyr Gly Phe Asn Ala Lys Arg Leu Lys Glu Thr Tyr Ser Ser Tyr  
 290 295 300  
 25 Glu Gly Asp Val Ala Thr Pro Ile Phe Asp Tyr Ile Tyr Thr Tyr Lys  
 305 310 315 320  
 Ala Leu Thr Ser Met Ala Thr Pro Ser Thr Glu Ala Gln Val Ala Val  
 325 330 335  
 30 Tyr Leu Asn Pro Ser Thr Asp Arg Leu Val Ile Leu Ala Asn Gly Ile  
 340 345 350  
 Thr His Leu Ser Met Tyr Asp Leu Gln Gly Lys Leu Ile Arg Asp Cys  
 355 360 365  
 Ala Leu Ser Gly Asp Lys Val Glu Met Gly Val Gly Ser Leu Thr Lys  
 370 375 380  
 35 Gly Thr Tyr Leu Leu Lys Val Asn Thr Asp Gln Gly Ala Phe Val Arg  
 385 390 395 400  
 Lys Val Val Ile Arg  
 405

40 (2) INFORMATION FOR SEQ ID NO:529

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 2037 base pairs  
 45 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

50 (iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:  
 55 (A) ORGANISM: *Porphyromonas gingivalis*

(ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 60 (B) LOCATION 1...2037

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:529

GTAATGGACT ACAAACTCAC TTCTCGATT C AAGCCACGG GCGACCAGCC GGAAGCCATT 60  
 CGCCAACTCG TACAGGGCAT CAACGAAGGG ATGCCGGCTC AGACGCTGCT CGGCGTAACG 120  
 65 GGTTCCGGCA AAACCTTTAC GGTGGCTAAC GTGGTGGCGG CGGTCAATCG TCCGACCCCTT 180  
 GTCCTGAGTC ACAACAAGAC CTTGGCAGCA CAGCTATACG GAGAGTTCAA AGCCTTCTTC 240  
 CCGGAGATG CGGTGGAGTA TTTCGTCAGC TACTACGACT ACTATCAGCC CGAGGCCTAC 300  
 CTCGCCGTCA CAGACACCTA TATCGAAAGG GACATGGCCA TCAACGCGGA GATCGAAAAA 360  
 70 CTGCGATTGA GGGCCACGGC TTCGCTCCTG TCAGGGCGGA AAGATGTGCT TGTGGTCAGC 420  
 TCCGTATCCT GTCTCTACGG TATGGCCAAT CCTGAAGCTT TTTCCGAAAA GTGATCAGC 480  
 CTGCACACGG GACAAAGGGC AGACAGGGAT CATTTTATCC GCCTGCTGGT AGAGAGCTAC 540  
 TACACGAACA ATAAAGTAGA GTTCGAGAGC GGCAACTTCC GTGTCAAAGG CGACAGCGTG 600  
 GACATATGCC CCGCCGTAGA AGGTTATGAC GGCGTGSCAT ACAGGGTGGA GTTTTGGGAT 660  
 75 GGAGAGSTCG AGCGGCTGAG TACCTTCGAT CCGCGAACGG GACGGGAATA CGGCCTGCTG 720  
 TCGGAGCTGA AGATATATCC GSCCAATCTC TTCGTGACGA CTAAAGGAGCA GGTGGATCGG 780

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	GCAGTAGGSA	AAATCGATGT	GGATCTGGGC	GCACAGGTCS	ATTTCTGAA	AGAAATCGGC	840
	AAACCATATG	AAGCCAAACG	CTTGTATGAG	CGGGTCACGT	ATGACTTGGA	AATGATCCGT	900
	GAGTTGGGTT	ATTGTTCCGG	TATAGAGAAC	TATTCCGCGT	ACTTCGACGG	CCGTGACGG	960
5	GGCGAACGTC	CTTTCTGTCT	GTTGGATTAT	TTCCCGSAGG	ATTTCTGTGT	GGTCATAGAC	1020
	GAAAGCCATG	TAACGATACC	GCAGATACGT	GCCATGTACG	GAGGCGATCG	TTCCGCGAAG	1080
	GAGAATCTGG	TCGAATACGG	ATTCCGCGTG	CCTGCCGCTC	TCGACAATCG	GCCGCTTCGC	1140
	TTCCAGCAGT	TCGAAGCTCT	CACCCCCCGG	ACCCTTTATA	TCAGTGCCAC	GCCTGCCGAC	1200
	TATGAGCTGA	ACAGAAGCGA	ASGCGTGATC	GTCGAGCAGC	TGATCCGTCC	GACCGGACTG	1260
10	CTGGATCCCA	TCATCGACGT	CAAGCCGACG	GCAAAACCAAG	TGGACGATCT	GATGGAGGAG	1320
	ATAGCACGCT	GCATCGAAAA	GAAAGAGCGC	GTACTGGTAA	CGACCCTGAC	CAAACGSTATG	1380
	GCAGAGGAGC	TTAGCGAATA	CCTGCTACGC	CACGCTATCA	GCACCGGCTA	CATACACAGC	1440
	GATGTGGACA	CGCTGGAGCG	TGTGCGTATC	ATGGAAGACC	TGGCAAGGG	GGTCTACGAT	1500
	GCACTCATCG	GGGTGAATCT	GCTCCGCGAA	GGATTGGACT	TGCCGGAAGT	TTGCTTGTGT	1560
	GCTATTCTGG	ATGCGGATAA	GGAAGGATTC	CTGCGCTCGC	ATCGTTCCGT	CACGAGACT	1620
15	GCAGGACGTC	CGCGCCGGCA	CATTTCATCT	TCTACGCGGA	CAAGATCACC		1680
	GACAGTATGC	AGCTCACCAT	GGACGAGACT	GCACGCGGAC	GCGCAAAGCA	ACTGGCCTAC	1740
	AACGAAGCGC	ACGGCATCAC	CCCCCAACAG	ATAGTGAAGA	ACAGTGCTGC	CATTTGGGGA	1800
	GAAGGCGATG	TGTGGGCTTT	GCAATCCGAT	ACAGAATCCG	GTGCGTACAT	AGAAGAGAGC	1860
	AGCATGGTGG	CTGCGGATCC	TTTGGCCGAC	TATCTGAGCA	AACCCAGGCT	GGAAGCACTC	1920
20	ATTGCTTCGA	CCAAGAAGCA	AATGCTGGCA	GCAGCCAAAG	AGCTGGACTT	TCTGGAAGCG	1980
	GCACGACTTC	GGGACGAAGC	CGCAGGATTG	GAAAAGAAAC	TGGAGCAACT	CACAGCC	2037

## (2) INFORMATION FOR SEQ ID NO:530

25

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 2034 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular

30

(ii) MOLECULE TYPE: DNA (genomic)

35

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

40

(A) ORGANISM: *Porphyromonas gingivalis*

(ix) FEATURE:

- (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...2034

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:530

	ATGGACTACA	AACTCACTTC	TCGATTCAAG	CCCAAGGGCG	ACCAGCCGGA	AGCCATTCCG	60
	CAACTCSTAC	AGGGCATCAA	CGAAGGGATG	CGGCTCAGA	CGCTGCTCGG	CGTAACGGGT	120
	TCGGGCAAAA	CTTTACGGT	GGCTAACGTG	GTGGCGGCGG	TCAATCGTCC	GACCTTTGTC	180
50	CTGAGTCACA	ACAAGACCTT	GGCAGCACAG	CTATACGGAG	AGTTCAAAGC	CTTCTTCCCC	240
	GAGAATGCGG	TGGAGTATTT	CGTCAGCTAC	TACGACTACT	ATCAGCCCCG	GGCTACCTC	300
	CCCGTCACAG	ACACCTATAT	CGAAAAGGAC	ATGSCCATCA	ACGCGGAGAT	CGAAAAACTG	360
	CGATTGAGGG	CCACGGCTTC	GCTCCTGTCA	GGGCGGAAAG	ATGTGCTTGT	GGTCAGCTCC	420
	GTATCGTGTC	TCTACGGTAT	GGCCAATCCT	GAAGCTTTTT	CCGAAAAGST	GATCAGCCTG	480
55	CACACGGGAC	AAAGGGCAGA	CAGGGATCAT	TTTATCCGCC	TGCTGGTAGA	GAGCTACTAC	540
	ACGAACAATA	AAGTAGAGTT	CGAGAGCGGC	AACTTCCGTG	TCAAAGGCGA	CAGCGTGGAC	600
	ATATTCCTCCG	CCGTAGAAGG	TTATGACGGC	GTGGCATACA	GGTGGAGTTT	TTGGGATGGA	660
	GAGSTCGAGC	GGCTGAGTAC	CTTCGATCCG	CGAACGGGAC	GGGAATACGG	CCTGCTGTCC	720
	GAGCTGAAGA	TATATCCGGC	CAATCTCTTC	GTGACGACTA	AGGAGCAGGT	GGATCGGGCA	780
60	GTAGGGAAAA	TCGATGTGGA	TCTGGGCGCA	CAGGTGCGAT	TTCTGAAAGA	AATCGGCAAA	840
	CCATATGAAG	CCAAACGCTT	GTATGAGCGG	GTCACTATG	ACTTGGAAAT	GATCCGTGAG	900
	TTGGGTATTT	GTTCGGGTAT	AGAGAACTAT	TGCGCTACT	TCGACGGCCG	TGACGCGGGC	960
	GAACGTCCTT	TCTGTCTGTT	GGATTATTTC	CCGGAGGATT	TCTGTGTTGT	CATAGACGAA	1020
	AGCCATGTAA	CGATACCGCA	GATACGTGCC	ATGTACGGAG	GCGATCGTTC	GCGCAAGGAG	1080
65	AATCTGGTCC	AATACGGATT	CGCCTGCGT	GCCGCTCTCG	ACAATCGGCC	GCTTCGCTTC	1140
	GACGAGTTCC	AAGCTCTCAC	CCCCCGGACC	CTTTATATCA	GTGCCACGCC	TGCCGACTAT	1200
	GAGCTGAACA	GAAGCGAAGG	CGTGATCGTC	GAGCAGCTGA	TCCGTCCGAC	CGGACTGCTG	1260
	GATCCCATCA	TCGACGTCAA	GCCGACGGCA	AACCAAGTGG	ACGATCTGAT	GGAGGAGATA	1320
70	GCACGCTGCA	TCGAAAAGAA	AGAGCGCGTA	CTGTAACGGA	CCCTGACCAA	ACGTATGGCA	1380
	GAGGAGCTTA	GCGAATACCT	GCTACGCCAC	GGTATCAGCA	CGGCTACAT	ACACAGCGAT	1440
	GTGGACACGC	TGGAGCGTGT	GCGTATCATG	GAAGACTTGC	GCAAGGGGGT	CTACGATGCA	1500
	CTCATCGGGG	TGAATCTGCT	CCGCGAAGGA	TTGGAATTGC	CGGAAGTTTC	GCTTGTGGCT	1560
	ATTCTGGATG	CGGATAAGGA	AGGATTCCCTG	CGCTCGCATC	GTTCGCTCAC	GCAGACTGCA	1620
	GACGCTGCGG	CCCGGCACAT	TCATGGGCGT	GTCTCTTTCT	ACGCGGACAA	GATCACCGAC	1680
75	AGTATGACAGC	TCAACCATGGA	CGAGACTGCA	CGCCGACGCG	CAAAGCAACT	GGCTACAAC	1740

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GAAGCGCACG GCATCACCCC CCAACAGATA GTGAAGAACA GTGCTGCCAT TTGGGGAGAA 1800  
 GGGCATGTGT CGGCCTTGCA ATCCGATACA GAATCCGGTG CSTACATAGA AGAGAGCAGC 1860  
 ATGTGGGCTG CCGATCCTTT GGGCGACTAT CTGAGCAAAC CCAAGCTGGA AGCACTCATT 1920  
 GCTTCGACCA AGAAGCAAAT GCTGGCAGCA GCCAAGAGC TGGACTTTCT GGAAGCGGCA 1980  
 5 CGACTTCGGG ACGAAGCCGC ACGATTGGAA AAGAACTGG AGCAACTCAC AGCC 2034

(2) INFORMATION FOR SEQ ID NO:531

- 10 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 679 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear
- 15 (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- 20 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Porphyromonas gingivalis
- (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (E) LOCATION 1...679
- 25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:531

Val Met Asp Tyr Lys Leu Thr Ser Arg Phe Lys Pro Thr Gly Asp Gln  
 1 5 10 15  
 30 Pro Glu Ala Ile Arg Gln Leu Val Gln Gly Ile Asn Glu Gly Met Pro  
 20 25 30  
 Ala Gln Thr Leu Leu Gly Val Thr Gly Ser Gly Lys Thr Phe Thr Val  
 35 40 45  
 Ala Asn Val Val Ala Ala Val Asn Arg Pro Thr Leu Val Leu Ser His  
 50 55 60  
 35 Asn Lys Thr Leu Ala Ala Gln Leu Tyr Gly Glu Phe Lys Ala Phe Phe  
 65 70 75 80  
 Pro Glu Asn Ala Val Glu Tyr Phe Val Ser Tyr Tyr Asp Tyr Tyr Gln  
 85 90 95  
 40 Pro Glu Ala Tyr Leu Pro Val Thr Asp Thr Tyr Ile Glu Lys Asp Met  
 100 105 110  
 Ala Ile Asn Ala Glu Ile Glu Lys Leu Arg Leu Arg Ala Thr Ala Ser  
 115 120 125  
 45 Leu Leu Ser Gly Arg Lys Asp Val Leu Val Val Ser Ser Val Ser Cys  
 130 135 140  
 Leu Tyr Gly Met Ala Asn Pro Glu Ala Phe Ser Glu Lys Val Ile Ser  
 145 150 155 160  
 Leu His Thr Gly Gln Arg Ala Asp Arg Asp His Phe Ile Arg Leu Leu  
 165 170 175  
 50 Val Glu Ser Tyr Tyr Thr Asn Asn Lys Val Glu Phe Glu Ser Gly Asn  
 180 185 190  
 Phe Arg Val Lys Gly Asp Ser Val Asp Ile Phe Pro Ala Val Glu Gly  
 195 200 205  
 55 Tyr Asp Gly Val Ala Tyr Arg Val Glu Phe Trp Asp Gly Glu Val Glu  
 210 215 220  
 Arg Leu Ser Thr Phe Asp Pro Arg Thr Gly Arg Glu Tyr Gly Leu Leu  
 225 230 235 240  
 Ser Glu Leu Lys Ile Tyr Pro Ala Asn Leu Phe Val Thr Thr Lys Glu  
 245 250 255  
 60 Gln Val Asp Arg Ala Val Gly Lys Ile Asp Val Asp Leu Gly Ala Gln  
 260 265 270  
 Val Asp Phe Leu Lys Glu Ile Gly Lys Pro Tyr Glu Ala Lys Arg Leu  
 275 280 285  
 65 Tyr Glu Arg Val Thr Tyr Asp Leu Glu Met Ile Arg Glu Leu Gly Tyr  
 290 295 300  
 Cys Ser Gly Ile Glu Asn Tyr Ser Arg Tyr Phe Asp Gly Arg Asp Ala  
 305 310 315 320  
 Gly Glu Arg Pro Phe Cys Leu Leu Asp Tyr Phe Pro Glu Asp Phe Leu  
 325 330 335  
 70 Leu Val Ile Asp Glu Ser His Val Thr Ile Pro Gln Ile Arg Ala Met  
 340 345 350  
 Tyr Gly Gly Asp Arg Ser Arg Lys Glu Asn Leu Val Glu Tyr Gly Phe  
 355 360 365  
 75 Arg Leu Pro Ala Ala Leu Asp Asn Arg Pro Leu Arg Phe Asp Glu Phe  
 370 375 380

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Glu Ala Leu Thr Pro Arg Thr Leu Tyr Ile Ser Ala Thr Pro Ala Asp  
 385 390 395 400  
 Tyr Glu Leu Asn Arg Ser Glu Gly Val Ile Val Glu Gln Leu Ile Arg  
 405 410 415  
 5 Pro Thr Gly Leu Asp Pro Ile Ile Asp Val Lys Pro Thr Ala Asn  
 420 425 430  
 Gln Val Asp Asp Leu Met Glu Glu Ile Ala Arg Cys Ile Glu Lys Lys  
 435 440 445  
 10 Glu Arg Val Leu Val Thr Thr Leu Thr Lys Arg Met Ala Glu Glu Leu  
 450 455 460  
 Ser Glu Tyr Leu Leu Arg His Gly Ile Ser Thr Gly Tyr Ile His Ser  
 465 470 475 480  
 Asp Val Asp Thr Leu Glu Arg Val Arg Ile Met Glu Asp Leu Arg Lys  
 485 490 495  
 15 Gly Val Tyr Asp Ala Leu Ile Gly Val Asn Leu Leu Arg Glu Gly Leu  
 500 505 510  
 Asp Leu Pro Glu Val Ser Leu Val Ala Ile Leu Asp Ala Asp Lys Glu  
 515 520 525  
 20 Gly Phe Leu Arg Ser His Arg Ser Leu Thr Gln Thr Ala Gly Arg Ala  
 530 535 540  
 Ala Arg His Ile His Gly Arg Val Ile Phe Tyr Ala Asp Lys Ile Thr  
 545 550 555 560  
 Asp Ser Met Gln Leu Thr Met Asp Glu Thr Ala Arg Arg Arg Ala Lys  
 565 570 575  
 25 Gln Leu Ala Tyr Asn Glu Ala His Gly Ile Thr Pro Gln Gln Ile Val  
 580 585 590  
 Lys Asn Ser Ala Ala Ile Trp Gly Glu Gly Asp Val Ser Ala Leu Gln  
 595 600 605  
 30 Ser Asp Thr Glu Ser Gly Ala Tyr Ile Glu Glu Ser Ser Met Val Ala  
 610 615 620  
 Ala Asp Pro Leu Ala Asp Tyr Leu Ser Lys Pro Lys Leu Glu Ala Leu  
 625 630 635 640  
 Ile Ala Ser Thr Lys Lys Gln Met Leu Ala Ala Ala Lys Glu Leu Asp  
 645 650 655  
 35 Phe Leu Glu Ala Ala Arg Leu Arg Asp Glu Ala Ala Arg Leu Glu Lys  
 660 665 670  
 Lys Leu Glu Gln Leu Thr Ala  
 675

40 (2) INFORMATION FOR SEQ ID NO:532

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 678 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
 (ii) MOLECULE TYPE: protein  
 (iii) HYPOTHETICAL: YES  
 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Porphyromonas gingivalis  
 (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...678  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:532

60 Met Asp Tyr Lys Leu Thr Ser Arg Phe Lys Pro Thr Gly Asp Gln Pro  
 1 5 10 15  
 Glu Ala Ile Arg Gln Leu Val Gln Gly Ile Asn Glu Gly Met Pro Ala  
 20 25 30  
 65 Gln Thr Leu Leu Gly Val Thr Gly Ser Gly Lys Thr Phe Thr Val Ala  
 35 40 45  
 Asn Val Val Ala Ala Val Asn Arg Pro Thr Leu Val Leu Ser His Asn  
 50 55 60  
 Lys Thr Leu Ala Ala Gln Leu Tyr Gly Glu Phe Lys Ala Phe Phe Pro  
 65 70 75 80  
 70 Glu Asn Ala Val Glu Tyr Phe Val Ser Tyr Tyr Asp Tyr Tyr Gln Pro  
 85 90 95  
 Glu Ala Tyr Leu Pro Val Thr Asp Thr Tyr Ile Glu Lys Asp Met Ala  
 100 105 110  
 75 Ile Asn Ala Glu Ile Glu Lys Leu Arg Leu Arg Ala Thr Ala Ser Leu  
 115 120 125

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	Leu	Ser	Gly	Arg	Lys	Asp	Val	Leu	Val	Val	Ser	Ser	Val	Ser	Cys	Leu
	130						135					140				
	Tyr	Gly	Met	Ala	Asn	Pro	Glu	Ala	Phe	Ser	Glu	Lys	Val	Ile	Ser	Leu
	145					150					155					160
5	His	Thr	Gly	Gln	Arg	Ala	Asp	Arg	Asp	His	Phe	Ile	Arg	Leu	Leu	Val
					165					170						175
	Glu	Ser	Tyr	Tyr	Thr	Asn	Asn	Lys	Val	Glu	Phe	Glu	Ser	Gly	Asn	Phe
					180					185					190	
10	Arg	Val	Lys	Gly	Asp	Ser	Val	Asp	Ile	Phe	Pro	Ala	Val	Glu	Gly	Tyr
					195			200					205			
	Asp	Gly	Val	Ala	Tyr	Arg	Val	Glu	Phe	Trp	Asp	Gly	Glu	Val	Glu	Arg
					210			215					220			
	Leu	Ser	Thr	Phe	Asp	Pro	Arg	Thr	Gly	Arg	Glu	Tyr	Gly	Leu	Leu	Ser
	225					230					235					240
15	Glu	Leu	Lys	Ile	Tyr	Pro	Ala	Asn	Leu	Phe	Val	Thr	Thr	Lys	Glu	Gln
					245					250					255	
	Val	Asp	Arg	Ala	Val	Gly	Lys	Ile	Asp	Val	Asp	Leu	Gly	Ala	Gln	Val
					260				265					270		
20	Asp	Phe	Leu	Lys	Glu	Ile	Gly	Lys	Pro	Tyr	Glu	Ala	Lys	Arg	Leu	Tyr
					275			280					285			
	Glu	Arg	Val	Thr	Tyr	Asp	Leu	Glu	Met	Ile	Arg	Glu	Leu	Gly	Tyr	Cys
					290			295				300				
	Ser	Gly	Ile	Glu	Asn	Tyr	Ser	Arg	Tyr	Phe	Asp	Gly	Arg	Asp	Ala	Gly
	305					310					315					320
25	Glu	Arg	Pro	Phe	Cys	Leu	Leu	Asp	Tyr	Phe	Pro	Glu	Asp	Phe	Leu	Leu
					325					330					335	
	Val	Ile	Asp	Glu	Ser	His	Val	Thr	Ile	Pro	Gln	Ile	Arg	Ala	Met	Tyr
					340					345				350		
30	Gly	Gly	Asp	Arg	Ser	Arg	Lys	Glu	Asn	Leu	Val	Glu	Tyr	Gly	Phe	Arg
					355			360					365			
	Leu	Pro	Ala	Ala	Leu	Asp	Asn	Arg	Pro	Leu	Arg	Phe	Asp	Glu	Phe	Glu
					370			375				380				
	Ala	Leu	Thr	Pro	Arg	Thr	Leu	Tyr	Ile	Ser	Ala	Thr	Pro	Ala	Asp	Tyr
	385					390					395					400
35	Glu	Leu	Asn	Arg	Ser	Glu	Gly	Val	Ile	Val	Glu	Gln	Leu	Ile	Arg	Pro
					405					410					415	
	Thr	Gly	Leu	Leu	Asp	Pro	Ile	Ile	Asp	Val	Lys	Pro	Thr	Ala	Asn	Gln
					420				425					430		
40	Val	Asp	Asp	Leu	Met	Glu	Glu	Ile	Ala	Arg	Cys	Ile	Glu	Lys	Lys	Glu
					435			440					445			
	Arg	Val	Leu	Val	Thr	Thr	Leu	Thr	Lys	Arg	Met	Ala	Glu	Glu	Leu	Ser
					450			455				460				
	Glu	Tyr	Leu	Leu	Arg	His	Gly	Ile	Ser	Thr	Gly	Tyr	Ile	His	Ser	Asp
	465					470					475					480
45	Val	Asp	Thr	Leu	Glu	Arg	Val	Arg	Ile	Met	Glu	Asp	Leu	Arg	Lys	Gly
					485					490					495	
	Val	Tyr	Asp	Ala	Leu	Ile	Gly	Val	Asn	Leu	Leu	Arg	Glu	Gly	Leu	Asp
					500				505				510			
50	Leu	Pro	Glu	Val	Ser	Leu	Val	Ala	Ile	Leu	Asp	Ala	Asp	Lys	Glu	Gly
					515			520					525			
	Phe	Leu	Arg	Ser	His	Arg	Ser	Leu	Thr	Gln	Thr	Ala	Gly	Arg	Ala	Ala
					530			535				540				
	Arg	His	Ile	His	Gly	Arg	Val	Ile	Phe	Tyr	Ala	Asp	Lys	Ile	Thr	Asp
	545					550					555					560
55	Ser	Met	Gln	Leu	Thr	Met	Asp	Glu	Thr	Ala	Arg	Arg	Arg	Ala	Lys	Gln
					565					570					575	
	Leu	Ala	Tyr	Asn	Glu	Ala	His	Gly	Ile	Thr	Pro	Gln	Gln	Ile	Val	Lys
					580				585					590		
60	Asn	Ser	Ala	Ala	Ile	Trp	Gly	Glu	Gly	Asp	Val	Ser	Ala	Leu	Gln	Ser
					595			600					605			
	Asp	Thr	Glu	Ser	Gly	Ala	Tyr	Ile	Glu	Glu	Ser	Ser	Met	Val	Ala	Ala
					610			615					620			
	Asp	Pro	Leu	Ala	Asp	Tyr	Leu	Ser	Lys	Pro	Lys	Leu	Glu	Ala	Leu	Ile
					625			630			635					640
65	Ala	Ser	Thr	Lys	Lys	Gln	Met	Leu	Ala	Ala	Ala	Lys	Glu	Leu	Asp	Phe
					645					650					655	
	Leu	Glu	Ala	Ala	Arg	Leu	Arg	Asp	Glu	Ala	Ala	Arg	Leu	Glu	Lys	Lys
					660				665					670		
70	Leu	Glu	Gln	Leu	Thr	Ala										
					675											

# INTERNATIONAL SEARCH REPORT

International application No.  
PCT/AU 98/01023

<b>A. CLASSIFICATION OF SUBJECT MATTER</b>																						
Int Cl <sup>6</sup> : C12N 15/31; C07K 14/195; A61K 38/00, 38/16, 39/00																						
According to International Patent Classification (IPC) or to both national classification and IPC																						
<b>B. FIELDS SEARCHED</b>																						
Minimum documentation searched (classification system followed by classification symbols) See Electronic Database box below																						
Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched See Electronic Database box below																						
Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)																						
Medline	porphyromonas gingivalis, bacterial proteins, peptides, bacterial vaccines																					
CA	porphyromonas gingivalis, genes microbial, antigens																					
WPAT	porphyromonas or porphyromonas gingivalis, C07K 07, 014/195: C12N 15/31 + *Seq IDS 265, 528, 340, 341																					
<b>C. DOCUMENTS CONSIDERED TO BE RELEVANT</b>																						
Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.																				
A	Derwent abstract 95-3513214/45 WO 95/26404 (MEITO SANGYO KK) 5 October 1995.	all																				
A	Derwent abstract 95-147309/19 WO 95/09181 (KYOWA HAKKO KOGYO KK) 6 April 1995.	all																				
<input type="checkbox"/> Further documents are listed in the continuation of Box C <input checked="" type="checkbox"/> See patent family annex																						
<p>* Special categories of cited documents:</p> <table border="0"> <tr> <td>"A"</td> <td>document defining the general state of the art which is not considered to be of particular relevance</td> <td>"T"</td> <td>later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention</td> </tr> <tr> <td>"E"</td> <td>earlier application or patent but published on or after the international filing date</td> <td>"X"</td> <td>document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone</td> </tr> <tr> <td>"L"</td> <td>document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)</td> <td>"Y"</td> <td>document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art</td> </tr> <tr> <td>"O"</td> <td>document referring to an oral disclosure, use, exhibition or other means</td> <td>"&amp;"</td> <td>document member of the same patent family</td> </tr> <tr> <td>"P"</td> <td>document published prior to the international filing date but later than the priority date claimed</td> <td></td> <td></td> </tr> </table>			"A"	document defining the general state of the art which is not considered to be of particular relevance	"T"	later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention	"E"	earlier application or patent but published on or after the international filing date	"X"	document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone	"L"	document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)	"Y"	document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art	"O"	document referring to an oral disclosure, use, exhibition or other means	"&"	document member of the same patent family	"P"	document published prior to the international filing date but later than the priority date claimed		
"A"	document defining the general state of the art which is not considered to be of particular relevance	"T"	later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention																			
"E"	earlier application or patent but published on or after the international filing date	"X"	document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone																			
"L"	document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)	"Y"	document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art																			
"O"	document referring to an oral disclosure, use, exhibition or other means	"&"	document member of the same patent family																			
"P"	document published prior to the international filing date but later than the priority date claimed																					
Date of the actual completion of the international search 11 January 1999		Date of mailing of the international search report 28 JAN 1999																				
Name and mailing address of the ISA/AU AUSTRALIAN PATENT OFFICE PO BOX 200 WODEN ACT 2606 AUSTRALIA Facsimile No.: (02) 6285 3929		Authorized officer  PHILIPPA WYRDEMAN Telephone No.: (02) 6283 2554																				

# INTERNATIONAL SEARCH REPORT

International application No.  
PCT/AU 98/01023

## Box I Observations where certain claims were found unsearchable (Continuation of item 1 of first sheet)

This international search report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☐ Claims Nos.:  
because they relate to subject matter not required to be searched by this Authority, namely:
2. ☒ Claims Nos.: **1 to 34 in part**  
because they relate to parts of the international application that do not comply with the prescribed requirements to such an extent that no meaningful international search can be carried out, specifically:

The claims are directed to a very large number of polypeptides and nucleotides such that it is economically unfeasible to perform a full and comprehensive search on all the claimed sequences.

3. ☐ Claims Nos.:  
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a)

## Box II Observations where unity of invention is lacking (Continuation of item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

1. ☐ As all required additional search fees were timely paid by the applicant, this international search report covers all searchable claims
2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.
3. ☐ As only some of the required additional search fees were timely paid by the applicant, this international search report covers only those claims for which fees were paid, specifically claims Nos.:
4. ☐ No required additional search fees were timely paid by the applicant. Consequently, this international search report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

### Remark on Protest

- ☐ The additional search fees were accompanied by the applicant's protest.
- ☐ No protest accompanied the payment of additional search fees.



## INTERNATIONAL SEARCH REPORT

Information on patent family members

International application No.  
PCT/AU 98/01023

This Annex lists the known "A" publication level patent family members relating to the patent documents cited in the above-mentioned international search report. The Australian Patent Office is in no way liable for these particulars which are merely given for the purpose of information.

Patent Document Cited in Search Report				Patent Family Member	
WO	95/26404	EP	753577		
WO	95/09181	EP	726276	JP	7097395
END OF ANNEX					

